

Annex VIII: Strategy for the selection of *Streptococcus agalactiae*-specific amplification primers from tuf sequences.

5	<i>S. agalactiae</i>	305	334	517	542	SEQ ID NO:
	<i>S. agalactiae</i>	CCAGAA	CGTGATAC	ACTT...GGAC	AACGTTGGTG	TTCTTCTTCG TG 207
	<i>S. agalactiae</i>	CCAGAA	CGTGATAC	ACTT...GGAC	AACGTTGGTG	TTCTTCTTCG TG 208
	<i>S. agalactiae</i>	CCAGAA	CGTGATAC	ACTT...GGAC	AACGTTGGTG	TTCTTCTTCG TG 209
	<i>S. agalactiae</i>	CCAGAA	CGTGATAC	ACTT...GGAC	AACGTTGGTG	TTCTTCTTCG TG 210
10	<i>S. anginosus</i>	CCAGAA	CGTGATAC	ACTT...GGAC	AACGTTGGTG	TTCTTCTTCG TG 211
	<i>S. anginosus</i>	CCAGAA	CGTGATAC	ACTT...GGAC	AACGTTGGTG	TTCTTCTTCG TG 212
	<i>S. bovis</i>	CCAGAA	CGTGATAC	ACTT...GGAC	AACGTTGGTG	TTCTTCTTCG TG 213
	<i>S. gordonii</i>	CCAGAA	CGTGATAC	ACTT...GGAC	AACGTTGGTG	TTCTTCTTCG TG 214
	<i>S. mutans</i>	CCAGAA	CGTGATAC	ACTT...GGAC	AACGTTGGTG	TTCTTCTTCG TG 215
15	<i>S. pneumoniae</i>	CCAGAA	CGTGATAC	ACTT...GGAC	AACGTTGGTG	TTCTTCTTCG TG 216
	<i>S. sanguinis</i>	CCAGAA	CGTGATAC	ACTT...GGAC	AACGTTGGTG	TTCTTCTTCG TG 217
	<i>S. sobrinus</i>	CCAGAA	CGTGATAC	ACTT...GGAC	AACGTTGGTG	TTCTTCTTCG TG 218
	<i>B. cepacia</i>	CCAGAA	CGTGATAC	ACTT...GGAC	AACGTTGGTG	TTCTTCTTCG TG 219
	<i>B. fragilis</i>	CCAGAA	CGTGATAC	ACTT...GGAC	AACGTTGGTG	TTCTTCTTCG TG 220
20	<i>B. subtilis</i>	CCAGAA	CGTGATAC	ACTT...GGAC	AACGTTGGTG	TTCTTCTTCG TG 221
	<i>C. diphtheriae</i>	CCAGAA	CGTGATAC	ACTT...GGAC	AACGTTGGTG	TTCTTCTTCG TG 222
	<i>C. trachomatis</i>	CCAGAA	CGTGATAC	ACTT...GGAC	AACGTTGGTG	TTCTTCTTCG TG 223
	<i>E. coli</i>	CCAGAA	CGTGATAC	ACTT...GGAC	AACGTTGGTG	TTCTTCTTCG TG 224
	<i>G. vaginalis</i>	CCAGAA	CGTGATAC	ACTT...GGAC	AACGTTGGTG	TTCTTCTTCG TG 225
25	<i>S. aureus</i>	CCAGAA	CGTGATAC	ACTT...GGAC	AACGTTGGTG	TTCTTCTTCG TG 226
	Selected sequences	GAA	CGTGATAC	ACAACCTTT A	G	AAGAAGAACCA CCAACGTTG

SEQ ID NO: 550b

SEQ ID NO: 549

Selected species-specific

primer sequences:

30 The sequence numbering refers to the *Streptococcus agalactiae* tuf gene fragment (SEQ ID NO: 209). Nucleotides in capitals are identical to the selected sequence or match that sequence. Mismatches are indicated by lower cases.

a "R" "y" "M" "K" "W" and "S" designate nucleotide positions which are degenerated. "R" stands for A or G; "y" stands for C or T; "M" stands for A or C; "K" stands for G or T; "W" stands for A or T; "S" stands for C or G.

b This sequence is the reverse-complement of the above tuf sequence.

Annex IX: Strategy for the selection of *Streptococcus agalactiae*-specific hybridization probes from *tuf* sequences.

5	<i>S. acidominimus</i>	401	GGTACTGT TaaagTCAAT GACGAAGTTG AAATCGTTGG	431 433	TATCAAGAGC GAAATCTCTA	AAGCAGTTGT TA	470	SEQ ID NO:
	<i>S. agalactiae</i>		GGTACTGT TCGTGTCAAC GACGAAGTTG AAATCGTTGG		TATTAAGAGG GAAATCTCTA	AAGCAGTTGT TA	206	
	<i>S. agalactiae</i>		GGTACTGT TCGTGTCAAC GACGAAGTTG AAATCGTTGG		TATTAAGAGG GAAATCTCTA	AAGCAGTTGT TA	209	
10	<i>S. agalactiae</i>		GGTACTGT TCGTGTCAAC GACGAAGTTG AAATCGTTGG		TATTAAGAGG GAAATCTCTA	AAGCAGTTGT TA	-	
	<i>S. agalactiae</i>		GGTACTGT TCGTGTCAAC GACGAAGTTG AAATCGTTGG		TATTAAGAGG GAAATCTCTA	AAGCAGTTGT TA	207	
	<i>S. anginosus</i>		GGTACTGT TaaagTCAAC GACGAAGTTG AAATCGTTGG		TATTAAGAGG GAAATCTCTA	AAGCAGTTGT TA	210	
	<i>S. anginosus</i>		GGTACTGT TaaagTCAAC GACGAAGTTG AAATCGTTGG		TATTAAGAGG GAAATCTCTA	AAGCAGTTGT TA	208	
	<i>S. bovis</i>		GGTACTGT TaaagTCAAC GACGAAGTTG AAATCGTTGG		TATTAAGAGG GAAATCTCTA	AAGCAGTTGT TA	211	
15	<i>S. anginosus</i>		GGTACTGT TaaagTCAAC GACGAAGTTG AAATCGTTGG		TATTAAGAGG GAAATCTCTA	AAGCAGTTGT TA	212	
	<i>S. cricetus</i>		GGTACTGT TaaagTCAAC GACGAAGTTG AAATCGTTGG		TATTAAGAGG GAAATCTCTA	AAGCAGTTGT TA	221	
	<i>S. cristatus</i>		GGTACTGT TaaagTCAAC GACGAAGTTG AAATCGTTGG		TATTAAGAGG GAAATCTCTA	AAGCAGTTGT TA	212	
	<i>S. downei</i>		GGTACTGT TaaagTCAAC GACGAAGTTG AAATCGTTGG		TATTAAGAGG GAAATCTCTA	AAGCAGTTGT TA	213	
	<i>S. dysgalactiae</i>		GGTACTGT TaaagTCAAC GACGAAGTTG AAATCGTTGG		TATTAAGAGG GAAATCTCTA	AAGCAGTTGT TA	214	
20	<i>S. equi equi</i>		GGTACTGT TaaagTCAAC GACGAAGTTG AAATCGTTGG		TATTAAGAGG GAAATCTCTA	AAGCAGTTGT TA	215	
	<i>S. ferus</i>		GGTACTGT TaaagTCAAC GACGAAGTTG AAATCGTTGG		TATTAAGAGG GAAATCTCTA	AAGCAGTTGT TA	216	
	<i>S. gordonii</i>		GGTACTGT TaaagTCAAC GACGAAGTTG AAATCGTTGG		TATTAAGAGG GAAATCTCTA	AAGCAGTTGT TA	217	
	<i>S. macacae</i>		GGTACTGT TaaagTCAAC GACGAAGTTG AAATCGTTGG		TATTAAGAGG GAAATCTCTA	AAGCAGTTGT TA	218	
	<i>S. gordonii</i>		GGTACTGT TaaagTCAAC GACGAAGTTG AAATCGTTGG		TATTAAGAGG GAAATCTCTA	AAGCAGTTGT TA	219	
25	<i>S. mutans</i>		GGTACTGT TaaagTCAAC GACGAAGTTG AAATCGTTGG		TATTAAGAGG GAAATCTCTA	AAGCAGTTGT TA	220	
	<i>S. oralis</i>		GGTACTGT TaaagTCAAC GACGAAGTTG AAATCGTTGG		TATTAAGAGG GAAATCTCTA	AAGCAGTTGT TA	222	
	<i>S. parvaquiniis</i>		GGTACTGT TaaagTCAAC GACGAAGTTG AAATCGTTGG		TATTAAGAGG GAAATCTCTA	AAGCAGTTGT TA	223	
	<i>S. pneumoniae</i>		GGTACTGT TaaagTCAAC GACGAAGTTG AAATCGTTGG		TATTAAGAGG GAAATCTCTA	AAGCAGTTGT TA	224	
	<i>S. pyogenes</i>		GGTACTGT TaaagTCAAC GACGAAGTTG AAATCGTTGG		TATTAAGAGG GAAATCTCTA	AAGCAGTTGT TA	-	
30	<i>S. ratti</i>		GGTACTGT TaaagTCAAC GACGAAGTTG AAATCGTTGG		TATTAAGAGG GAAATCTCTA	AAGCAGTTGT TA	225	
	<i>S. salivarius</i>		GGTACTGT TaaagTCAAC GACGAAGTTG AAATCGTTGG		TATTAAGAGG GAAATCTCTA	AAGCAGTTGT TA	-	
	<i>S. sanguinis</i>		GGTACTGT TaaagTCAAC GACGAAGTTG AAATCGTTGG		TATTAAGAGG GAAATCTCTA	AAGCAGTTGT TA	-	
	<i>S. sobrinus</i>		GGTACTGT TaaagTCAAC GACGAAGTTG AAATCGTTGG		TATTAAGAGG GAAATCTCTA	AAGCAGTTGT TA	226	
	<i>S. suis</i>		GGTACTGT TaaagTCAAC GACGAAGTTG AAATCGTTGG		TATTAAGAGG GAAATCTCTA	AAGCAGTTGT TA	-	
35	<i>S. uberis</i>		GGTACTGT TaaagTCAAC GACGAAGTTG AAATCGTTGG		TATTAAGAGG GAAATCTCTA	AAGCAGTTGT TA	227	
	<i>S. vestibularis</i>		GGTACTGT TaaagTCAAC GACGAAGTTG AAATCGTTGG		TATTAAGAGG GAAATCTCTA	AAGCAGTTGT TA	228	
	Selected sequences		GGTACTGT TaaagTCAAC GACGAAGTTG AAATCGTTGG		TATTAAGAGG GAAATCTCTA	AAGCAGTTGT TA	229	
	Selected sequences		ACTGT TCGTGTCAAC GACGAAGTTG AAATCGTTGG		TATTAAGAGG GAAATCTCTA	AAGCAGTTGT TA	230	
							231	
40	Selected species-specific hybridization probes		TTTCA ACTTCGTCGT TGACACGAAC AGT		CGTTGG TATTAAGAGG GAAATCTCTA	AAGCAGTTGT		
			SEQ ID NO: 582 ^a					
45	The sequence numbering refers to the <i>Streptococcus agalactiae</i> <i>tuf</i> gene fragment (SEQ ID NO: 209). Nucleotides in capitals are identical to the selected sequence or match that sequence. Mismatches are indicated by lower cases.		TTTCA ACTTCGTCGT TGACACGAAC AGT		CAACTG CTTTTGGAT ATCTTCTTTA ATACCAAC			
	^a This sequence is the reverse-complement of the above <i>tuf</i> sequence.							

Annex X: Strategy for the selection of *Streptococcus agalactiae*-specific amplification primers from *atpD* sequences.

SEQ ID
NO:

5	<i>S. agalactiae</i>	39	TT GATTGCTTAT AAAATGGCG ATAGTCACA AAAAGTAGTA...TARGGATA	80	203	234	368	399	ATTAGCACCT TACTTAAAG GTGCTAAAG	380
	<i>S. agalactiae</i>	TT	GATTGCTTAT AAAATGGCG ATAGTCACA AAAAGTAGTA...TARGGATA			TTTC...CTT			ATTAGCACCT TACTTAAAG GTGCTAAAG	379
	<i>S. agalactiae</i>	TT	GATTGCTTAT AAAATGGCG ATAGTCACA AAAAGTAGTA...TARGGATA			TTTC...CTT			ATTAGCACCT TACTTAAAG GTGCTAAAG	381
	<i>S. agalactiae</i>	TT	GATTGCTTAT AAAATGGCG ATAGTCACA AAAAGTAGTA...TARGGATA			TTTC...CTT			ATTAGCACCT TACTTAAAG GTGCTAAAG	382
	<i>S. agalactiae</i>	TT	GATTGCTTAT AAAATGGCG ATAGTCACA AAAAGTAGTA...TARGGATA			TTTC...CTT			ATTAGCACCT TACTTAAAG GTGCTAAAG	383
10	<i>S. agalactiae</i>	TT	GATTGCTTAT AAAATGGCG ATAGTCACA AAAAGTAGTA...TARGGATA			TTTC...CTT			ATTAGCACCT TACTTAAAG GTGCTAAAG	-
	<i>S. bovis</i>	TT	GATTGCTTAT AAAATGGCG ATAGTCACA AAAAGTAGTA...TARGGATA			TTTC...CTT			ATTAGCACCT TACTTAAAG GTGCTAAAG	387
	<i>S. salivarius</i>	TT	GATTGCTTAT AAAATGGCG ATAGTCACA AAAAGTAGTA...TARGGATA			TTTC...CTT			ATTAGCACCT TACTTAAAG GTGCTAAAG	-
	<i>S. pneumoniae</i>	CT	GTGCTGTTAT AAGATGAGC AAAATGCTAA AAGATGCTG...TAAAGATA			TTTC...CTT			ATTAGCACCT TACTTAAAG GTGCTAAAG	-
	<i>S. pneumoniae</i>	TT	GATTGCTTAT AAAATGGCG ATAGTCACA AAAAGTAGTA...TARGGATA			TTTC...CTT			ATTAGCACCT TACTTAAAG GTGCTAAAG	-
15	<i>S. pyogenes</i>	CT	GTGCTGTTAT AAGATGAGC AAAATGCTAA AAGATGCTG...TAAAGATA			TTTC...CTT			ATTAGCACCT TACTTAAAG GTGCTAAAG	-
	<i>S. anginosus</i>	TT	GATTGCTTAT AAAATGGCG ATAGTCACA AAAAGTAGTA...TARGGATA			TTTC...CTT			ATTAGCACCT TACTTAAAG GTGCTAAAG	-
	<i>S. sanguinis</i>	CT	GTGCTGTTAT AAGATGAGC AAAATGCTAA AAGATGCTG...TAAAGATA			TTTC...CTT			ATTAGCACCT TACTTAAAG GTGCTAAAG	-
	<i>S. mutans</i>	TT	GATTGCTTAT AAAATGGCG ATAGTCACA AAAAGTAGTA...TARGGATA			TTTC...CTT			ATTAGCACCT TACTTAAAG GTGCTAAAG	-
	<i>B. anthracis</i>	GT	AAACAGAGC AAGGAAAGC G...AAGCAT GAACTTAACA...TGAAGCAA			TTTC...CTT			ATTAGCACCT TACTTAAAG GTGCTAAAG	247
	<i>B. cereus</i>	TT	GATTGCTTAT AAAATGGCG ATAGTCACA AAAAGTAGTA...TARGGATA			TTTC...CTT			ATTAGCACCT TACTTAAAG GTGCTAAAG	248
20	<i>E. faecium</i>	TT	GATTGCTTAT AAAATGGCG ATAGTCACA AAAAGTAGTA...TARGGATA			TTTC...CTT			ATTAGCACCT TACTTAAAG GTGCTAAAG	292
	<i>E. gallinarum</i>	TT	GATTGCTTAT AAAATGGCG ATAGTCACA AAAAGTAGTA...TARGGATA			TTTC...CTT			ATTAGCACCT TACTTAAAG GTGCTAAAG	293
	<i>E. faecalis</i>	TT	GATTGCTTAT AAAATGGCG ATAGTCACA AAAAGTAGTA...TARGGATA			TTTC...CTT			ATTAGCACCT TACTTAAAG GTGCTAAAG	291
	<i>E. coli</i>	TT	GATTGCTTAT AAAATGGCG ATAGTCACA AAAAGTAGTA...TARGGATA			TTTC...CTT			ATTAGCACCT TACTTAAAG GTGCTAAAG	-
	<i>L. monocytogenes</i>	Ta	CGATGCTCTT GAGGTGCAAA ATGTAAGTA GCTGCTGCTG...TAAAGATA			TTTC...CTT			ATTAGCACCT TACTTAAAG GTGCTAAAG	324
25	<i>S. aureus</i>	GT	TATGATGCTG CCAAGAGAG AAGGTACACAT AAGCTTAACA...TGAAGCAA			TTTC...CTT			ATTAGCACCT TACTTAAAG GTGCTAAAG	366
	<i>S. epidermidis</i>	ca	CATCGAAGT CCAAGAGAG ATGGAAGCTT CCAAGTAAACA...TGAAGCAA			TTTC...CTT			ATTAGCACCT TACTTAAAG GTGCTAAAG	370
	Selected sequences		ATTGCTTAT AAAATGGCG ATAGTCACA AAAAGTAGTA...TARGGATA			TTTC...CTT			ATTAGCACCT TACTTAAAG GTGCTAAAG	

SEQ ID NO: 625^a
CGTTG AAGACACGAC CCAAGTATC C

SEQ ID NO: 626^a
TACCACCTTT TAAGTAAGGT GCTAAT

SEQ ID NO: 627
ATTGCTTAT AAAATGGCG ATAGTC

Selected species-specific primers

SEQ ID NO: 628
AAAATGGCG ATAGTCACA AAAAGTAGTA

Selected species-specific primers

35 The sequence numbering refers to the *Streptococcus agalactiae* *tuf* gene fragment (SEQ ID NO: 380). Nucleotides in capitals are identical to the selected sequence or match that sequence. Mismatches are indicated by lower cases. Dots indicate gaps.

^a This sequence is the reverse-complement of the above *tuf* sequence.

[illegible]

The sequence numbering refers to the *Candida albicans* *tuf* gene fragment (SEQ ID NO: 408). Nucleotides in capitals are identical to the selected sequence SEQ ID NO: 577 or match that sequence. Mismatches are indicated by lower cases. Mismatches for SEQ ID NO: 578 are indicated by underlined nucleotides.

a "R" "Y" "M" "K" "W" and "S" designate nucleotide positions which are degenerated. "R" stands for A or G; "Y" stands for C or T; "M" stands for A or C; "K" stands for G or T; "W" stands for A or T; "S" stands for C or G. "I" stands for inosine which is a nucleotide analog that can bind to any of the four nucleotides A, C, G or T.

b *C. albicans* primers have been described in previous patent (application WO 98/20157, SEQ ID NO. 11-12)

c This sequence is the reverse-complement of the above *tuf* sequence.

Ann x XII: Strategy for the selection of *Staphylococcus*-specific amplification primers from *tuf* sequences.

		310	340	652	682	SEQ ID NO:
5	<i>S. aureus</i>	A CAGGCCGCTGT	TGAACGTGGT	CAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTTAT GC 179
	<i>S. aureus</i>	A CAGGCCGCTGT	TGAACGTGGT	CAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTTAT GC 176
	<i>S. aureus</i>	A CAGGCCGCTGT	TGAACGTGGT	CAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTTAT GC 177
	<i>S. aureus aureus</i>	A CAGGCCGCTGT	TGAACGTGGT	CAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTTAT GC 180
	<i>S. auricularis</i>	A CAGGCCGCTGT	TGAACGTGGT	CAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTTAT GC 181
10	<i>S. capitis</i>	A CAGGCCGCTGT	TGAACGTGGT	CAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTTAT GC 182
	<i>S. caseolyticus</i>	A CAGGCCGCTGT	TGAACGTGGT	CAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTTAT GC 183
	<i>S. cohnii</i>	A CAGGCCGCTGT	TGAACGTGGT	CAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTTAT GC 184
	<i>S. epidermidis</i>	A CAGGCCGCTGT	TGAACGTGGT	CAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTTAT GC 185
	<i>S. epidermidis</i>	A CAGGCCGCTGT	TGAACGTGGT	CAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTTAT GC 186
15	<i>S. haemolyticus</i>	A CAGGCCGCTGT	TGAACGTGGT	CAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTTAT GC 188
	<i>S. haemolyticus</i>	A CAGGCCGCTGT	TGAACGTGGT	CAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTTAT GC 189
	<i>S. haemolyticus</i>	A CAGGCCGCTGT	TGAACGTGGT	CAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTTAT GC 191
	<i>S. hominis hominis</i>	A CAGGCCGCTGT	TGAACGTGGT	CAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTTAT GC 193
20	<i>S. hominis</i>	A CAGGCCGCTGT	TGAACGTGGT	CAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTTAT GC 194
	<i>S. hominis</i>	A CAGGCCGCTGT	TGAACGTGGT	CAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTTAT GC 195
	<i>S. hominis</i>	A CAGGCCGCTGT	TGAACGTGGT	CAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTTAT GC 196
	<i>S. hominis</i>	A CAGGCCGCTGT	TGAACGTGGT	CAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTTAT GC 197
	<i>S. lugdunensis</i>	A CAGGCCGCTGT	TGAACGTGGT	CAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTTAT GC 198
25	<i>S. saprophyticus</i>	A CAGGCCGCTGT	TGAACGTGGT	CAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTTAT GC 199
	<i>S. saprophyticus</i>	A CAGGCCGCTGT	TGAACGTGGT	CAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTTAT GC 200
	<i>S. saprophyticus</i>	A CAGGCCGCTGT	TGAACGTGGT	CAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTTAT GC 201
	<i>S. sciuri sciuri</i>	A CAGGCCGCTGT	TGAACGTGGT	CAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTTAT GC 187
30	<i>S. warneri</i>	A CAGGCCGCTGT	TGAACGTGGT	CAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTTAT GC 192
	<i>S. warneri</i>	A CAGGCCGCTGT	TGAACGTGGT	CAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTTAT GC 202
	<i>S. warneri</i>	A CAGGCCGCTGT	TGAACGTGGT	CAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTTAT GC 78
	<i>B. subtilis</i>	A CTGGCCGCTGT	AGAACCGGGA	CAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTTAT GC -
	<i>E. coli</i>	A CCGGTCGCTGT	AGAACCGGGA	CAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTTAT GC -
35	<i>L. monocytogenes</i>	A CTGGACGCTGT	TGAACGTGGT	CAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTTAT GC -
	Selected sequences	GGCCGCTGT	TGAACGTGGT	CAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTTAT GC -
	Selected genus-specific primer sequences ^a :	GGCCGCTGT	TGAACGTGGT	CAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTTAT GC -
		SEQ ID NO: 553	SEQ ID NO: 575 ^a	SEQ ID NO: 707 ^a	SEQ ID NO: 707 ^a	SEQ ID NO: 707 ^a
		GGCCGCTGT	TGAACGTGGT	CAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTTAT GC -
		GGCCGCTGT	TGAACGTGGT	CAATCAAG...CACTTACCA	GAAGGTACTG	AAATGGTTAT GC -

The sequence numbering refers to the *Staphylococcus aureus tuf* gene fragment (SEQ ID NO: 179). Nucleotides in capitals are identical to the selected sequence or match that sequence. Mismatches are indicated by lower cases. "N" indicate incomplete sequence data.

^a This sequence is the reverse-complement of the above *tuf* sequence. "R" stands for A or G; "Y" stands for C or G. "Y" stands for A or G; "Y" stands for C or G. "I" stands for inosine which T; "M" stands for A or C; "K" stands for G or T; "W" stands for A or T; "S" stands for C or G. "I" stands for inosine which is a nucleotide analog that can bind to any of the four nucleotides A, C, G or T.

Annex XIII: Strategy for the selection of the *Staphylococcus* genus-specific hybridization probe from *tuf* sequences.

5		400	425	SEQ ID NO:
	<i>S. aureus</i>	G TTGAAATGTT CCGTAAATTA TTAGA	179	
	<i>S. aureus</i>	G TTGAAATGTT CCGTAAATTA TTAGA	176	
	<i>S. aureus</i>	G TTGAAATGTT CCGTAAATTA TTAGA	177	
10	<i>S. aureus</i>	G TTGAAATGTT CCGTAAATTA TTAGA	178	
	<i>S. aureus aureus</i>	G TTGAAATGTT CCGTAAATTA TTAGA	180	
	<i>S. auricularis</i>	G TAGAAATGTT CCGTAAATTA TTAGA	181	
	<i>S. capitis capitis</i>	G TAGAAATGTT CCGTAAATTA TTAGA	182	
	<i>S. caseolyticus</i>	G TAGAAATGTT CCGTAAATTA TTAGA	183	
15	<i>S. cohnii</i>	G TAGAAATGTT CCGTAAATTA TTAGA	184	
	<i>S. epidermidis</i>	G TAGAAATGTT CCGTAAATTA TTAGA	185	
	<i>S. haemolyticus</i>	G TAGAAATGTT CCGTAAATTA TTAGA	186	
	<i>S. haemolyticus</i>	G TAGAAATGTT CCGTAAATTA TTAGA	189	
	<i>S. haemolyticus</i>	G TAGAAATGTT CCGTAAATTA TTAGA	190	
20	<i>S. haemolyticus</i>	G TAGAAATGTT CCGTAAATTA TTAGA	188	
	<i>S. hominis</i>	G TAGAAATGTT CCGTAAATTA TTAGA	196	
	<i>S. hominis</i>	G TAGAAATGTT CCGTAAATTA TTAGA	194	
	<i>S. hominis hominis</i>	G TAGAAATGTT CCGTAAATTA TTAGA	191	
	<i>S. hominis</i>	G TAGAAATGTT CCGTAAATTA TTAGA	193	
25	<i>S. hominis</i>	G TAGAAATGTT CCGTAAATTA TTAGA	195	
	<i>S. lugdunensis</i>	G TAGAAATGTT CCGTAAATTA TTAGA	197	
	<i>S. saprophyticus</i>	G TAGAAATGTT CCGTAAATTA TTAGA	198	
	<i>S. saprophyticus</i>	G TAGAAATGTT CCGTAAATTA TTAGA	200	
	<i>S. saprophyticus</i>	G TAGAAATGTT CCGTAAATTA TTAGA	199	
30	<i>S. sciuri sciuri</i>	G TTGAAATGTT CCGTAAATTA TTAGA	201	
	<i>S. warneri</i>	G TAGAAATGTT CCGTAAgTTA TTAGA	187	
	<i>S. warneri</i>	G TAGAAATGTT CCGTAAgTTA TTAGA	192	
	<i>S. warneri</i>	G TAGAAATGTT CCGTAAgTTA TTAGA	202	
	<i>S. warneri</i>	G TAGAAATGTT CCGTAAgTTA TTAGA	203	
35	<i>B. subtilis</i>	G TTGAAATGTT CCGTAAgcTt cTTGA	-	
	<i>E. coli</i>	G TTGAAATGTT CCGcAAAcTg cTGGA	78	
	<i>L. monocytogenes</i>	G TAGAAATGTT CCGTAAATTA cTAGA	-	
	Selected sequence	GAAATGTT CCGTAAATTA TT		
40	Selected genus-specific hybridization probe:	SEQ ID NO: 605 GAAATGTT CCGTAAATTA TT		

45 The sequence numbering refers to the *Staphylococcus aureus tuf* gene fragment (SEQ ID NO: 179). Nucleotides in capitals are identical to the selected sequence or match that sequence. Mismatches are indicated by lower cases.

		339	383 SEQ	ID NO:
		AG TtGGTGAAGA AgTtGAAATC ATcGGTtTaC ATGACACaTC TAA	179	
	<i>S. aureus</i>	AG TtGGTGAAGA AgTtGAAATC ATcGGTtTaC ATGACACaTC TAA	176	
	<i>S. aureus</i>	AG TtGGTGAAGA AgTtGAAATC ATcGGTtTaC ATGACACaTC TAA	177	
10	<i>S. aureus</i>	AG TtGGTGAAGA AgTtGAAATC ATcGGTtTaC ATGACACaTC TAA	178	
	<i>S. aureus</i>	AG TtGGTGAAGA AgTtGAAATC ATcGGTtTaC ATGACACaTC TAA	180	
	<i>S. aureus aureus</i>	AG TtGGTGAAGA AgTtGAAATC ATcGGTATga AaGACggTTC AAA	181	
	<i>S. auricularis</i>	AG TCGGTGAAGA AgTtGAAATC ATcGGTATCC AcGAaACTTC TAA	182	
	<i>S. capitis capitis</i>	AG TtGGTGAAGA AgTtGAAATC ATTGGTtTaa cTGAagaacC AAA	183	
15	<i>S. caseolyticus</i>	AG TtGGTGAAGA AgTtGAAATC ATcGGTATgC AaGAagaTTC CAA	184	
	<i>S. cohnii</i>	AG TCGGTGAAGA AgTtGAAATC ATcGGTATgC AcGAaACTTC TAA	185	
	<i>S. epidermidis</i>	AG TtGGTGAAGA AgTtGAAATC ATcGGTATgC AcGAaACTTC TAA	186	
	<i>S. haemolyticus</i>	AG TtGGTGAAGA AgTtGAAATC ATTGGTATCC ATGACACTTC TAA	189	
	<i>S. haemolyticus</i>	AG TtGGTGAAGA AgTtGAAATC ATTGGTATCC ATGACACTTC TAA	190	
20	<i>S. haemolyticus</i>	AG TtGGTGAAGA AgTtGAAATC ATTGGTATCC ATGACACTTC TAA	191	
	<i>S. haemolyticus</i>	AG TtGGTGAAGA AgTtGAAATt ATTGGTATCa AaGAaACTTC TAA	194	
	<i>S. hominis</i>	AG TtGGTGAAGA AgTtGAAATt ATTGGTATCa AaGAaACTTC TAA	199	
	<i>S. hominis hominis</i>	AG TtGGTGAAGA AgTtGAAATt ATTGGTATCa AaGAaACTTC TAA	193	
	<i>S. hominis</i>	AG TtGGTGAAGA AgTtGAAATt ATTGGTATCa AaGAaACTTC TAA	195	
25	<i>S. hominis</i>	AG TtGGTGAAGA AgTtGAAATt ATTGGTATCa AaGAaACTTC TAA	196	
	<i>S. hominis</i>	AG TtGGTGAAGA AgTtGAAATt ATTGGTATCa AaGAaACTTC TAA	197	
	<i>S. lugdunensis</i>	AG TCGGTGAAGA AgTtGAAATt ATTGGTATCC AcGAtACTAc TAA	197	
	<i>S. saprophyticus</i>	AG TCGGTGAAGA AATCGAAATC ATcGGTATgC AaGAagaATC CAA	198	
	<i>S. saprophyticus</i>	AG TCGGTGAAGA AATCGAAATC ATcGGTATgC AaGAagaATC CAA	200	
30	<i>S. saprophyticus</i>	AG TCGGTGAAGA AATCGAAATC ATcGGTATgC AaGAagaATC CAA	199	
	<i>S. sciuri sciuri</i>	TG TtGGTGAAGA AgTtGAAATC ATcGGTtTaa cTGAagaATC TAA	201	
	<i>S. warneri</i>	AG TtGGTGAAGA AgTtGAAATC ATcGGTtTaC ATGACACTTC TAA	187	
	<i>S. warneri</i>	AG TtGGTGAAGA AgTtGAAATC ATcGGTtTaC ATGACACTTC TAA	192	
	<i>S. warneri</i>	AG TtGGTGAAGA AgTtGAAATC ATcGGTtTaC ATGACACTTC TAA	202	
35	<i>S. warneri</i>	AG TtGGTGAAGA AgTtGAAATC ATcGGTtTaC ATGACACTTC TAA	203	
	<i>B. subtilis</i>	AG TCGGTGAAGA AgTtGAAATC ATcGGTtTtC AaGAagagag AAA	-	
	<i>E. coli</i>	AG TtGGTGAAGA AgTtGAAATC gTTGGTATCa AaGAgACTCa GAA	78	
	<i>L. monocytogenes</i>	AG TtGGTGAAGA AgTaGAAgTt ATcGGTATCg AaGAagaag AAA	-	
	Selected sequences	CGGTGAAGA AATCGAAATC A		

45 Selected species-specific hybridization probes: SEQ ID NO: 594
ATTGGTATCC ATGACACTTC
SEQ ID NO: 599
CGGTGAAGA AATCGAAATC A

50 The sequence numbering refers to the *Staphylococcus aureus* *tuf* gene fragment (SEQ ID NO: 179). Nucleotides in capitals are identical to the selected sequence or match that sequence. Mismatches are indicated by lower cases.

Annex XV: Strategy for the selection of *Staphylococcus aureus*-specific and of *Staphylococcus epidermidis*-specific hybridization probes from *tuf* sequences.

		521	547	592	617	SEQ ID NO:
10	<i>S. aureus</i>	TACACCACA TACTGAATTC	AAAGCAG...	TTCTTCTCa	AACTATCGtC	CACAATT 179
	<i>S. aureus</i>	TACACCACA TACTGAATTC	AAAGCAG...	TTCTTCTC~	~~~~~	178
	<i>S. aureus</i>	TACACCACA TACTGAATTC	AAAGCAG...	TTCTTCTCa	AACTATCGtC	CACAATT 176
	<i>S. aureus aureus</i>	TACACCACA TACTGAATTC	AAAGCAG...	TTCTTCTCa	AACTATCGtC	CACAATT 177
	<i>S. auricularis</i>	TACACCACA cACTaAATTC	ActGCAG...	TTCTTCTCa	AACTATCGtC	CACAATT 180
15	<i>S. capitis capitis</i>	CACACCACA cACTaAATTC	AAAGCGG...	TTCTTCTCT	AACTAcCGtC	CACAATT 181
	<i>S. caseolyticus</i>	TACTCCACA TACTaAATTC	AAAGCTG...	TTCTTCACT	AACTAcCGCC	CtCAGTT 182
	<i>S. cohnii</i>	TACACCACA cACaaAcTTt	AAAGCGG...	TTCTTCAgT	AACTATCGCC	CACAATT 183
	<i>S. epidermidis</i>	TACACCACA cACaaAATTC	AAAGCTG...	TTCTTCACT	AACTATCGCC	CACAATT 184
	<i>S. haemolyticus</i>	CACACCTCA cACaaAATTC	AAAGCGG...	TTCTTCACT	AACTATCGCC	CACAATT 185
20	<i>S. haemolyticus</i>	CACACCTCA cACaaAATTC	AAAGCAG...	TTCTTCaCa	AACTATCGtC	CACAATT 186
	<i>S. haemolyticus</i>	CACACCTCA cACaaAATTC	AAAGCAG...	TTCTTCaCa	AACTATCGtC	CACAATT 189
	<i>S. haemolyticus</i>	CACACCTCA cACaaAATTC	AAAGCAG...	TTCTTCaCa	AACTATCGtC	CACAATT 190
	<i>S. hominis</i>	CACACCTCA cACaaAATTC	AAAGCAG...	TTCTTCACT	AACTATCGtC	CACAATT 188
	<i>S. hominis</i>	TACACCTCA cACaaAATTC	AAAGCAG...	TTCTTCACT	AACTATCGtC	CACAATT 195
25	<i>S. hominis hominis</i>	TACACCTCA cACaaAATTC	AAAGCAG...	TTCTTCACT	AACTATCGtC	CACAATT 196
	<i>S. hominis</i>	TACACCTCA cACaaAATTC	AAAGCAG...	TTCTTCTCT	AACTATCGtC	CACAATT 191
	<i>S. hominis</i>	TACACCTCA cACaaAATTC	AAAGCAG...	TTCTTCTCT	AACTATCGtC	CACAATT 193
	<i>S. lugdunensis</i>	TACACCTCA cACTaAATTC	AAAGCTG...	TTCTTCTCa	AACTAcCGCC	CACAATT 194
	<i>S. saprophyticus</i>	TACACCACA TACaaAATTC	AAAGCGG...	TTCTTCACT	AACTAcCGCC	CACAATT 197
30	<i>S. saprophyticus</i>	TACACCACA TACaaAATTC	AAAGCGG...	TTCTTCACT	AACTAcCGCC	CACAATT 198
	<i>S. saprophyticus</i>	TACACCACA TACaaAATTC	AAAGCGG...	TTCTTCACT	AACTAcCGCC	CACAATT 199
	<i>S. sciuri sciuri</i>	CACACCTCA cACTaAATTC	AAAGCTG...	TTCTTCaCa	AACTAcCGCC	CACAATT 200
	<i>S. warneri</i>	TACACCACA TACaaAATTC	AAAGCGG...	~~~~~	~~~~~	192
35	<i>S. warneri</i>	TACACCACA TACaaAATTC	AAAGCGG...	TTCTTCAgT	AACTAcCGCC	CACAATT 187
	<i>S. warneri</i>	TACACCACA TACaaAATTC	AAAGCGG...	TTCTTCAgT	AACTAcCGCC	CACAATT 202
	<i>B. subtilis</i>	CACtCCACA cAgcaAATTC	AAAGCTG...	TTCTTCTCT	AACTAcCGtC	CtCAGTT -
	<i>E. coli</i>	CAAgCCgCA cACaaAgTTC	gAAtCTG...	TTCTTCAaa	ggCTAcCGtC	CgCAGTT -
40	<i>L. monocytogenes</i>	TACTCCACA cACTaAcTTC	AAAGCTG...	TTCTTCAac	AACTAcCGCC	CACAATT 78
	Selected sequences	ACCACA TACTGAATTC AAAG		TTCaCT	AACTATCGCC	CACA -
45	Selected species-specific hybridization probes:	SEQ ID NO: 585 ACCACA TACTGAATTC AAAG		SEQ ID NO: 593 TTCaCT AACTATCGCC CACA		

The sequence numbering refers to the *Staphylococcus aureus tuf* gene fragment (SEQ ID NO: 179). Nucleotides in capitals are identical to the selected sequence or match that sequence. Mismatches are indicated by lower cases. "~" indicate incomplete sequence data.

Ann x XVI: Strategy for the selection of the
Staphylococcus hominis-specific hybridization
 probe from *tuf* sequences.

		358	383	SEQ ID NO:
5		ATC ATcGGTtTac AtGAcACaTC TAA		179
	<i>S. aureus</i>	ATC ATcGGTtTac AtGAcACaTC TAA		176
	<i>S. aureus</i>	ATC ATcGGTtTac AtGAcACaTC TAA		177
	<i>S. aureus</i>	ATC ATcGGTtTac AtGAcACaTC TAA		178
10	<i>S. aureus</i>	ATC ATcGGTtTac AtGAcACaTC TAA		180
	<i>S. aureus aureus</i>	ATC ATcGGTATgA AAGAcggTTC AAA		181
	<i>S. auricularis</i>	ATC ATcGGTATCc AcGAAACTTC TAA		182
	<i>S. capitis capitis</i>	ATC ATTGGTtTaA ctGAAGAaAC AAA		183
	<i>S. caseolyticus</i>	ATC ATcGGTATgc AAGAAGaTTC CAA		184
15	<i>S. cohnii</i>	ATC ATcGGTATgc AcGAAACTTC TAA		185
	<i>S. epidermidis</i>	ATC ATTGGTATCc AtGAcACTTC TAA		186
	<i>S. haemolyticus</i>	ATC ATTGGTATCc AtGAcACTTC TAA		189
	<i>S. haemolyticus</i>	ATC ATTGGTATCc AtGAcACTTC TAA		190
	<i>S. haemolyticus</i>	ATT ATTGGTATCA AAGAACTTC TAA		188
20	<i>S. haemolyticus</i>	ATT ATTGGTATCA AAGAtACTTC TAA		196
	<i>S. hominis</i>	ATT ATTGGTATCA AAGAACTTC TAA		194
	<i>S. hominis</i>	ATT ATTGGTATCA AAGAACTTC TAA		191
	<i>S. hominis hominis</i>	ATT ATTGGTATCA AAGAACTTC TAA		193
	<i>S. hominis</i>	ATT ATTGGTATCA AAGAACTTC TAA		195
25	<i>S. hominis</i>	ATT ATTGGTATCc AcGAtACTaC TAA		197
	<i>S. lugdunensis</i>	ATC ATcGGTATgc AAGAAGaaTC CAA		198
	<i>S. saprophyticus</i>	ATC ATcGGTATgc AAGAAGaaTC CAA		200
	<i>S. saprophyticus</i>	ATC ATcGGTATgc AAGAAGaaTC CAA		199
	<i>S. saprophyticus</i>	ATC ATcGGTtTaA ctGAAGAaTC TAA		201
30	<i>S. sciuri sciuri</i>	ATC ATcGGTtTac AtGAcACTTC TAA		187
	<i>S. warneri</i>	ATC ATcGGTtTac AtGAcACTTC TAA		192
	<i>S. warneri</i>	ATC ATcGGTtTac AtGAcACTTC TAA		202
	<i>S. warneri</i>	ATC ATcGGTtTac AtGAcACTTC TAA		203
	<i>S. warneri</i>	ATC ATcGGTcTtc AAGAAGagag AAA		-
35	<i>B. subtilis</i>	ATC gTTGGTATCA AAGAgACTca GAA		78
	<i>E. coli</i>	GTT ATcGGTATCg AAGAAGaaag AAA		-
	<i>L. monocytogenes</i>	ATTGGTATCA AAGAACTTC		
	Selected sequence			
40	Selected species-specific hybridization probe:	SEQ ID NO: 597 ATTGGTATCA AAGAACTTC		

45 The sequence numbering refers to the *Staphylococcus aureus tuf* gene fragment (SEQ ID NO: 179). Nucleotides in capitals are identical to the selected sequence or match that sequence. Mismatches are indicated by lower cases.

Annex XVII: Strategy for the selection from *tuf* sequences of the amplification primers specific for the genus *Enterococcus*.

5	<i>E. avium</i>	270	TAGAATTAA TGGCTGCTGT TCACGAATA...ACGTGA AGATATCCAA CGTGGACAAG TA	580	SEQ ID NO:
	<i>E. casseliflavus</i>	298	TGGAATTAA TGGCTGCAGT TCACGAATA...TCGTGA AGATATCCAA CGTGGACAAG TA	58	
	<i>E. cecorum</i>	553	TAGAATTAA TGGCTGCAGT TCACGAATA...TCGTGA AGATATCCAA CGTGGACAAG TA	59	
10	<i>E. dispar</i>		TAGAATTAA TGGCTGCAGT TCACGAATA...TCGTGA AGATATCCAA CGTGGACAAG TA	60	
	<i>E. durans</i>		TTGAATTAA TGGCTGCAGT TCACGAATA...ACGTGA AGATATCCAA CGTGGACAAG TT	61	
	<i>E. faecalis</i>		TAGAATTAA TGGCTGCAGT TCACGAATA...ACGTGA AGATATCCAA CGTGGACAAG TA	607	
	<i>E. faecium</i>		TTGAATTAA TGGCTGCAGT TCACGAATA...ACGTGA AGATATCCAA CGTGGACAAG TT	608	
	<i>E. flavescens</i>		TGGAATTAA TGGCTGCAGT TCACGAATA...TCGTGA AGATATCCAA CGTGGACAAG TA	65	
	<i>E. gallinarum</i>		TGGAATTAA TGGCTGCAGT TCACGAATA...TCGTGA AGATATCCAA CGTGGACAAG TA	609	
15	<i>E. hirae</i>		TTGAATTGA TGGCTGCAGT TCACGAATA...ACGTGA AGATATCCAA CGTGGACAAG TT	67	
	<i>E. mundtii</i>		TGGAATTGA TGGCTGCAGT TCACGAATA...ACGTGA AGATATCCAA CGTGGACAAG TT	68	
	<i>E. pseudoavium</i>		TTGAATTGA TGGCTGCAGT TCACGAATA...ACGTGA AGATATCCAA CGTGGACAAG TT	69	
	<i>E. raffinosus</i>		TAGAATTAA TGGCTGCAGT TCACGAATA...ACGTGA AGATATCCAA CGTGGACAAG TA	70	
	<i>E. saccharolyticus</i>		TGGAATTAA TGGCTGCAGT TCACGAATA...TCGTGA AGATATCCAA CGTGGACAAG TA	71	
	<i>E. solitarius</i>		TGGAATTAA TGGCTGCAGT TCACGAATA...TCGTGA AGATATCCAA CGTGGACAAG TA	72	
20	<i>C. diphtheriae</i>		TCGAATTGA TGGCTGCAGT TCACGAATA...TCGTGA AGATATCCAA CGTGGACAAG TT	662 ^a	
	<i>G. vaginalis</i>		AGGAATTGA TGGCTGCAGT TCACGAATA...TCGTGA AGATATCCAA CGTGGACAAG TT	16	
	<i>B. cepacia</i>		TGGAATTGA TGGCTGCAGT TCACGAATA...TCGTGA AGATATCCAA CGTGGACAAG TA	179	
	<i>S. aureus</i>		TGGAATTGA TGGCTGCAGT TCACGAATA...TCGTGA AGATATCCAA CGTGGACAAG TA	179	
25	<i>B. subtilis</i>		TGGAATTGA TGGCTGCAGT TCACGAATA...TCGTGA AGATATCCAA CGTGGACAAG TA	179	
	<i>S. pneumoniae</i>		TGGAATTGA TGGCTGCAGT TCACGAATA...TCGTGA AGATATCCAA CGTGGACAAG TA	179	
	<i>E. coli</i>		TGGAATTGA TGGCTGCAGT TCACGAATA...TCGTGA AGATATCCAA CGTGGACAAG TA	179	
	<i>B. fragilis</i>		TGGAATTGA TGGCTGCAGT TCACGAATA...TCGTGA AGATATCCAA CGTGGACAAG TA	179	
	<i>C. trachomatis</i>		TGGAATTGA TGGCTGCAGT TCACGAATA...TCGTGA AGATATCCAA CGTGGACAAG TA	179	
30	Selected sequences ^a		AATTAA TGGCTGCAGT TGAYGA	22	
	Selected sequences ^a		TGA AGAYATCCAA CGTGGACAAG		
			TGA AGAYATCCAA CGTGGACAAG		
	Selected genus-specific primer sequences:		AATTAA TGGCTGCAGT TGAYGA		
35			SEQ ID NO: 656		
			SEQ ID NO: 657b		
			TTG TCCACGTTGG ATRCTTCA		
			SEQ ID NO: 271b		
			TTG TCCACGTTGG ATRCTTCA		

The sequence numbering refers to the *Enterococcus durans tuf* gene fragment (SEQ ID NO: 61). Nucleotides in capitals are identical to the selected sequence SEQ ID NO: 656 or 657 or match that sequence. Mismatches are indicated by lower cases. Mismatches for SEQ ID NO: 271 are indicated by underlined nucleotides.

^a "R" "Y" "M" "K" "W" and "S" designate nucleotide positions which are degenerated. "R" stands for A or G; "Y" stands for C or T; "M" stands for A or C; "K" stands for G or T; "W" stands for A or T; "S" stands for C or G. "I" stands for inosine which is a nucleotide analog that can bind to any of the four nucleotides A, C, G or T. This sequence is the reverse-complement of the above *tuf* sequence.

5

SEQ ID NO:

	423	462	524
<i>E. avium</i>	ACGAAGTT	GAAATCGTgag	GTATgctgca
<i>E. casseliflavus</i>	ACGAAGTT	GAAATCGTgag	GTATgctgca
<i>E. cecorum</i>	ACGAAGTT	GAAATCGTgag	GTATgctgca
<i>E. dispar</i>	ACGAAGTT	GAAATCGTgag	GTATgctgca
<i>E. durans</i>	ACGAAGTT	GAAATCGTgag	GTATgctgca
<i>E. faecalis</i>	ACGAAGTT	GAAATCGTgag	GTATgctgca
<i>E. faecium</i>	ACGAAGTT	GAAATCGTgag	GTATgctgca
<i>E. flavescens</i>	ACGAAGTT	GAAATCGTgag	GTATgctgca
<i>E. gallinarum</i>	ACGAAGTT	GAAATCGTgag	GTATgctgca
<i>E. hirae</i>	ACGAAGTT	GAAATCGTgag	GTATgctgca
<i>E. mundtii</i>	ACGAAGTT	GAAATCGTgag	GTATgctgca
<i>E. pseudoavium</i>	ACGAAGTT	GAAATCGTgag	GTATgctgca
<i>E. raffinosus</i>	ACGAAGTT	GAAATCGTgag	GTATgctgca
<i>E. saccharolyticus</i>	ACGAAGTT	GAAATCGTgag	GTATgctgca
<i>E. solitarius</i>	ACGAAGTT	GAAATCGTgag	GTATgctgca
<i>E. diptheriae</i>	ACGAAGTT	GAAATCGTgag	GTATgctgca
<i>C. vaginalis</i>	ACGAAGTT	GAAATCGTgag	GTATgctgca
<i>B. cepacia</i>	ACGAAGTT	GAAATCGTgag	GTATgctgca
<i>S. aureus</i>	ACGAAGTT	GAAATCGTgag	GTATgctgca
<i>B. subtilis</i>	ACGAAGTT	GAAATCGTgag	GTATgctgca
<i>S. pneumoniae</i>	ACGAAGTT	GAAATCGTgag	GTATgctgca
<i>E. coli</i>	ACGAAGTT	GAAATCGTgag	GTATgctgca
<i>B. fragilis</i>	ACGAAGTT	GAAATCGTgag	GTATgctgca
<i>C. trachomatis</i>	ACGAAGTT	GAAATCGTgag	GTATgctgca
Selected sequences	ACGAAGTT	GAAATCGTgag	GTATgctgca

Selected species-specific
probes sequences:

SEQ ID NO: 603	SEQ ID NO: 620
ATTTGTCGATTGCTACGTT	ATTTGTCGATTGCTACGTT

SEQ ID NO: 602
AAGTT GAAGTTGTTG GTATT

AGATT GAAGTTGTTG GTAT

The sequence numbering refers to the *Enterococcus faecalis* sequence. Dots indicate gaps. "R" stands for A or G; "Y" stands for C or U. "M" stands for A or C; "K" stands for G or T; "W" stands for A or T; "S" stands for C or G. "I" stands for inosine which is a nucleotide analog that can bind to any of the four nucleotides A, C, G or T.

45

Ann x XIX: Strategy for the selection of primers from tuf sequences for the identification of platelets contaminants.

[illegible]

The sequence numbering refers to the *E. coli* *tuf* gene fragment (SEQ ID NO: 78). Nucleotides in capitals are identical to the selected sequence or match that sequence. Mismatches are indicated by lower cases.

^a "R" "Y" "M" "K" "W" and "S" designate nucleotide positions which are degenerated. "R" stands for A or G; "Y" stands for C or T; "M" stands for A or C; "K" stands for G or T; "W" stands for A or T; "S" stands for C or G. "I" stands for inosine which is a nucleotide analog that can bind to any of the four nucleotides A, C, G or T. This sequence is the reverse-complement of the above tuf sequence.

^b

Annex XX: Strat gy for the s lection of th universal amplification primers from atpD sequences.

		616	657	781	812	SEQ ID NO:
5	C. glutamicum	GTGTTGGGTC AGATGGATGA GGCACCAGGA GTCCGTATG	CGC...CGTATG	CGT...CGTATG	CGTTCGCGCG TGGTTATCCA GCCAAC	-
	M. tuberculosis	GTATTGGGAC AGATGGACGA GCGCGCGGCG	ACCCGTATG	CGT...CGGATG	CGTTCGCGCG TGGGATACCA GCCCAC	-
	E. faecalis	GTGTTGGGAC AAATGAACGA ACCACCAGGT	GCTCGGATG	CGG...CGTATG	CGTTCGCGCG TGGGTTATCCA ACCAAC	291
	S. agalactiae	GTCTTTGGTC AAATGAATGA ACCACCAGGT	GCACGTATG	CGT...CGTATG	CGTTCAGCGG TGGGTTATCCA ACCAAC	380
	B. subtilis	GTATTGGGAC AAATGAACGA GCGCGCGGCG	GCACGTATG	CGT...CGTATG	CGTTCAGCGG TGGGTTATCCA GCGGAC	-
10	L. monocytogenes	GTATTGGGTC AAATGAACGA GCGCGCGGCG	GCACGTATG	CGT...CGTATG	CGTTCAGCGG TGGGTTATCCA ACCAAC	324
	S. aureus	GTATTGGGTC AAATGAACGA GCGCGCGGCG	GCACGTATG	CGT...CGTATG	CGTTCAGCGG TGGGTTATCCA ACCAAC	366
	A. baumannii	GTATTGGGTC AAATGAACGA GCGCGCGGCG	GCACGTATG	CGT...CGTATG	CGTTCAGCGG TGGGTTATCCA ACCAAC	243
	N. gonorrhoeae	GTATTGGGTC AAATGAACGA GCGCGCGGCG	GCACGTATG	CGT...CGTATG	CGTTCAGCGG TGGGTTATCCA ACCAAC	-
15	C. freundii	GTATTGGGTC AAATGAACGA GCGCGCGGCG	GCACGTATG	CGT...CGTATG	CGTTCAGCGG TGGGTTATCCA ACCAAC	264
	E. cloacae	GTATTGGGTC AAATGAACGA GCGCGCGGCG	GCACGTATG	CGT...CGTATG	CGTTCAGCGG TGGGTTATCCA ACCAAC	284
	E. coli	GTATTGGGTC AAATGAACGA GCGCGCGGCG	GCACGTATG	CGT...CGTATG	CGTTCAGCGG TGGGTTATCCA ACCAAC	669
	S. typhimurium	GTATTGGGTC AAATGAACGA GCGCGCGGCG	GCACGTATG	CGT...CGTATG	CGTTCAGCGG TGGGTTATCCA ACCAAC	351
20	K. pneumoniae	GTATTGGGTC AAATGAACGA GCGCGCGGCG	GCACGTATG	CGT...CGTATG	CGTTCAGCGG TGGGTTATCCA ACCAAC	317
	S. marcescens	GTATTGGGTC AAATGAACGA GCGCGCGGCG	GCACGTATG	CGT...CGTATG	CGTTCAGCGG TGGGTTATCCA ACCAAC	357
	Y. enterocolitica	GTATTGGGTC AAATGAACGA GCGCGCGGCG	GCACGTATG	CGT...CGTATG	CGTTCAGCGG TGGGTTATCCA ACCAAC	393
	B. cepacia	GTATTGGGTC AAATGAACGA GCGCGCGGCG	GCACGTATG	CGT...CGTATG	CGTTCAGCGG TGGGTTATCCA ACCAAC	-
	H. influenzae	GTATTGGGTC AAATGAACGA GCGCGCGGCG	GCACGTATG	CGT...CGTATG	CGTTCAGCGG TGGGTTATCCA ACCAAC	-
	M. pneumoniae	GTATTGGGTC AAATGAACGA GCGCGCGGCG	GCACGTATG	CGT...CGTATG	CGTTCAGCGG TGGGTTATCCA ACCAAC	670
25	H. pylori	GTATTGGGTC AAATGAACGA GCGCGCGGCG	GCACGTATG	CGT...CGTATG	CGTTCAGCGG TGGGTTATCCA ACCAAC	-
	B. fragilis	GTATTGGGTC AAATGAACGA GCGCGCGGCG	GCACGTATG	CGT...CGTATG	CGTTCAGCGG TGGGTTATCCA ACCAAC	-
	Selected sequences ^b	ATG CCITCIGCIG TIGGITAYCA RCC				
	Selected sequences ^b	ATG CCITCIGCIG TIGGITAYCA RCC				
30	Selected universal primers sequences :	SEQ ID NO: 562	SEQ ID NO: 563 ^a			
		C ARATGRAYCA RCCICIGGI GYIMGIATG	GGY TGRTAICCA CIGCIGAIGG DAT			
		SEQ ID NO: 564	SEQ ID NO: 563 ^a			
		TAYGGIC ARATGAAYCA RCCICIGGI AA	GGY TGRTAICCA CIGCIGAIGG CAT			

35 The sequence numbering refers to the *Escherichia coli* atpD gene fragment (SEQ ID NO: 669). Nucleotides in capitals are identical to the selected sequence SEQ ID NO: 562 or 563 or match that sequence. Mismatches are indicated by lower cases. Mismatches for SEQ ID NO: 664 and 563 are indicated by underlined nucleotides.

^a This sequence is the reverse-complement of the above atpD sequence.
^b "R" "Y" "M" "K" "W" "S" "D" and "H" designate nucleotide positions which are degenerated. "R" stands for A or G; "Y" stands for C or T; "M" stands for A or C; "K" stands for G or T; "W" stands for A or T; "S" stands for C or G; "D" stands for A, T or G; "H" stands for A, T or C. "I" stands for inosine which is a nucleotide analog that can bind to any of the four nucleotides A, C, G or T.

Annex XXI: Specific and ubiquitous primers for DNA amplification
(*recA* sequences)

5	SEQ ID NO.	Nucleotide sequence	Originating DNA fragment	
			SEQ ID NO.	Nucleotide position
0		Universal primers (<i>recA</i>)		
	919	5'-GGI CCI GAR TCI TMI GGI AAR AC	918	437-459
	920 ^C	5'-TCI CCV ATI TCI CCI TCI AIY TC	918	701-723
5	921	5'-TIY RTI GAY GCI GAR CAI GC	918	515-534
	922 ^C	5'-TAR AAY TTI ARI GCI YKI CCI CC	918	872-894
		Universal primers (<i>rad51</i>)		
0	935	5'-GGI AAR WSI CAR YTI TGY CAY AC	939	568-590
	936	5'-TCI SIY TCI GGI ARR CAI GG	939	1126-1145
		Universal primers (<i>dmcl</i>)		
5	937	5'-ATI ACI GAR GYI TTY GGI GAR TT	940	1038-1060
	938	5'-CYI GTI GYI SWI GCR TGI GC	940	1554-1573

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS: BERGERON, Michel G.¹, Quebec City
 BOISSINOT, Maurice¹, St-Augustin-de-Desmaures
 HULETSKY, Ann¹, Sillery,
 MÉNARD, Christian¹, St-Lambert-de-Lévis
 OUELLETTE, Marc¹, Quebec City
 PICARD, François J.¹, Cap-Rouge
 ROY, Paul H.², Loretteville

¹:Canadian citizenship

²:American citizenship

(ii) TITLE OF THE INVENTION: HIGHLY CONSERVED GENES AN THEIR USE
 TO GENERATE SPECIES-SPECIFIC, GENUS-SPECIFIC AND UNIVERSAL
 NUCLEIC ACID PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY
 DETECT AND IDENTIFY BACTERIAL, FUNGAL AND PARASITICAL
 PATHOGENS FROM CLINICAL SPECIMENS FOR DIAGNOSIS

(iii) NUMBER OF SEQUENCES: 940

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE:
 (B) STREET:
 (C) CITY:
 (D) STATE:
 (E) COUNTRY:
 (F) ZIP:

(v) COMPUTER READABLE:

(A) MEDIUM TYPE:
 (B) COMPUTER:
 (C) OPERATING:
 (D) SOFTWARE:

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION:
 (B) FILING DATE:
 (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION:
 (B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME:
 (B) REGISTRATION NUMBER:

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE:
 (B) TELEFAX:

2) INFORMATION FOR SEQ ID NO: 1

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Acinetobacter baumannii*
 (B) STRAIN: ATCC 19606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1

CAA	ACTCGTG	AGCACATCCT	TCTTTCTCGT	CAGGTAGGTG	TACCTTACAT	50
CAT	CGTATTC	TTAAACAAAT	GCGACCTTGT	TGATGACGAA	GAATTACTTG	100
AAT	TAGTAGA	AATGGAAGTA	CGTGAACCTC	TTTCTACTTA	TGACTTCCCA	150
GGT	GATGACA	CTCCAGTAAT	CCGTGGTTCA	GCTCTTGCA	CGCTTAACGG	200
TGA	AGCTGGT	CCTTACGGTG	AAGAATCAGT	TCTTGCTCTT	GTCAGCAGCAC	250
TTG	ACTCTTA	CATCCAGAG	CCAGAGCGTG	CAATCGACAA	AGCATTCTTG	300
ATG	CCAATCG	AAGACGTATT	CTCAATTTCT	GGTCGTGGTA	CAGTAGTAAC	350
AGG	CCGTGTT	GAAGCTGGTA	TCATCAAAGT	TGGTGAAGAA	GTCAGATCG	400
TTG	GTTATTA	AGATACAGTT	AAAACAACCTG	TAACTGGCGT	AGAAATGTTT	450
CGT	AACTTTC	TTGACGAAG	CCGTGCAGGT	GAGAACTGTG	GTATCTTACT	500
TCG	TGGTACT	AAGCGTGAAG	AAGTACAACG	TGGTCAAGTA	CTTGCTAAAC	550
CAG	GTAACAT	CAAGCCGCAC	ACTAAATTCG	ACGCAGAAGT	ATACGTACTT	600
TCT	AAAGAAG	AAGGTGGTCG	TCACACTCCA	TTCTTAAATG	GTTACCGTCC	650
ACAG	TCTAC	TTCCGTACAA	CTGACGTAA	TGGTGCRATC	CAGTTGAAAG	700
AAGG	CGTTGA	AATGGTAATG	CCAGGTGACA	ACGTTGAAAT	GTCAGTAGAA	750

2) INFORMATION FOR SEQ ID NO: 2

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Actinomyces meyeri*
 (B) STRAIN: ATCC 35568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2

CGG	TGCGATC	CTCGTGGTCG	CCGCGACCGA	CGGCCCCATG	GCCCAGACCC	50
GCG	AGCACGT	CCTGCTCGCC	CGTCAGGTCG	GCGTTCCAC	CATCCTCATC	100
GCC	CTCAACA	AGTCCGACAT	GGTTGACGAC	GAGGAAATGA	TGGAAGTGGT	150
CGA	GAGGAG	TGCCGCGACC	TGCTGGAGTC	CCAGGACTTC	GATCGCGATG	200
CCCC	GATCGT	CCAGGTTTCC	GCTCTGAAGG	CCCTCGAGGG	CGACGCGGAG	250
TGG	TTGCCA	AGATCGAGGA	GCTCATGGAG	GCTGTGGATT	CCTACATCCC	300
CAC	CCCCGAG	CGCGATATGG	ACAAGCCCTT	CCTCATGCCG	ATCGAGGACG	350
TCT	TACGAT	CACAGGTCGT	GGCACGGTCG	TCACGGGGCG	TGTTGAGCGT	400
GGC	AAGCTGC	CGATCAACTC	CGAGGTCGAG	ATCCTCGGTA	TCCGTGATCC	450

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CCAGAAGACC ACGGTCACCG GCATCGAGAT GTTCCACAAG TCGATGGACG 500
AGGCATGGGC CGGCGAGAAC TGTGGCCTGC TGCTGCGCGG TACCAAGCGC 550
GATGAGGTTG AGCGCGGCCA GGTGTGGGCC ATTCCCGGCT CCATCACGCC 600
TCACACCGAG TTCGAGGGCC AGGTTTACAT CCTCAAGAAG GAAGAGGGCG 650
5 GCCGTCACAA CCCGTTCTTC TCGAACTACC GTCCGCAGTT CTACTTCCGT 700
ACCACGGACG TGACCGGCGT CATCACCTC CCCGAGGGCA CCGACATGGT 750
CATGCCTGGC GACACCACCG AGATCTCCGT TCAGCTGATC CAGCCCATCG 800
CCATGGAGCC CGGCTGGGCT TCGCCA 826

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10

2) INFORMATION FOR SEQ ID NO: 3

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aerococcus viridans*
 (B) STRAIN: ATCC 11563

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3

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TGGTGCGATC TTAGTAGTAT CTGCTGCTGA TGGTCCAATG CCACAAACTC 50
GTGAGCACAT CCTTTTAGCT GGCCAAATCG GTGTTCTGCTC ATTCGTAGTA 100
30 TTCTTAAACA AAGTTGACCA AGTTGACGAT GAAGAATTAC TAGAATTAGT 150
TGAAATGGAA GTTCGTGACT TATTATCTGA GTACAACTAC CCAGGTGACG 200
ATCTACCTGT AATCGCTGGT TCTGCTTTAT TAGCATTACA AGGCGATGAA 250
GCTCAAGAAG CTAAAATCAT GGAATTAATG GAAGCTGTAG ACTCTTACAT 300
TCCAGAACCA GAACGTGACA ACGACAAACC ATTCATGATG CCAATTGAGG 350
35 ATGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG TCGTGTTGAA 400
CGTGGTGAAG TTCGTACAGG TGACGAAGTT GACATCGTTG GTATTGCTGA 450
ACAAATCGGT AAATCAGTTG TAACTGGTGT TGAAATGTTT CGTAAAAACT 500
TAGACTACGC TCAAGCTGGT GACAACATCG GTGCATTATT ACGTGGTGT 550
CAACGTGAAG ACATCCAACG TGGTCAAGTA TTGGCTGCTC CTGGTTCAAT 600
40 CACTCCACAT ACTAAATTTA AAGCGCAAGT TTACGTTTTA TCTAAAGAAG 650
AAGGTGGACG TCATACACCA TTCTTAACTA ACTACCGTCC ACAATTCTAC 700
TTCCGTACTA CTGACATTAC TGGTGTTATC ACTTTACCAG AAGACGTAGC 750
TATGGTTATG CCTGGTGACA ACGTTGATAT GGACGTTGAA TTGATTCAAC 800
CAGTTGCGAT CGAAGATGGT ACTAAATTCT CTATC 835
45

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2) INFORMATION FOR SEQ ID NO: 4

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 827 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 60 (A) ORGANISM: *Achromobacter xylosoxidans* subsp.
denitrificans

(B) STRAIN: ATCC 15173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4

5	CCTGGTGGTG	TCGGCCGCTG	ACGGCCCGAT	GCCGCAAACG	CGCGAACACA	50
	TCCTGCTGAG	CCGCCAGGTT	GGCGTGCCGT	ACATCATCGT	CTTCCTGAAC	100
	AAGGCCGACA	TGGTTGACGA	CGCCGAGCTG	CTTGAGCTGG	TGGAAATGGA	150
	AGTTCGCGAR	CTGCTGAGCA	AGTACGACTT	CCCGGGCGAC	GACACCCCGA	200
	TCGTGAAGGG	TTCGGCCAAG	CTGGCGCTGG	AAGGCGACAA	GGGCGAACTG	250
10	GGCGAACAGG	CCATCATGGC	GCTGGCCGCT	GCGCTGGACT	CGTACATCCC	300
	GACGCCTGAG	CGTGCCGTTG	ACGGCGCGTT	CCTGATGCCG	GTTGAAGACG	350
	TGTTCTCGAT	CTCGGGTCGC	GGCACCCTGG	TGACCGGCCG	TATCGAACGC	400
	GGCATCATCA	AGGTTCGGCGA	GGAAATCGAA	ATCGTCGGTC	TGGTGCCGAC	450
	GGTGAAGACG	ACCTGCACGG	GCGTGGAAT	GTTCCGCAAG	CTGCTGGACC	500
15	AAGGTCAAGC	CGGCGACAAC	GTGGGCATCC	TRCTGCGCGG	CACCAAGCGT	550
	GAAGACGTCC	AGCGCGGCCA	GGTTCTGGCC	AAGCCGGGCT	CGATACCCCC	600
	GCACACGGAC	TTCACGTCCG	AGGTGTACAT	CCTGTCCAAG	GAAGAAGGCG	650
	GCCGTACAC	TCCGTTCTTC	CAAGGCTATC	GTCCCCAGTT	CTACTTCCCG	700
	ACGACGGACG	TGACGGGCAC	GATCGAGCTG	CCGGCCGACA	AGGAAATGGT	750
20	CCTGCCGGGC	GACAACGTGG	CCATGACGGT	CAAGCTGCTG	GCTCCGATCG	800
	CCATGGAAGA	AGGCCTGCGT	TCGCCAC			827

25 2) INFORMATION FOR SEQ ID NO: 5

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 823 bases
	(B)	TYPE: Nucleic acid
30	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

(A)	ORGANISM: <i>Anaerorhabdus furcosus</i>
(B)	STRAIN: ATCC 25662

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5

40	TGGATCAATC	CTAGTAGTTG	CTGCAACTGA	TGGACCAATG	CCTCAAACCTC	50
	GTGAACATAT	CTTACTTGCT	CGTCAAGTAG	GTGTTCCAAG	AATGGTTGTA	100
	TTCTTGAACA	AATGCGACAT	GGTTGAAGAT	GAAGAATTAA	TCGACCTTGT	150
	TGAAATGGAA	GTTCGTGAAC	TTCTAAGTGC	TTACGGTTTC	GAAGGTGATG	200
45	ATACACCAGT	TATCCGTGGT	TCTGCATTAA	AATCTCTTGA	AGGAAATGCT	250
	GATTGGGAAG	CAAAAGTTGC	TGAATTAATG	GATGCAGTTG	ACTCTTGGAT	300
	TCCAACCTCA	ACTCATGAAA	CAGACAAACC	ATTCTTAATG	GCTGTTGAAG	350
	ATGTATTAC	AATTACAGGT	CGTGGTACAG	TTGCTACTGG	ACGTGTTGAA	400
	CGTGGAACAT	TAAACCTTAA	CGAAGAAGTT	GAAATCGTTG	GTATTTCATGA	450
50	TACTAAGAAA	TCAGTTGTTA	CTGGTATCGA	AATGTTCCGT	AAATTATTAG	500
	ACTATGCTGA	AGCAGGAGAC	AACATTGGTG	CATTATTACG	TGGTGTTTCT	550
	CGTGATGAAA	TCGAACGTGG	ACAATGTCTA	GCTAAACCTG	GATCAGTTAC	600
	TCCACATACA	GCTTTCAAAG	CTCAAGTATA	CGTATTAACT	AAAGAAGAAG	650
	GTGGACGTCA	TACACCATTG	GTAACATACT	ACCGTCCTCA	ATTCTATTTC	700
55	CGTACAACCTG	ACGTAACAGG	AGTTGTTAAA	CTTCCTGAAG	GTAAGTAAAT	750
	GGTTATGCCT	GGAGACAACA	TCGAAATGAT	CGTTGAATTA	ATCGCTCCAA	800
	TCGCTGTTGA	ACAAGGAACT	AAG			823

60

2) INFORMATION FOR SEQ ID NO: 6

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus anthracis*
 (B) STRAIN: 4229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6

	CGGCGGTATC	TTAGTAGTAT	CTGCTGCTGA	TGGCCCAATG	CCTCAAACATC	50
	GTGAGCACAT	CCTTCTTTCT	CGTCAAGTAG	GTGTACCTTA	CATCGTTGTA	100
	TTCTTAAACA	AATGCGACAT	GGTAGACGAC	GAAGAATTAT	TAGAATTAGT	150
20	AGAAATGGAA	GTTGCGGACC	TATTATCTGA	ATACGGATTC	CCAGGCGACG	200
	ACATTCCTGT	AATCAAAGGT	TCTGCTCTTA	AAGCTCTTCA	AGGAGAAGCT	250
	GATTGGGAAG	CAAAAATCAT	TGAATTAATG	GCTGAAGTTG	ATGCTTACAT	300
	CCCAACTCCA	GAACGTGAAA	CTGACAAACC	ATTCTTAATG	CCTGTAGAGG	350
	ACGTATTCTC	TATCACAGGT	CGTGGTACAG	TTGCTACTGG	TCGTGTTGAG	400
25	CGCGGTATCG	TTAAAGTTGG	TGACGTAGTA	GAAATCATCG	GTCTTGCTGA	450
	AGAAAATGCT	TCTACAACTG	TAACCTGGTG	AGAGATGTTC	CGTAAACTTC	500
	TTGACCAAGC	TCAAGCTGGA	GACAACATCG	GTGCTTTACT	TCGTGGGGTT	550
	GCTCGTGAAG	ACATCCAACG	TGGACAAGTA	CTTGCAAAAA	GCGGTTCTGT	600
	AAAAGCTCAC	GCTAAATTCA	AAGCTGAAGT	TTTCGTATTA	TCTAAAGAAG	650
30	AAGGTGGACG	TCACACTCCA	TTCTTCGCTA	ACTACCGTCC	TCAGTTCTAC	700
	TTCCGTACAA	CTGACGTAAC	TGGTATCATC	CAATTACCAG	AAGGTACTGA	750
	AATGGTAATG	CCTGGTGACA	ACATCGAAAT	GACTATCGAA	CTTATCGCTC	800
	CAATCGCTAT	CGAAGAGGGA	ACTAA			825

2) INFORMATION FOR SEQ ID NO: 7

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
 (B) STRAIN: ATCC 14579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7

	CGGCGGTATC	TTAGTAGTAT	CTGCTGCTGA	TGGCCCAATG	CCTCAAACAC	50
	GTGAGCACAT	CCTTCTTTCT	CGTCAAGTAG	GTGTCCTTA	CATCGTTGTA	100
55	TTCTTAAACA	AATGCGACAT	GGTAGATGAC	GAAGAATTAT	TAGAATTAGT	150
	AGAAATGGAA	GTTGCGGACC	TATTATCTGA	ATACGGATTC	CCAGGCGACG	200
	ACATTCCTGT	AATCAAAGGT	TCTGCTCTTA	AAGCTCTTCA	AGGAGAAGCT	250
	GATTGGGAAG	CAAAAATCAT	TGAATTAATG	GCTGAAGTTG	ATGCTTACAT	300
	CCCAACTCCA	GAACGTGAAA	CTGACAAACC	ATTCTTAATG	CCTGTAGAGG	350
60	ACGTATTCTC	TATCACAGGT	CGTGGTACAG	TTGCTACTGG	TCGTGTTGAG	400

	CGCGGTATCG	TTAAAGTTGG	TGACGTAGTA	GAAATCATCG	GTCTTGCTGA	450
	AGAAAAATGCT	TCTACAACTG	TAACTGGTGT	AGAGATGTTC	CGTAAACTTC	500
	TTGACCAAGC	TCAAGCTGGA	GACAACATCG	GTGCTTTACT	TCGTGGGGTT	550
5	GCTCGTGAAG	ACATCCAACG	TGGACAAGTA	CTTGCAAAAA	GCGGTTCTGT	600
	AAAAGCTCAC	GCTAAATTCA	AAGCTGAAGT	TTTCGTATTA	TCTAAAGAAG	650
	AAGGTGGACG	TCACACTCCA	TTCTTCGCTA	ACTACCGTCC	TCAGTTCTAC	700
	TTCCGTACAA	CTGACGTAAC	TGGTATCATC	CAATTACCAG	AAGGTACTGA	750
	AATGGTAATG	CCTGGTGACA	ACATTGAAAT	GACTATCGAA	CTTATCGCTC	800
10	CAATCGCTAT	CGAAGAGGGA	ACTAAATTC			829

2) INFORMATION FOR SEQ ID NO: 8

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 20 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacteroides distasonis*
 25 (B) STRAIN: ATCC 8503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8

30	CGGTGCTATC	ATCGTAGTTG	CTGCTACTGA	TGGTCCTATG	CCTCAAACCTC	50
	GCGAGCACAT	CCTTTTGGCT	CGTCAGGTAA	ACGTTCCGAG	ATTGGTTGTA	100
	TTCATGAACA	AGTGTGACAT	GGTTGACGAC	GAGGAAATGT	TGGAATTGGT	150
	TGAGATGGAG	ATGAGAGAGT	TGCTTTTCATT	CTATCAATTC	GACGGTGACA	200
	ACACTCCGAT	CATCCGTGGT	TCTGCTCTTG	GTGCATTGAA	CGGTGATGCT	250
	CAATGGGAAG	ATAAAGTAAT	GGAGTTGATG	GAAGCTTGTTG	ATACTTGGAT	300
35	TCCTCTGCCT	CCGCGCGAAA	TCGACAAGCC	GTTCTTGATG	CCGGTTGAGG	350
	ACGTATTCTC	AATCACGGGT	CGTGGTACTG	TTGCTACAGG	TCGTATCGAG	400
	ACAGGTATTG	TTAAGGTTGG	TGAGGAAGTT	CAGATCATCG	GTCTTGCGCG	450
	TGCTGGTAAG	AAATCTGTTG	TTACAGGTGT	TGAGATGTTC	CGTAAGTTAT	500
	TGGATCAAGG	TGAGGCTGGT	GATAACGTTG	GTTTGTGCT	TCGCGGTATC	550
40	GATAAGAATG	AGATCAAGCG	TGGTATGGTA	ATCTGCCACC	CGGGTCAGGT	600
	TAAAGAGCAT	TCTAAGTTCA	AGGCTGAGGT	TTATATCTTG	AAGAAAGAGG	650
	AAGGTGGTCG	TCACACTCCG	TTCCACAACA	AATATCGTCC	TCAGTTCTAT	700
	ATCCGTACAT	TGGATGTAAC	TGGTGAGATC	ACTTTGCCGG	AAGGAAGTGA	750
	AATGGTAATG	CCGGGTGATA	ACGTAACGAT	CGAGGTTGAG	TTGATCTATC	800
45	CGGTAGCATG	TAGCGTAG				818

2) INFORMATION FOR SEQ ID NO: 9

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 639 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*

(B) STRAIN: R763

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9

5	GGTCCTATGC	CTCAAACACG	TGAACACATC	TTGTTATCAC	GTAACGTTGG	50
	TGTACCATAC	ATCGTTGTTT	TCTTAAACAA	AATGGATATG	GTTGATGACG	100
	AAGAATTACT	AGAATTAGTT	GAAATGGAAG	TTCGTGACTT	ATTGTCAGAA	150
	TATGACTTCC	CAGGCGACGA	TGTTCTGTGA	ATCGCTGGTT	CTGCTTTGAA	200
	AGCTCTTGAA	GGCGATGCTT	CATACGAAGA	AAAAATCATG	GAATTAATGG	250
10	CTGCAGTTGA	CGAATACGTT	CCAACTCCAG	AACGTGACAC	TGACAAACCA	300
	TTCATGATGC	CAGTCGAAGA	CGTATTCTCA	ATCACTGGAC	GTGGTACTGT	350
	TGCTACAGGC	CGTGTGGAAC	GTGGACAAGT	TCGCGTTGGT	GACGAAGTTG	400
	AAATCGTTGG	TATTGCTGAA	GAAACTGCTA	AAACAACGTG	AACTGGTGTT	450
	GAAATGTTCC	GTAAATTGTT	AGACTATGCT	GAAGCAGGGG	ATAACATTGG	500
15	TGCATTGCTA	CGTGGTGTTG	CTCGTGAAGA	CATCCAACGT	GGACAAGTAT	550
	TGGCTAAAGC	TGGTACAATC	ACACCTCATA	CAAAATTTAA	AGCTGAAGTT	600
	TACGTTTTTA	CAAAAGAAGA	AGGTGGACGT	CACACACCA		639

20

2) INFORMATION FOR SEQ ID NO: 10

(i) SEQUENCE CHARACTERISTICS:

25	(A)	LENGTH: 692 bases
	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

(A)	ORGANISM: <i>Staphylococcus saprophyticus</i>
(B)	STRAIN: CSG 197

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10

	GAACACATTC	TTTTATCACG	TAACGTTGGT	GTTCCAGCAT	TAGTTGTATT	50
	CTTAAACAAA	GTTGACATGG	TTGACGATGA	AGAATTATTA	GAATTAGTAG	100
	AAATGGAAGT	TCGTGACTTA	TTAAGCGAAT	ATGACTTCCC	AGGTGACGAT	150
40	GTACCTGTAA	TCTCTGGTTC	TGCATTAAAA	GCTTTAGAAG	GCGACGCTGA	200
	CTATGAGCAA	AAAATCTTAG	ACTTAATGCA	AGCTGTTGAT	GACTTCATTC	250
	CAACACCAGA	ACGTGATTCT	GACAAACCAT	TCATGATGCC	AGTTGAGGAC	300
	GTATTCTCAA	TCACTGGTTC	TGGTACTGTT	GCTACAGGCC	GTGTTGAACG	350
	TGGTCAAATC	AAAGTCGGTG	AAGAAATCGA	AATCATCGGT	ATGCAAGAAG	400
45	AATCAAGCAA	AACAACGTG	ACTGGTGTAG	AAATGTTCCG	TAAATTATTA	450
	GACTACGCTG	AAGCTGGTGA	CAACATTGGT	GCATTATTAC	GTGGTGTTTC	500
	ACGTGATGAC	GTACAACGTG	GTCAAGTTTT	AGCTGCTCCT	GGTACTATTA	550
	CACCACATAC	AAAATTCAAA	GCGGATGTTT	ACGTTTTTATC	TAAAGATGAA	600
	GGTGGTCGTC	ATACACCAT	CTTCACTAAC	TACCGCCAC	AATTCTATTT	650
50	CCGTACTACT	GACGTAACTG	GTGTTGTAA	CTTACCAGAA	GG	692

2) INFORMATION FOR SEQ ID NO: 11

55

(i) SEQUENCE CHARACTERISTICS:

60	(A)	LENGTH: 808 bases
	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Bacteroides vulgatus*
(B) STRAIN: ATCC 8482

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11

```

10 TTATTGTTTG TGCTGCAACT GATGGTCCGA TGCCTCAGAC TCGTGAACAC      50
   ATCCTGTTGG CTCGTCAGGT AAACGTACCT CGTTTGGTTG TTTTCTTGAA      100
   CAAGTGTGAT ATGGTTGATG ATGAAGAAAT GTTGAATTG GTAGAAATGG      150
   AAATGCGTGA ATTGCTTTCA TTCTATGATT TCGATGGTGA TAATACTCCT      200
   ATTATTCGTG GTTCTGCATT AGGTGCTTTG AATGGTGTTT CTCAATGGGA      250
15 AGATAAAGTA ATGGAGTTGA TGGATGCAGT TGATACTTGG ATTCCATTGC      300
   CTCCGCGTGA TATTGATAAA CCTTCTTTGA TGCCTGTTGA AGACGTGTTT      350
   TCTATCACTG GTCGTGGTAC TGTGCTACA GGTGCTATCG AAGCTGGTAT      400
   TATCCATGTA GGTGACGAAG TTGAAATTCT TGGTTTGGGT GAAGATAAGA      450
   AATCAGTTGT TACTGGCGTT GAAATGTTCC GTAAATTATT GGATCAAGGT      500
20 GAAGCTGGTG ATAATGTTGG TTTGTTGTTG CGTGGTATCG AAAAAACGA      550
   AATCAAACGT GGTATGATTT TGTGTAAGCC GGGTCAGGTT AAGGCTCACT      600
   CTAAGTTCAA AGCTGAGGTT TATATCTTGA AGAAAGAAGA AGGTGGTCTG      650
   CATACTCCGT TCCATAACAA GTATCGTCTT CAGTTCTACT TCGCTACTAT      700
   GGACTGTACA GGTGAAATCA CTTTGCCGGA AGGAACTGAA ATGGTAATGC      750
25 CTGGTGATAA CGTAACTATT ACAGTTGAGT TGATCTACCC GGTTCATTG      800
   AATGTAGG                                     808

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30 2) INFORMATION FOR SEQ ID NO: 12

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 838 bases
(B) TYPE: Nucleic acid
35 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bartonella henselae*
(B) STRAIN: ATCC 49882

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12

```

45 TGGTGCGATT TTGGTTGTTT CAGCTGCTGA TGGTCCGATG CCTCAAACAC      50
   GTGAGCATAT TCTTCTTGCC CGTCAGGTTG GTGTTCCAGC GATTGTTGTT      100
   TTTCTTAATA AGGTTGATCA GGTGATGAT GCTGAGCTTT TGGAGCTTGT      150
   TGAGCTTGAA GTTCGGGAGT TATTGTCGAA ATATGATTTT CCAGGAGACG      200
50 ATATTCCGAT CGTTAAAGGT TCTGCTTTGG CAGCGCTTGA AGATAAAGAT      250
   AAAAGCATTG GTGAAGATGC GGTTGCTCTT TTGATGAGTG AAGTTGATAA      300
   TTATATACCG ACGCCTGAAC GTCCTGTTGA TCAGCCGTTT TTGATGCCAA      350
   TTGAAGATGT TTTTTTCGATT TCGGGTCTGT GAACTGTTGT GACGGGTCGT      400
   GTTGAGCGTG GTGTTATTAA GGTGTTGTTG GAAGTTGAGA TTATCGGCAT      450
55 TCGTCCAAC TCTAAGACAA CAGTTACAGG GGTGAAATG TTCCGCAAGC      500
   TTTTAGATCA GGGGCAAGCG GGTGATAATA TTGGAGCGCT GCTTCGTGGT      550
   ATTGATCGTG AAGGGATTGA GCGTGGACAA GTTTTGGCGA AGCCTGCTTC      600
   GGTACACCT CATAAGAGAT TTAAAGCAGA GGCTTACATT TTGACGAAAG      650
   ATGAAGGTGG TCGTCATACT CCATTTTTC CGAATTATCG TCCTCAGTTT      700
60 TATTTCCGTA CTACGGATGT AACGGGAATT GTTACGCTTC CAGAAGGTAC      750

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AGAGATGGTT ATGCCTGGTG ATAATGTTGC TATGGATGTC TCTCTGATTG 800
 TTCCAATTGC CATGGAAGAA AAAC TTCGTT TTGCTATC 838

5

2) INFORMATION FOR SEQ ID NO: 13

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 839 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bifidobacterium adolescentis*
 (B) STRAIN: ATCC 15703

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13

25 TGGCGCCATC CTTGTTGTGG CCGCCACCGA CGGCCCGATG GCTCAGACCC 50
 GCGAGCACGT GCTGCTCGCT CGTCAGGTGG GCGTCCCGAA GATCCTCGTC 100
 GCTCTGAACA AGTGCGATAT GGTGACGAC GACGAGCTCA TCGAGCTCGT 150
 TGAGGAAGAG GTCCGTGACC TCCTCGACGA AAATGGCTTC GATCGCGATT 200
 GCCCGGTTCAT CCACGTGTCC GCTTACGGCG CACTGCACGA TGACGCTCCG 250
 GACCACGAGA AGTGGGTTGA GCAGATCAAG AAGCTCATGG ACGCCGTCGA 300
 TGACTACATC CCGACCCCGG TCCACGATCT GGACAAGCCG TTCCTGATGC 350
 CGATCGAAGA TGTCTTCACC ATCTCCGGCC GTGGCACCGT GGTGACCGGC 400
 CGTGTCGAGC GTGGTAAGCT CCCGGTCAAC TCCAACGTCG AGATCGTCGG 450
 30 CATCCGTCCG ACCCAGACCA CCACCGTCAC CTCCATCGAG ACCTTCCACA 500
 AGCAGATGGA CGAGTGCAG GCTGGCGACA ACACCGGTCT GCTGCTCCGC 550
 GGCATCAACC GTGACCAGGT CGAGCGTGGC CAGGTTCTGG CTGCTCCGGG 600
 CTCCGTGACC CCGCACACCA AGTTCGAGGG CGAAGTCTAC GTGCTGACCA 650
 35 AGGACGAAGG CGGCCGTCAC TCGCCGTTCT TCTCCAATA CCGTCCGCAG 700
 TTCTACTTCC GTACCACCGA CGTCACCGGC GTCATCACCC TGCCGGAAGG 750
 CGTTGAGATG GTGCAGCCGG GCGATCACGC TACCTTCGGC GTTGAGCTGA 800
 TCCAGCCGAT CGCTATGGAA GAGGGCCTGA CCTTCGCAG 839

40

2) INFORMATION FOR SEQ ID NO: 14

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 839 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bifidobacterium dentium*
 (B) STRAIN: ATCC 27534

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14

60 TGGCGCTATC CTCGTTGTGG CCGCCACCGA CGGCCCGATG GCTCAGACCC 50
 GCGAGCACGT GCTGCTCGCT CGTCAGGTGG GCGTGCCGCG TATCCTCGTC 100
 GCCCTGAACA AGTGCGATAT GGTGACGAC GAAGAGCTCA TCGAGCTCGT 150

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TGAGGAAGAG GTCCGTGACC TCCTCGACGA AAACGGCTTC GATCGCGATT 200
GCCCCGGTCAT CCACACCTCC GCCTACGGCG CGCTGCACGA TGACGCTCCG 250
GACCACGACA AGTGGGTTGA GTCCGTCAAG GAACTCATGA AGGCCGTCGA 300
CGAGTACATC CCGACCCCGA CCCACGATCT GGACAAGCCG TTCCTGATGC 350
5 CGATCGAAGA TGTGTTACAC ATCTCCGGCC TCCAACGTTG AGATCGTCGG 400
CGTGTGCGAGC GTGGTAAGCT CCCGGTCAAC TCCAACGTTG AGATCGTCGG 450
CATCCGTCCG ACCCAGACCA CCACCGTCAC CTCCATCGAG ACCTTCCACA 500
AGCAGATGGA CGAGTGCAG GCTGGCGACA ACACCGGTCT GCTGCTCCGC 550
GGCATCAACC GTGACCAGGT CGAGCGTGGC CAGGTTCTGG CTGCTCCGGG 600
10 CTCCGTGACC CCGCACACCA AGTTCGAGGG CGAAGTCTAC GTGCTGACCA 650
AGGACGAAGG CGGCCGTCAC TCGCCGTTCT TCTCCAATA CCGTCCGCAG 700
TTCTACTTCC GTACACCGA CGTACCCGGC GTCATCACCC TGCCGGAAGG 750
CGTTGAGATG GTGCAGCCGG GCGATCACGC TACCTTCGGC GTTGAGCTGA 800
TCCAGCCGAT CGCTATGGAA GAGGGCCTGA CCTTCGCAG 839
15

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2) INFORMATION FOR SEQ ID NO: 15

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20 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 838 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
25 (ii) MOLECULE TYPE: Genomic DNA
    (vi) ORIGINAL SOURCE:
    (A) ORGANISM: Brucella abortus
30 (B) STRAIN: S2308

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15

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35 TGGCGCGATC CTGGTGGTTT CGGCTGCTGA CGGCCCGATG CCGCAGACCC 50
GCGAGCACAT CCTGCTTGCC CGTCAGGTTG GCGTTCCGGC GATCGTCGTG 100
TTCCTCAACA AGTGCAGACCA GGTGACGAT GCAGAACTGC TCGAACTGGT 150
TGAAGTGGAA GTGCGCGAAC TTCTGTCGAA GTACGAATTC CCCGGCGACG 200
AAATCCCGAT CATCAAGGGC TCGGCTCTTG CTGCTCTGGA AGATTCTTCC 250
AAGGAACTGG GCGAAGATGC CATCCGCAAC CTGATGGACG CGGTTGACAG 300
40 CTACATTCCG ACCCCGGAAC GCCCGATCGA CCAGCCGTTT CTGATGCCGA 350
TCGAAGACGT GTTCTCGATC TCCGGCCGTG GTACGGTTGT GACGGGTTCG 400
GTTGAGCGCG GTATCGTTAA GGTCCGTGAA GAAGTTGAAA TCGTCGGCAT 450
CAAGGCGACG ACGAAGACCA CGGTTACCGG CGTTGAAATG TTCCGCAAGC 500
TGCTCGACCA GGGCCAGGCT GGCAGACAAC TTGGCGCGCT GATCCGCGGC 550
45 GTTGGCCGTG AAGACGTTGA ACGCGGCCAG GTTCTCTGCA AGCCGGGTTC 600
TGTGAAGCCG CACACCAAGT TTAAGGCAGA AGCCTATATT CTGACCAAGG 650
ACGAAGGTGG CCGTCATACG CCGTTCTTCA CCAACTACCG TCCGCAGTTC 700
TACTTCCGTA CGACGGACGT GACGGGTGTT GTGACGCTTC CGGCTGGCAC 750
GGAAATGGTC ATGCCTGGCG ATAACGTCGC CATGGACGTT ACCCTGATCG 800
50 TGCCGATCGC CATGGAAGAG AAGCTTCGCT TCGCTATC 838

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2) INFORMATION FOR SEQ ID NO: 16

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55 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 771 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
60 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Burkholderia cepacia*
(B) STRAIN: LSPQ 2217

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16

10	GGCAGCAGAC	GGCCCGATGC	CGCAAACGCG	TGAGCACATC	CTGCTGGCGC	50
	GTCAGGTTGG	CGTTCCGTAC	ATCATCGTGT	TCCTGAACAA	GTGCGACATG	100
	GTGGACGACG	CCGAAGTGT	CGAGCTGGTC	GAGATGGAAG	TTCGCGAACT	150
	CCTGTCAAG	TACGACTTCC	CGGGCGACGA	CACGCCGATC	GTGAAGGGTT	200
	CGGCGAAGCT	GGCGCTGGAA	GGCGACACGG	GCGAGCTGGG	CGAAGTGGCG	250
15	ATCATGAGCC	TGGCCGACGC	GCTGGACACG	TACATCCCGA	CGCCGGAGCG	300
	TGCAGTTGAC	GGCGCGTTCC	TGATGCCGGT	GGAAGACGTG	TTCTCGATCT	350
	CGGGCCGCGG	TACGGTGGTG	ACGGGTCGTG	TCGAGCGCGG	CATCGTGAAG	400
	GTCGGCGAAG	AAATCGAAAT	CGTCGGTATC	AAGCCGACGG	TGAAGACGAC	450
	CTGCACGGGC	GTTGAAATGT	TCCGCAAGCT	GCTGGACCAA	GGTCAAGCAG	500
20	GCGACAACGT	TGGTATCCTG	CTGCGCGGCA	CGAAGCGTGA	AGACGTGGAG	550
	CGTGGCCAGG	TTCTGGCGAA	GCCGGGTTCTG	ATCACGCCGC	ACACGCACTT	600
	CACGGCTGAA	GTGTACGTGC	TGAGCAAGGA	CGAAGGCCGC	CGTCACACGC	650
	CGTTCTTCAA	CAACTACCGT	CCGCAGTTCT	ACTTCCGTAC	GACGGACGTG	700
	ACGGGCTCGA	TCGAGCTGCC	GAAGGACAAG	GAAATGGTGA	TGCCGGGCGA	750
25	CAACGTGTCTG	ATCACGGTGA	A			771

2) INFORMATION FOR SEQ ID NO: 17

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 829 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cedecea davisae*
(B) STRAIN: ATCC 33431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17

45	GGCGCTATCC	TGGTTGTTGC	TGCGACTGAT	GGCCCAATGC	CACAGACCCG	50
	TGAGCACATC	CTGCTGGGTC	GTCAGGTTGG	CGTTCCGTAC	ATCATCGTGT	100
	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTA	150
	GAAATGGAAG	TTCGTGAACT	TCTGTCCCAG	TACGACTTCC	CGGGCGACGA	200
	TACTCCAATC	GTTCGTGGTT	CTGCTCTGAA	AGCGCTGGAA	GGCGAAGCAG	250
50	AGTGGGAAGC	TAAAATCGTT	GAGCTGGCTG	GCTACCTGGA	TTCTTACATC	300
	CCTGAGCCAG	AGCGTGCTAT	CGATAAGCCG	TTCCTGCTGC	CAATCGAAGA	350
	CGTATTCTCC	ATCTCCGGCC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAGC	400
	GCGGTATCAT	CAAAGTTGGT	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAT	450
	ACTGCGAAAT	CTACCTGTAC	CGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
55	CGAAGGCCGT	GCTGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTATCAAAC	550
	GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCAGG	CTCTATCAAG	600
	CCACACACCA	AGTTCGAATC	TGAAGTGATC	ATCCTGTCCA	AAGACGAAGG	650
	CGGCCGTGAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700
	GTACAACCTGA	CGTGACCGGC	ACCATCGAAC	TGCCAGAAGG	CGTTGAGATG	750
60	GTAATGCCTG	GCGACAACAT	CAAATGGTT	GTTACCCTGA	TCCACCCAAT	800

CGCGATGGAT GACGGTCTGC GTTTCGCAA

829

5 2) INFORMATION FOR SEQ ID NO: 18

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cedecea neteri*
 (B) STRAIN: ATCC 33855

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18

20 CGCTATCCTG GTTGTGCTG CGACTGACGG CCCTATGCCT CAGACCCGTG 50
 AGCACATCCT GCTGGGTCGT CAGGTTGGCG TTCCTTACAT CATCGTGTTT 100
 CTGAACAAAT GTGACATGGT TGATGACGAA GAGCTGCTGG AGCTGGTTGA 150
 25 AATGGAAGTT CGTGAACCTT TGTCTCAGTA CGACTTCCCG GGCGATGACA 200
 CTCCAATCAT CCGTGGTTCT GCTCTGAAAG CGCTGGAAGG CGAAGCAGAG 250
 TGGGAAGCTA AAATYGTGTA GCTGGCTGGC TTCCTGGATT CCTACATCCC 300
 AGAACCAGTA CGTGCAATCG AYCTGCCGTT CCTGCTGCCA ATCGAAGACG 350
 TATTCTCCAT CTCCGGCCGT GGTACCGTTG TTACCGGTCTG TGTAGAGCGC 400
 GGTATCGTTA AAGTGGGCGA AGAAGTAGAA ATCGTTGGTA TCAAAGATAC 450
 30 TGCGAAATCT ACCTGTACCG GCGTTGAAAT GTTCCGCAA CTGCTGGACG 500
 AAGGCCGTGC TGGTGAGAAC GTTGGTGTTC TGCTGCGTGG TATCAAACGT 550
 GAAGAAATCG AACGTGGTCA GGTCTGCTG AAGCCAGGCT CTATCAAGCC 600
 GCACACCAAG TTCGAATCTG AAGTGTACAT CCTGTCCAA GACGAAGGCG 650
 GCCGTCTATC TCCGTTCTTC AAAGGCTACC GTCCACAGTT CTACTTCCGT 700
 35 ACAACTGACG TGACCGGTAC CATCGAACTG CCAGAAAGGCG TAGAGATGGT 750
 AATGCCAGGC GACAACATCA AAATGGTTGT TACCCTGATC CACCCAATCG 800
 CGATGGACGA CCGTCTGCGT TTCG 824

40 2) INFORMATION FOR SEQ ID NO: 19

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 bases
 45 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cedecea lapagei*
 (B) STRAIN: ATCC 33432

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19

CGCTATTCTG GTTGTGCTG CAACTGACGG CCCTATGCCT CAGACCCGTG 50
 AGCACATCCT GCTGGGTCGC CAGGTTGGCG TTCCTTACAT CATCGTGTTT 100
 CTGAACAAAT GTGACATGGT TGATGACGAA GAGCTGCTGG AGCTGGTAGA 150
 60 AATGGAAGTT CGTGAACCTT TGTCTCAGTA CGACTTCCCA GGCGATGATA 200

CCCC AATCAT CCGTGGTTCT GCTCTGAAAG CGCTGGAAGG CGAAGCAGAG 250
 TGGGAAGCTA AAATCGTTGA GCTGGCTGGC TTCCTGGATT CCTACATCCC 300
 AGAACCAGTA CGTGCAATCG ACCTGCCGTT CCTGCTGCCA ATCGAAGACG 350
 TATTCTCCAT CTCCGGCCGT GGTACCGTTG TKACCGGTCG TG TAGAGCGC 400
 5 GGTATCGTTA AAGTGGGCGA AGAAGTAGAA ATCGTTGGTA TCAAAGATAC 450
 TGC GAAATCT ACCTGTACTG GCGTTGAAAT GTTCCGCAA CTGCTGGACG 500
 AAGGCCGTGC TGGTGAGAAC GTTGGTGTTT TGCTGCGTGG TATCAAACGT 550
 GAAGAAATCG AACGTGGTCA GGTCTGGCT AAGCCAGGCT CTATCAAGCC 600
 GCACACCAAG TTCGAATCTG AAGTGATACAT CCTGTCCAAA GACGAAGGCG 650
 10 GCCGTCATAC TCCGTTCTTC AARGGCTACC GTCCACAGTT CTACTTCCGT 700
 ACCACTGACG TGACCGGTAC CATCGAACTG CCAGAAGGCG TAGAGATGGT 750
 AATGCCAGGT GACAACATCA AAATGGTTGT TACCCTGATC CACCCAATCG 800
 CGATGGACGA CCGTCTGCGT TTCGCAA 827

15

2) INFORMATION FOR SEQ ID NO: 20

(i) SEQUENCE CHARACTERISTICS:
 20 (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: Genomic DNA
 25 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Chlamydia pneumoniae*
 (B) STRAIN: CLW 029

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20

GCGGAGCTAT CCTAGTCGTT TCAGCTACAG ACGGAGCTAT GCCACAACT 50
 AAAGAACATA TCTTGCTAGC TCGCCAGGTT GGAGTTCCTT ATATCGTTGT 100
 35 TTTCTTGAAT AAAGTAGATA TGATCTCTCA AGAAGATGCT GAACTTATTG 150
 ACCTTGTTGA GATGGAACCTT AGTGAGCTTC TTGAAGAAAA AGGCTACAAA 200
 GGATGCCCTA TTATCCGTGG TTCTGCTTTG AAAGCTCTTG AAGGTGATGC 250
 AAATTATATC GAAAAAGTTC GAGAACTTAT GCAAGCTGTG GATGACAACA 300
 TCCCTACACC AGAAAGAGAA ATTGATAAGC CTTTCTTAAT GCCTATCGAA 350
 40 GACGTATTCT CAATCTCTGG TCGTGGTACT GTGGTTACAG GAAGAATCGA 400
 GCGTGGAATC GTTAAAGTTT CTGATAAAGT TCAGCTCGTG GGATTAGGAG 450
 AGACTAAAGA AACAAATCGTT ACTGGAGTCG AAATGTTTCA GAAAGAACTT 500
 CCTGAAGGTC GTGCAGGAGA AAACGTTGGT TTACTCCTCA GAGGTATTGG 550
 AAAGAACGAT GTTGAAAGAG GTATGGTGGT TTGTCAGCCT AACAGCGTGA 600
 45 AGCCTCATAC GAAATTTAAG TCAGCTGTTT ACGTTCTTCA GAAAGAAGAA 650
 GCGCGACGTC ATAAGCCTTT CTTCAGCGGA TACAGACCTC AGTTCTTCTT 700
 CCGTACTACA GACGTGACAG GAGTCGTAAC TCTTCCTGAA GGAAGTGAAG 750
 TGGTAATGCC TGGAGATAAC GTTGAGCTTG ATGTTGAGCT CATTGGAACA 800
 GTTGCTCTTG AAGAAGGAAT GAGATTTGCA A 831

50

2) INFORMATION FOR SEQ ID NO: 21

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Chlamydia psittaci*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21

	TGGAGCGATT	CTCGTTGTTT	CCGCTACTGA	CGGTGCGATG	CCTCAGACCA	50
	AAGAACATAT	TCTTTTGGCG	AGACAGGTTG	GTGTTCTTA	CATCGTTGTT	100
10	TTCCTTAACA	AAATCGATAT	GATTTCTCAA	GAAGATGCTG	AGCTCGTAGA	150
	CTTAGTTGAA	ATGGAATTGT	CCGAACCTCT	AGAAGAAAAA	GGTTATAAAG	200
	GTTGCCCAAT	TATCCGTGGT	TCTGCTTTGA	AAGCCTTAGA	AGGTGATGCA	250
	AGCTACGTTG	AAAAAATTCG	CGAGTTAATG	CAAGCAGTGG	ATGATAACAT	300
	CCCTACTCCA	GAGCGTGAAG	TTGATAAGCC	TTTCTTAATG	CCTATCGAAG	350
15	ACGTATTCTC	TATTTCTGGT	CGTGGTACTG	TGGTCACAGG	ACGTATCGAG	400
	CGTGGAATCG	TTAAAGTGGG	TGATAAAGTA	CAGATTGTTG	GTTTAAGAGA	450
	TACTAGAGAG	ACAATTGTTA	CCGGTGTGGA	AATGTTTCAGA	AAAGAACTTC	500
	CAGAAGGTCA	AGCAGGGGAA	AACGTTGGTT	TGCTCCTCAG	AGGTATCGGT	550
	AAGAATGACG	TTGAACGTGG	TATGGTTATC	TGCCAACCTA	ATAGCGTGAA	600
20	ATCTCACACA	CAATTTAAAG	GTGCTGTCTA	CATTCTACAA	AAAGAAGAGG	650
	GTGGACGTCA	TAAACCTTTC	TTTACCGGAT	ACAGACCTCA	GTTCTTCTTC	700
	CGTACAACAG	ATGTTACAGG	TGTTGTAAct	CTCCCAGAAG	GTACAGAGAT	750
	GGTTATGCCA	GGCGATAACG	TTGAATTCTGA	AGTTCAATTA	ATTAGCCCAG	800
25	TAGCTCTAGA	AGAAGGTATG	AGATTT			826

2) INFORMATION FOR SEQ ID NO: 22

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Chlamydia trachomatis*

(B) STRAIN: LGV 12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22

	GGGGCTATTC	TAGTAGTTTC	TGCAACAGAC	GGAGCTATGC	CTCAAACATAA	50
45	AGAGCATATT	CTTTTGGCAA	GACAAGTTGG	GGTTCCTTAC	ATCGTTGTTT	100
	TTCTCAATAA	AATTGACATG	ATTTCCGAAG	AAGACGCTGA	ATTGGTCGAC	150
	TTGGTTGAGA	TGGAGTTGGC	TGAGCTTCTT	GAAGAGAAAG	GATACAAAGG	200
	GTGTCCAATC	ATCAGAGGTT	CTGCTCTGAA	AGCTTTGGAA	GGGGATGCTG	250
	CATACATAGA	GAAAGTTCGA	GAGCTAATGC	AAGCCGTCGA	TGATAATATC	300
50	CCTACTCCAG	AAAGAGAAAT	TGACAAGCCT	TTCTTAATGC	CCATTGAGGA	350
	CGTGTCTCT	ATCTCCGGAC	GAGGAACGTG	AGTAACTGGA	CGTATTGAGC	400
	GTGGAATTGT	TAAAGTTTCC	GATAAAGTTC	AGTTGGTCGG	TCTTAGAGAT	450
	ACTAAAGAAA	CGATTGTTAC	TGGGGTTGAA	ATGTTTCAGAA	AAGAAGTCCC	500
	AGAAGGTTCG	GCAGGAGAGA	ATGTTGGATT	GCTCCTCAGA	GGTATTGGTA	550
55	AGAACGATGT	GGAAAGAGGA	ATGGTTGTTT	GCTTGCCAAA	CAGTGTTAAA	600
	CCTCATACAC	GGTTTAAGTG	TGCTGTTTAC	GTTCTGCAAA	AAGAAGAAGG	650
	TGGACGACAT	AAGCCTTTCT	TCACAGGATA	TAGACCTCAA	TTCTTCTTCC	700
	GTACAACAGA	CGTTACAGGT	GTGGTAACCT	TGCCTGAGGG	AGTTGAGATG	750
60	GTCATGCCTG	GGGATAACGT	TGAGTTTGAA	GTGCAGTTGA	TTAGCCCTGT	800
	GGCTTTAGAA	GAAGGTATGA	GA			822

2) INFORMATION FOR SEQ ID NO: 23

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Chryseobacterium meningosepticum*
 (B) STRAIN: CDC B7681

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23

20	CGGAGCTATC	TTAGTATGTG	CTGCTACAGA	TGGTCCAATG	CCTCAAACCTA	50
	GAGAACACAT	CCTACTTTGC	CGTCAGGTAA	ACGTACCTAG	AATTGTTGTG	100
	TTCATGAACA	AAGTTGACAT	GGTAGATGAT	CCAGAATTGT	TAGAGCTTGT	150
	TGAGCTTGAA	CTTAGAGATC	TATTATCTAC	TTACGAATAT	GATGGTGATA	200
	ACTCTCCAGT	AATTCAAGGT	TCTGCTCTTG	GTGCTCTTAA	CGGTGATGCT	250
	ACTCTCCAGT	AATTCAAGGT	TCTGCTCTTG	GTGCTCTTAA	CGGTGATGCT	300
25	AAGTGGGTAG	CTACTGTAGA	AGCTCTAATG	GATGCTGTTG	ATACTTGAT	350
	CGAGCAACCA	GTAAGAGATT	CTGATAAGCC	ATTCTTATG	CCAATCGAAG	400
	ACGTATTCTC	TATTACAGGT	AGAGGTAAGT	TAGCAACTGG	TAGAATCGAG	450
	GCTGGTGTA	TCAACACAGG	TGATCCTGTT	GACATCGTAG	GTATGGGTGA	500
	CGAGAAGTTA	ACTTCTACTA	TTACAGGTGT	TGAGATGTTT	AGAAAAATCC	550
30	TAGACAGAGG	TGAAGCTGGT	GATAACGTAG	GTCTATTGTT	GAGAGGTATT	600
	GAAAAGACTG	ACATCAAGAG	AGGTATGGTT	ATCGCTAAGA	AAGATTTCAGT	650
	TAAGCCACAC	AAGAAATTCA	AAGCTGAGGT	TTATATCCTT	TCTAAAGAAG	700
	AAGGTGGACG	TCACACTCCA	TTCCACAACA	AATACCGTCC	TCAGTTCTAT	750
	GTAAGAACTA	CTGACGTTAC	AGGTGAAATC	TTCTTACCAG	AAGGTGTAGA	800
35	AATGGTAATG	CCTGGTGATA	ACTTAACTAT	CACTGTAGAA	TTGTTACAAC	835
	CAATCGCTCT	TAACGAGGGT	CTTAGATTCTG	CGATC		

2) INFORMATION FOR SEQ ID NO: 24

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter amalonaticus*
 (B) STRAIN: ATCC 25405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24

55	CGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACTC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	100
	TTCCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	AGAAATGGAA	GTTTCGTGAAC	TTCTGTCTCA	GTACGATTTC	CCGGGCGACG	200
60	ACACCCCGAT	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGACGCA	250

GAGTGGGAAG CGAAAATCAT CGAACTGGCC GGCTTCCTGG ATTCTTACAT 300
 CCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG 350
 ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAA 400
 CGCGGTATCA TCAAAGTGGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA 450
 5 GACTGCCAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAAGTGTGCTGG 500
 ACGAAGGCCG TCGGGGTGAG AACGTTGGTG TTCTGCTGCG TGGTATCAAA 550
 CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCCG GCWCCATCAA 600
 GCCGCACACC ATGTTTCAAT CYGAAGTGTA CATCCTGTCC AAAGACGAAG 650
 GCGGCCCGTCA TACTCCGTTT TTCAAAGGCT ACCGTCCGCA GTTCTACTTC 700
 10 CGTACAACCTG ACGTGAAGTG CACCATCGAA CTGCCGGAAG GCGTTGAGAT 750
 GGTAAATGCCG GGCAGACAAC TCAAATGGT TGTACCCTG ATCCACCCGA 800
 TCGCGATGGA CGACGG 816

15

2) INFORMATION FOR SEQ ID NO: 25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter braakii*
 (B) STRAIN: ATCC 43162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25

CGCGATCCTG GTTGTGCTG CAACTGACGG CCCGATGCCG CAGACTCGTG 50
 AGCACATCCT GCTGGGTCGY CAGGTAGGCG TTCCGTACAT CATCGTGTTT 100
 CTGAACAAAT GCGACATGGT TGATGACGAA GAGCTGCTGG AACTGGTAGA 150
 35 AATGGAAGTT CGTGAAGTTC TGTCTCAGTA CGATTTCCCG GCGACGACA 200
 CGCCGATCGT TCGTGGTTCT GCTCTGAAAG CGCTGGAAGG CGAWGCAGAG 250
 TGGGAAGCGA AAATCATCGA ACTGGCTGGC TTCCTGGATT CTTACATCCC 300
 GGAACCAGAG CGTGCGATTG ACAAGCCGTT CCTGCTGCCT ATCGAAGACG 350
 TATTCTCCAT CTCTGGTCGT GGTACCGTTG TTACCGGTCG TGTAAGAGCGC 400
 40 GGTATCATCA AAGTTGGTGA AGAAGTTGAA ATCGTTGGTA TCAARGACAC 450
 TGCTAAGTCT ACCTGTACTG GCGTTGAAAT GTTCCGCAA CTGCTGGACG 500
 AAGGCCGTGC TGGTGAGAAC GTTGGTGTTC TGCTGCGTGG TATCAAGCGT 550
 GAAGAAATCG AACGTGGTCA GGTACTGGCT AAGCCGGGCT CTATCAAGCC 600
 GCACACCAAG TTCGAATCTG AAGTGTACAT TCTGTCCAAA GACGAAGGCG 650
 45 GCCGTCATAC TCCGTTCTTC AARGGCTACC GTCCGCAGTT CTACTTCCGT 700
 ACTACTGACG TGACTGGTAC CATCGAAGTG CCGGAAGGCG TTGAGATGGT 750
 AATGCCGGGC GACAACATCA AAATGGTTGT TACCCTGATC CACCCAATCG 800
 CGATGGACGA CGGTCTGCGT TTCGC 825

50

2) INFORMATION FOR SEQ ID NO: 26

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter koseri*
 (B) STRAIN: ATCC 27156

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26

	CGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCCGATG	CCGCAGACCC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	100
10	TTCCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	TGAGATGGAA	GTGCGTGAAC	TGCTGTCTCA	GTACGATTTC	CCGGGCGACG	200
	ACACGCCGAT	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGAMGCT	250
	GAGTGGGAAG	CGAAAATCAT	CGAACTGGCT	GGCTACCTGG	ATTCTTACAT	300
	CCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	GTTCTGTCTG	CCGATCGAAG	350
15	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
	CGCGGTATCA	TCAAAGTGGG	CGAAGAAAGT	GAAATYGTTG	GTATCAAAGA	450
	GACTGCGAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TGCAACGTGG	TCAGGTACTG	GCTAAGCCGG	GYTCCATCAA	600
20	GCCGCACACC	AAGTTCGAAT	CTGAAGTGTA	CATYCTGTCY	AAAGATGAAG	650
	GCGGCCGTCA	TACTCCGTTC	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACAACCTG	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
	GGTAATGCCG	GGCGACAACA	TCAAATGGT	TGTTACCCTG	ATCCACCCGA	800
25	TCGCGAGGAC	GACGGTCTGC	GTTTCGCAA			829

2) INFORMATION FOR SEQ ID NO: 27

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter farmeri*
 (B) STRAIN: ATCC 51112

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27

	CGCGATCCTG	GTTGTTGCTG	CGACTGACGG	CCCGATGCCG	CAGACTCGTG	50
45	AGCACATCCT	GCTGGGTCGT	CAGGTAGGCG	TTCCGTACAT	CATCGTGTTT	100
	CTGAACAAAT	GCGACATGGT	TGATGACGAA	GAGCTGCTGG	AACTGGTAGA	150
	GATGGAAGTT	CGTGAAGTGC	TGTCTCAGTA	CGATTTCCCG	GGCGACGACA	200
	CGCCGATCGT	TCGTGGTTCT	GCTCTGAAAG	CGCTGGAAGG	CGACGCAGAG	250
	TGGGAAGCGA	AAATCATCGA	ACTGGCAGGC	TTCTTGGATT	CTTACATCCC	300
50	GGAACCAGAG	CGTGCGATTG	ACAAGCCGTT	CCTGCTGCCG	ATCGAAGACG	350
	TATTCTCCAT	CTCTGGTCGT	GGTACCGTTG	TTACCGGTCG	TGTAGAGCGC	400
	GGTATCATCA	AAGTGGGTGA	AGAAGTTGAA	ATCGTTGGTA	TCAAAGAGAC	450
	TGCCAAGTCT	ACCTGTACTG	GCGTTGAAAT	GTTCCGCAAA	CTGCTGGACG	500
	AAGGCCGTGC	TGGTGAGAAC	GTAGGTGTTT	TGCTGCGTGG	TATCAAACGT	550
55	GAAGAAATCG	AACGTGGTCA	GGTACTGGCT	AAGCCGGGCW	CCATCAAGCC	600
	RCACACTATG	TTCGAATCTG	AAGTGTACAT	TCTGTCCAAA	GACGAAGGCG	650
	GCCGTCATAC	TCCGTTCTTC	AAAGGCTACC	GTCCGCAGTT	CTACTTCCGT	700
	ACGACTGACG	TGACTGGCAC	CATCGAACTG	CCGGAAGGTG	TTGAGATGGT	750
	TATGCCGGGC	GACAACATCA	AAATGGTTGT	TACCCTGATC	CACCCGATCG	800
60	CGATGGACGA	CGGTCTGCGT	TTCGCAA			827

2) INFORMATION FOR SEQ ID NO: 28

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 797 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter freundii*
 (B) STRAIN: ATCC 8090

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28

20	CCTGGTTGTT	GCTGCGACTG	ACGGCCCGAT	GCCGCAGACT	CGTGAGCACA	50
	TCCTGCTGGG	TCGTCAGGTA	GGCGTTCCGT	ACATCATCGT	GTTCTGAAC	100
	AAATGCGACA	TGGTTGATGA	CGAAGAGCTG	CTGGAAGTGG	TAGAAATGGA	150
	AGTTCGTGAA	CTTCTGTCTC	AGTACGATTT	CCCGGGCGAC	GACACTCCGA	200
	TCGTTTCGTGG	TTCTGCTCTG	AAAGCGCTGG	AAGGCGAAGC	AGAGTGGGAA	250
25	GCGAAAATCA	TCGAACTGGC	TGGCTTCCTG	GATTCTTACA	TCCCAGAACC	300
	AGAGCGTGCG	ATTGACAAGC	CGTTCCTGCT	GCCTATCGAA	GACGTATTCT	350
	CCATCTCCGG	TCGTGGTACC	GTTGTTACCG	GTCGTGTAGA	GCGCGGTATC	400
	ATCAAAGTTG	GTGAAGAAGT	TGAAATCGTT	GGTATCAAAG	AGACTGCTAA	450
	GTCTACCTGT	ACTGGCGTTG	AAATGTTCCG	CAAAGTCTG	GACGAAGGCC	500
30	GTGCTGGTGA	GAACGTTGGT	GTTCTGCTGC	GTGGTATCAA	ACGTGAAGAA	550
	ATCGAACGTG	GTCAGGTACT	GGCTAAGCCG	GGCTCTATCA	AGCCGCACAC	600
	CAAGTTCGAA	TCTGAAGTGT	ACATTCTGTC	CAAAGACGAA	GGCGGCCGTC	650
	ATACTCCGTT	CTTCAAAGGC	TACCGTCCGC	AGTTCTACTT	CCGTACTACT	700
	GACGTGACTG	GTACCATCGA	ACTGCCGGAA	GGCGTAGAGA	TGGTAATGCC	750
35	GGGCGACAAC	ATCAAAATGG	TTGTTACCCT	GATCCACCCA	ATCGCGA	797

2) INFORMATION FOR SEQ ID NO: 29

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter sedlakii*
 (B) STRAIN: ATCC 51115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29

55	CGGCGCGATC	CTGGTTGTTG	CCGCGACTGA	CGGCCCGATG	CCGCAGACCC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	100
	TTCCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	AGAGATGGAA	GTTTCGTGAAC	TGCTGTCTCA	GTACGATTTT	CCGGGCGACG	200
	ACACGCCGAT	CGTTCGTGGT	TCAGCTCTGA	AAGCGCTGGA	AGGCGACGCA	250
60	GAGTGGGAAG	CGAAAATCAT	CGAACTGGCT	GGCTTCCTGG	ATTCTTACAT	300

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TCCGGAACCA GAGCGTGC GA TTTGACAAGCC GTTCCTGCTG CCGATCGAAG 350
ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAG 400
CGCGGTATCA TCAAAGTGGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA 450
GACTGCCGAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAAGTGTCTGG 500
5 ACGAAGGCCG TCGGGGTGAG AACGTAGGTG TTCTGCTGCG TGGTATCAAA 550
CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCGAAGCCGG GCACCATCAA 600
GCCGCACACC AAGTTCGAAT CTGAAGTGTA TATTCTGTCC AAAGATGAAG 650
GCGGCCGTCA TACTCCGTTT TTCAAAGGCT ACCGTCCGCA GTTCTACTTC 700
CGTACAAC TG ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTAGAGAT 750
10 GGTAATGCCG GCGACAACA TCAAATGGT TGTTACCTG ATCCACCCGA 800
TCGCGATGGA CGACGGTCTG CGTTTC 826

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15 2) INFORMATION FOR SEQ ID NO: 30

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 823 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Citrobacter werkmanii*
(B) STRAIN: ATCC 51114

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30

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30 GCGATCCTGG TTGTTGCTGC GACTGACGGC CCGATGCCGC AGACTCGTGA 50
GCACATCCTG CTGGGTCGTC AGGTAGGCGT TCCGTACATC ATCGTGTTC 100
TGAACAAATG CGACATGGTT GATGACGAAG AGCTGCTGGA ACTGGTAGAA 150
ATGGAAGTTC GTGAAC TTCT GTCTCAGTAC GATTTC CCGG GCGACGACAC 200
35 TCCGATCGTT CGTGGTTCTG CTCTGAAAGC GCTGGAAGGC GAAGCAGAGT 250
GGGAAGCGAA AATCATCGAA CTGGCTGGCT TTCTGGATTC TTACATCCCG 300
GAACCAGAGC GTGCGATTGA CAAGCCGTTT CTGCTRCCTA TCGAAGACGT 350
ATTCTCCATC TCCGGTCGTG GTACCGTTGT TACCGGTCGT GTAGAGCGCG 400
GTATCATCAA AGTTGGTGAA GAAGTTGAAA TCGTTGGTAT CAAAGACACC 450
40 GCTAAGTCTA CCTGTACCGG CGTTGAAATG TTCCGCAAAC TGCTGGACGA 500
AGGCCGTGCT GGTGAGAACG TTGGTGTTC GCTGCGTGGT ATCAAACGTG 550
AAGAAATCGA ACGTGGTCAG GTACTGGCTA AGCCGGGCTC TATCAAGCCG 600
CACACCAAGT TCGAATCTGA AGTGATACAT CTGTCCAAAG ACGAAGGCGG 650
CCGTCATACT CCGTTCTTCA AAGGCTACCG TCCGCAGTTC TACTTCCGTA 700
45 CTACTGACGT GACTGGTACC ATCGAAGTGC CGGAAGGCGT AGAGATGGTA 750
ATGCCGGGCG ACAACATYAA AATGGTTGTT ACYCTGATCC ACCCGATCGC 800
GATGGACGAC GGTCTGCGTT TCG 823

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50 2) INFORMATION FOR SEQ ID NO: 31

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 826 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter youngae*
 (B) STRAIN: ATCC 29935

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31

	GGCGCGATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCGATGC	CGCAGACTCG	50
	TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	100
	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTA	150
10	GAAATGGAAG	TTCGTGAACT	TCTGTCTCAG	TACGATTTC	CGGGCGACGA	200
	TACGCCGATC	GTTTCGTGGT	CTGCTCTGAA	AGCGCTGGAA	GGCGAAGCAG	250
	AGTGGGAAGC	GAAAATCATC	GAAGTGGCTG	GCTTCCTGGA	TTCTTACATC	300
	CCGGAACCAG	AACGTGCTAT	CGATAAGCCG	TTCCTGCTGC	CAATCGAAGA	350
	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACTGGT	CGTGTAGAAC	400
15	GCGGTATCAT	CAAAGTTGGT	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAG	450
	ACTGCCAAGT	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCTGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTATCAAAC	550
	GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CTCTATCAAG	600
	CCGCACACCA	AGTTCGAATC	TGAAGTGTAC	ATTCTGTCCA	AAGACGAAGG	650
20	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	700
	GTACTACTGA	CGTGACGGGT	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	750
	GTAATGCCGG	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TCCACCCAAT	800
	CGCGATGGAT	GACGGTCTGC	GTTTCG			826

25

2) INFORMATION FOR SEQ ID NO: 32

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 841 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium perfringens*
 (B) STRAIN: ATCC 13124

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32

	CGGAGCTATA	TTAGTTTGTT	CAGCAGCTGA	TGGTCCAATG	CCTCAAACAA	50
	GAGAGCACAT	CTTATTATCA	TCAAGAGTTG	GAGTTGACCA	CATCGTAGTA	100
45	TTCTTAAACA	AAGCAGATAT	GGTTGACGAC	GAAGAATTAT	TAGAATTAGT	150
	TGAAATGGAA	GTTAGAGAGT	TATTAAGCGA	GTACAACTTC	CCAGGAGACG	200
	AYATTCCAGT	AATCAARGGA	TCAGCTTTAG	TAGCATTAGA	AAACCCAACT	250
	GACGAAGCTG	CAACAGCTTG	TATCAGAGAG	TTAATGGATG	CTGTAGATAG	300
	CTACATCCCA	ACACCAGAAA	GAGCAACAGA	TAAGCCATTC	TTAATGCCAG	350
50	TAGAGGACGT	ATTCAACAATC	ACTGGTAGAG	GAACAGTTGC	AACAGGAAGA	400
	GTTGAAAGAG	GAGTTCTACA	TGTAGGAGAC	GAAGTAGAAG	TAATCGGATT	450
	AACTGAAGAA	AGAAGAAAAA	CTGTTGTAAC	AGGAATCGAA	ATGTTTCAGAA	500
	AGTTATTAGA	TGAAGCACAA	GCTGGAGATA	ACATCGGAGC	ATTATTAAGA	550
	GGTATCCAAA	GAAGTGAAT	CGAAAGAGGT	CAAGTTTTAG	CTCAAGTTGG	600
55	AACAATCAAC	CCACACAAAA	AATTCGTAGG	TCAAGTATAC	GTAAGTAAAA	650
	AAGAAGAAGG	TGGAAGACAT	ACTCCATTCT	TCGATGGATA	CAGACCACAA	700
	TTCTACTTCA	GAACAACAGA	CGTTACAGGA	TCAATCAAAT	TACCAGAAGG	750
	AATGGAAATG	GTTATGCCTG	GAGACCACAT	CGACATGGAA	GTTGAATTAA	800
60	TCACAGAAAT	CGCTATGGAY	GAAGGATTAA	GATTCGCTAT	C	841

2) INFORMATION FOR SEQ ID NO: 33

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Comamonas acidovorans*
 (B) STRAIN: ATCC 15668

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33

20	CGGCGCCATC	CTGGTGTGCT	CGGCCGCTGA	CGGCCCCATG	CCCCAGACCC	50
	GCGAGCACAT	CCTGCTGGCC	CGTCAGGTGG	GCGTGCCCTA	CATCATCGTG	100
	TTCCTGAACA	AGTGCGACAT	GGTGGACGAC	GAAGAGCTGC	TGGAAGTGGT	150
	CGAAATGGAA	GTGCGCGAGC	TGCTTGCCAA	GTACGACTTC	CCCGGCGACG	200
	ACACCCCCAT	CATCCGCGGC	TCGGCCAAGC	TGGCCCTGGA	AGGCGACCAG	250
	TCCGACAAGG	GCGAACCTGC	CATCCTGCGC	CTGGCTGAAG	CACTGGACTC	300
25	CTACATCCCC	ACGCCCCGAGC	GCGCTGTGGA	CGGCGCCTTT	GCAATGCCCG	350
	TGGAAGACGT	GTTCTCGATC	TCTGGCCGTG	GCACCGTGGT	GA CTGGCCGT	400
	ATCGAGCGCG	GCATCATCAA	GGTCGGCGAA	GAAATCGAAA	TCGTCGGTAT	450
	CCGCGACACC	CAGAAGACCA	TCGTCACCGG	CGTGGAAATG	TTCCGCAAGC	500
	TGCTGGACCA	AGGTCAAGCT	GGCGACAACG	TGGGTCTGCT	GCTGCGCGGC	550
30	ACCAAGCGTG	AAGACGTGGA	ACGCGGCCAA	GTGCTGTGCA	AGCCCGGCTC	600
	CATCAAGCCC	CACACCCACT	TCACGGCTGA	GGTGTACGTG	CTGTCCAAGG	650
	ACGAAGGTGG	TCGCCACACT	CCGTTCTTCA	ACA ACTACCG	TCCCCAGTTC	700
	TATTTCCGTA	CGACCGACGT	GACCGGCTCC	ATCGAGCTGC	CCGCCGACAA	750
	GGAAATGGTG	ATGCCTGGCG	ACAACGTGTC	GATCACCCTC	AAGCTGATCG	800
35	CCCCCATCGC	CATGGAAGAA	GG			822

2) INFORMATION FOR SEQ ID NO: 34

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 702 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium bovis*
 (B) STRAIN: ATCC 7715

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34

55	GCCGCGAGACC	CGTGAGCACG	TCCTCCTGGC	CCGTCAGGTC	GGTGTGCCCT	50
	ACATCCTCGT	CGCCCTCAAC	AAGTGCGACA	TGGTCGACGA	CGAGGACCTC	100
	ATCGAGCTCG	TCGAGATGGA	GGTCCGTGAG	CTCCTCGCCG	AGCAGGACTA	150
	CGACGAGGAC	GCCCCGATCA	TCCACATCTC	CGCCCTCAAG	GCCCTCGAGG	200
	GTGACCCGGA	GTGGACGCAG	CGCATCGTCG	ACCTCATGAA	GGCCTGCGAC	250
60	GACGCCATCC	CGGATCCGGA	GCGCGAGACG	GACAAGCCGT	TCCTCATGCC	300

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GATCGAGGAC ATCTTCACGA TCACCGGCCG CGGCACCGTC GTCACGGGCC 350
GTGTCGAGCG TGGCATCCTC AACGTCAACG AGGAGGTCGA GATCCTGGGT 400
ATCTGCGAGA ACTCCCAGAA GACGACCGTC ACCTCCATCG AGATGTTCAA 450
CAAGTTCCTC GACACGGCCG AGGCCGGCGA CAACGCCGCC CTGCTGCTCC 500
5 GTGGCCTGAA GCGCGAGGAC GTCGAGCGTG GCCAGATCGT GGCCAAGCCG 550
GGCGCCTACA CGCCGCACAC CGAGTTCGAG GGCTCCGTGT ACATCCTCTC 600
CAAGGACGAG GGTGGCCGCC ACACGCCGTT CTTGACAAC TACCGTCCGC 650
AGTTCTACTT CCGGACGACC GACGTCACCG GCGTCGTCAA GCTGCCGGAG 700
GG 702
10

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2) INFORMATION FOR SEQ ID NO: 35

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15 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 689 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
20

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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25 (A) ORGANISM: Corynebacterium cervicis
    (B) STRAIN: NCTC 10604

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35

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30 GGCTCAGACC CGCGAGCACG TTCTGCTTGC TCGCCAGGTT GGC GTTCCGA 50
CGATCCTGGT TGCCCTCAAC AAGGCCGATA TGGTCGACGA TGAGGAAATG 100
CTGGAGCTCG TTGAGGAAGA GTGCCGCGAC CTGCTCGAGT CCCAGGACTT 150
CGATCGTGAC GCCCCGATCA TCCAGGTTTC CGCGCTGAAG GCTCTCGAAG 200
GTGATCCGCA GTGGGTTGCT AAGGTCGAGG AGCTCATGGA GGCAGTCGAC 250
ACCTTCGTGC GACTCCTGA GCGCGACATG GACAAGCCGT TCCTCATGCC 300
35 GATCGAAGAC GTCTTCACCA TCACCGGCCG TGGCACCGTT GTTACCGGTC 350
GTGTTGAGCG TGGCAAGCTC CCGATCAACT CTGAGGTTGA AATCCTCGGT 400
ATCCGCGAAC CGCAGAAGAC CACCGTTACC GGTATCGAGA TGTTCCACAA 450
GTCCATGGAT GAAGCATGGG CAGGCGAGAA CTGTGGTCTC CTCCTGCGTG 500
GCACCAAGCG CGATGAGGTT GAGCGCGGTC AGGTCGTTGC CGTTCCCGGT 550
40 TCGATACCC CGCACACCAA CTTACCGGA CAGGTCTACA TCCTCAAGAA 600
GGAAGAAGGC GGTGTCACA ACCCGTTCTT CTCGAACTAC CGTCCGCAGT 650
TCTACTTCCG CACCACGGAC GTGACCGGCG TCATCACCC 689

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45

2) INFORMATION FOR SEQ ID NO: 36

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50 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 804 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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55 (A) ORGANISM: Corynebacterium flavescens
    (B) STRAIN: ATCC 10340

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36

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GGTTGTTGCT GCAACCGATG GTCCTATGCC GCAGACCCGC GAGCACGTTC      50
TTCTGGCTCG CCAGGTTGGC GTTCCTTACA TCCTCGTTGC TCTTAACAAG      100
TGCGACATGG TTGATGATGA GGAAATCATC GAGCTCGTTG AGATGGAAAT      150
5 CCGCGAACTG CTCGCTGAGC AGGACTACGA CGAGGATGCC CCCATCATCC      200
ACATCTCCGC TCTCAAGGCT CTTGAGGGTG ACGAGAAGTG GGTACAGGCC      250
ATCGTCGACC TCATGCAGGC CTGCGATGAC TCCATTCCGG ATCCGGAGCG      300
CGAGACCGAC AAGCCCTTCC TCATGCCTAT CGAGGACATC TTCACCATCA      350
CCGGCCGCGG TACCGTTGTT ACCGGCCGTG TTGAGCGTGG CGTTTTGAAG      400
10 GTCAACGAGG ATGTTGAGAT CATCGGCATC AAGGAGAAAGT CCATCTCCAC      450
CACCGTTACC GGTATCGAAA TGTTCCGCAA GATGATGGAC TACACCGAGG      500
CTGGCGACAA CTGTGGTCTG CTTCTGCGTG GTACCAAGCG TGAAGAGGTC      550
GAGCGCGGCC AGGTTGTTAT CAAGCCGGGC GCCTACACCC CCCACACCAA      600
GTTCGAGGGT TCCGTCTACG TCCTCAAGAA GGAAGAGGGC GGCCGCCACA      650
15 CCCC GTTCAT GGACAACTAC CGTCCGCAGT TCTACTCCG TACCACTGAC      700
GTGACCGGCG TTGTTCACCT GCCTGAGGGC ACCGAGATGG TCATGCCTGG      750
CGACAACGTT GATATGACCG TTGAGTCTAT CCAGCCCGTC GCTAGGATGA      800
GGGC

```

20

2) INFORMATION FOR SEQ ID NO: 37

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 692 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium kutscheri*
 (B) STRAIN: ATCC 15677

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37

```

TGCCTCAGAC CCGTGAGCAC GTTCTTCTTG CTCGCCAGGT TGGCGTTCCT      50
TACATCCTCG TTGCTCTTAA CAAGTGCGAC ATGGTTGACG ATGAGGAAAT      100
40 CATCGAGCTC GTTGAGATGG AAGTTCGCGA GCTTCTTGCT GAGCAGGAGT      150
ACGATGAAGA GGCTCCAATC ATCCACATCT CTGCTTTGAA GGCTCTTGAG      200
GGCGACGAGA AGTGGACTCA GGCCATCATC GACCTCATGC AGGCTTGTA      250
TGA CTCCATC CCAGATCCAG AGCGTGAGAC CGACAAGCCA TTCCTCATGC      300
CTATCGAGGA TATCTTCACC ATCACC GGTC GTGGCACC GTTTACCGGT      350
45 CGTGTGAGC GCGGTTCTT GAAGGTGAAT GAGGACGTCG AGATCATCGG      400
CATCAAGGAG AAGTCCACCA CTACTACCGT TACCGGTATC GAAATGTTCC      450
GTAAGCTTCT TGATTACACC GAAGCTGGCG ATA ACTGTGG TCTGCTTCTT      500
CGTGGTATCA AGCGCGAAGA CGTTGAGCGT GGTCAGGTTG TTGTTAAGCC      550
AGGCGCTTAC ACACCTCACA CCGAGTTCGA GGGCTCTGTT TACGTTCTTT      600
50 CCAAGGACGA GGGCGGCCGC CACACCCCAT TCTTCGACAA CTACCGTCCA      650
CAGTTCTACT TCCGCACCAC TGACGTTACC GGTGTTGTGA AG      692

```

55 2) INFORMATION FOR SEQ ID NO: 38

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 797 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Corynebacterium minutissimum*

(B) STRAIN: ATCC 23348

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38

10 CCTGGTTGTT GCTGCAACCG ATGGCCCGAT GCCGCAGACC CGCGAGCACG 50
 TTCTTCTGGC CCGCCAGGTT GCGGTTCCGT ACATCCTCGT TGCCTGAAC 100
 AAGTGTGACA TGGTTGACGA TGAGGAAATC ATCGAGCTCG TTGAGATGGA 150
 15 GATCCCGTGAG CTGCTCGCTG AGCAGGACTA CGACGAGGAA GCTCCGATCG 200
 TTCACATCTC CGCTCTGAAG GCTCTTGAGG GCGACGAGAA GTGGGCACAG 250
 TCCATCGTTG ACCTGATGCA GGCTTGCGAT GACTCCATCC CGGATCCGGA 300
 GCGCGAGCTG GACAAGCCGT TCCTGATGCC GATCGAGGAC ATCTTCACCA 350
 TTACCGGCCG CGGTACCGTT GTTACCGGCC GTGTTGAGCG TGGCTCCCTG 400
 AACGTTAACG AGGACATCGA GATCATCGGT ATCAAGGACA AGTCCATGTC 450
 20 CACCACCGTT ACCGGTATCG AGATGTTCCG CAAGATGATG GACTACACCG 500
 AGGCTGGCGA CAACTGTGGT CTGCTTCTGC GTGGTACCAA GCGTGAAGAG 550
 GTTGAGCGTG GCCAGGTTTG CATCAAGCCG GGCGCTTACA CCCC GCACAC 600
 CAAGTTCGAG GGTTCCTGCT ACGTCCTGAA GAAGGAAGAG GGCGGCCGCC 650
 ACACCCCGTT CATGGACAAC TACCGTCCGC AGTTCTACTT CCGCACCACC 700
 25 GACGTCACCG GTGTCATCAA GCTGCCGGAG GGCACCGAGA TGGTCATGCC 750
 GGGCGACAAC GTTGAGATGT CCGTAGAGCT GATCCAGCCG GTCGCTA 797

30 2) INFORMATION FOR SEQ ID NO: 39

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 702 bases

(B) TYPE: Nucleic acid

35 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Corynebacterium mycetoides*

(B) STRAIN: ATCC 21134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39

45 GCCGCAGACC CGCGAGCACG TTCTTCTGGC CCGCCAGGTC GGCGTCCCCT 50
 ACATCCTCGT TGCGCTGAAC AAGTGCGACA TGGTTGATGA TGAGGAGATC 100
 ATCGAGCTCG TGGAGATGGA GGTCCGTGAG CTGCTCGGCG AGCAGGACTA 150
 CGACGAGGAC GCCCCCATCA TCCACATCTC CGCTCTGAAG GCTCTCGAGG 200
 50 GCGACGAGAA GTGGGTTTCA TCCGTGCTCG ACCTCATGCA GGCGTGCGAC 250
 GACTCCATCC CGGATCCGGT CCGCGAGACC GACCGCGACT TCCTGATGCC 300
 GATCGAGGAC ATCTTCACCA TCTCCGGCCG CGGCACCGTG GTTACCGGTC 350
 GTGTGGAGCG CGGCGTGCTC AACCTCAACG ACGAGGTGCA GATCATCGGC 400
 ATCCGCGACA AGTCCCAGAA GACCACCGTC ACCTCCATCG AGATGTTCAA 450
 55 CAAGCTGCTC GATACCGCTG AGGCAGGCGA CAACGCGGCT CTGCTGCTCC 500
 GCGGTCTGAA GCGCGAGGAC GTCGAGCGTG GCCAGGTTGT CATCAAGCCG 550
 GGCGCCTACA CCCC GCACAC CAAGTTCGAG GGTTCCTGCT ACGTCTGTC 600
 CAAGGACGAG GGCGGCCGCC ACACCCCGTT CTTGACAAC TACCGTCCGC 650
 60 AGTTCTACTT CCGCACCACC GACGTGACCG GTGTTGTGAA GCTGCCGGAG 700
 GG 702

2) INFORMATION FOR SEQ ID NO: 40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 674 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium pseudogenitalium*
 (B) STRAIN: ATCC 33038

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40

20	GCTCGCCAGG TTGGCGTTCC TTACATCCTC GTTGCCTGA ACAAGTGCGA	50
	CATGGTTGAT GATGAGGAAA TCATCGAGCT CGTTGAGATG GAGATCCGTG	100
	AGCTGCTCGC AGAGCAGGAT TACGATGAGG AAGCTCCTAT CGTTCACATC	150
	TCCGCTCTGA AGGCCCTCGA GGGCGATGAC AAGTGGGTAC AGTCCGTCGT	200
	TGATCTGATG GAAGCCTGCG ACAACTCCAT CCCGGATCCG GAGCGCGCTA	250
25	CCGACCAGCC GTTCCTGATG CCTATCGAGG ACATCTTCAC CATTACCGGC	300
	CGCGGTACCG TTGTTACCGG CCGTGTGAG CGTGGCCGTC TGAACGTCAA	350
	CGAGGACGTT GAGATCATCG GTATCCAGGA GAAGTCCAG ACCACCACCG	400
	TTACCGGTAT CGAGATGTTT CGCAAGATGA TGGACTACAC CGAGGCTGGC	450
	GACAACTGTG GTCTGCTTCT GCGTGGTACC AAGCGTGAGG ACGTTGAGCG	500
30	TGGCCAGGTT GTTATCAAGC CGGGCGCTTA CACCCGCGAC ACCAAGTTCG	550
	AGGGCTCCGT CTACGTCCTG AAGAAGGAAG AGGGCGGCCG CCACACCCCG	600
	TTCATGAACA ACTACCGTCC GCAGTTCTAC TTCCGTACCA CGGACGTTAC	650
	CGGTGTTGTT CACCTGCCAG AGGG	674

2) INFORMATION FOR SEQ ID NO: 41

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 694 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium renale*
 (B) STRAIN: ATCC 19412

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41

55	TGCCTCAGAC CCGTGAGCAC GTTCTGCTTG CTCGTCAGGT CGGCGTTCCT	50
	TACATCCTCG TTGCACTGAA CAAGTGCAGC ATGGTCGACG ACGAAGAAAT	100
	CATCGAGCTC GTCGAGATGG AAATCCGTGA ACTGCTCGCA GAGCAGGACT	150
	ACGATGAGGA AGCTCCTATC GTTCACATCT CCGCTCTGGG CGCCCTGAAC	200
	GGCGAGCAGA AGTGGGTTGA CTCCATCGTC GAACTGATGG AAGCTTGCGA	250
	CAACTCCATC CCAGACCCAG TTCGCGACAT CGACCACCCA TTCCTGATGC	300
	CTATCGAGGA CATCTTCACC ATTACCGGTC GCGGTACCGT TGTTACCGGC	350
60	CGTGTCGAGC GTGGCCGTCT CAACGTCAAC GAAGAAGTTG AGATCATCGG	400

TATCAAGGAC AAGTCCCAGA AGACCACCGT CACCGGTATC GAGATGTTCC 450
 GCAAGATGCT GGACTACACC GAAGCTGGCG ACAACTGTGG TCTGCTGCTC 500
 CGCGGCATCG GCCGTGAGGA TGTCGAGCGT GGCCAGGTTA TCATCAAGCC 550
 AGGCGCTTAC ACCCCTCACT CTGAGTTCTGA GGGCTCTGTC TACGTCCTGT 600
 5 CCAAGGACGA GGGTGGCCGC CACACCCCAT TCTTCGACAA CTACCGTCCA 650
 CAGTTCTACT TCCGACCAC CGACGTGACC GCGTTGTGC ACCT 694

10 2) INFORMATION FOR SEQ ID NO: 42

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 687 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Corynebacterium ulcerans*
 (B) STRAIN: NCTC 8665

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42

25 GCCGCAGACC CGCGAGCACG TTCTGCTGGC TCGCCAGGTT GCGTTTCKT 50
 ACATCCTSGT TGCACTGAAC AAGTGCACG TGGTTGACGA TGAGGARCTC 100
 CTSGAGCTCG TCGAGATGGA GGTCCGCGAG CTGCTGGCTG AGCAGGACTA 150
 CGACGAGGAA GCTCCGRTCG TTCACATCTC CGCWCTGAAC GCCCTGGACG 200
 30 GCGACSAAGAA GTGGGCTVAC TCCATCCTCG AGCTGATGCA GGCTTGCGAC 250
 GAGTCCATCC CGGATCCGGA GCGCGAGACC GACAAGCCGT TCCTGATGCC 300
 GATTGAGGAC ATCTTCACCA TTACCGGTCTG CCGYACCGTT GTTACCGGCC 350
 GTGTTGAGCG TGGCDTCCTG AACGTSAAAG ACGASGTTGA GATCATGGGY 400
 ATCCGGGAGA AGTCCCAGAA GACCACCGTY ACCKSCATCG AGATGTTCAA 450
 35 CAAGMTGMTG GACWCCGCAG AGGCTGGCGA CAACGCTGSW CTGCTGCTGC 500
 GTGGTMTSAA GCGTGAGGAC GTTGAGCGTG GCCAGATCAT CGYTAAGCCG 550
 GCGGCKTACA CCCCACACAC CGAGTTCGAG GGCTCCGTCT ACGTCCCTGTC 600
 CAAGGACGAG GCGGCGCGCC ACACCCCGTT CTTGACAAC TACCGTCCGC 650
 40 AGTTCTACTT CCGCACCACC GACGTSACCG GTGTTGT 687

2) INFORMATION FOR SEQ ID NO: 43

45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 778 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Corynebacterium urealyticum*
 55 (B) STRAIN: ATCC 43042

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43

60 CTGTTGTTG CTGCAACCGA TGGCCCGATG CCGCAGACCC GTGAGCACGT 50
 TCTGCTGGCT CGCCAGGTTG GCGTTCCGTA CATCTCGTT GCACTGAACA 100

```

    AGTGCACAT GGTGACGAT GAGGAGCTCC TCGAGCTCGT CGAGATGGAG 150
    GTCCGCGAGC TTCTGGCTGA GCAGGACTAC GACGAGGAGG CTCCGGTCTG 200
    CCCGATCTCC GCACTGGGCG CCCTGGACGG CGATCAGAAG TGGGTCGACT 250
    CCATCCTCGA GCTCATGAAG GCTTGCGACG AGTCCATCCC GGACCCGGAG 300
    5 CGCGAGACCG ACAAGCCGTT CCTGATGCCG GTTGAGGACA TCTTCACCAT 350
    TACCGGTCGC GGCACCGTCG TTACCGGCCG TGTGAGCGT GGCGTCCTGA 400
    ACCTGAACGA CGAGGTCGAG ATCCTGGGCA TCCGCGAGAA GTCCACCAAG 450
    ACCACCGTCA CCTCCATCGA GATGTTCAAC AAGCTGCTGG ACACCGCAGA 500
    GGCTGGCGAC AACGCTGCAC TGCTGCTGCG TGGTCTGAAG CGTGAGGACG 550
    10 TCGAGCGAGG CCAGATCATC GCTAAGCCGG GCGCTTACAC CCCGCACACC 600
    GAGTTCGAGG GCTCCGTCTA CGTCCTGTCC AAGGACGAGG GCGGCCGTCA 650
    CACCCCGTTC TTCGACAACT ACCGTCCGCA GTTCTACTTC CGTACCACCG 700
    ACGTCACCGG TGTCGTTACC CTGCCAGAGG GCACCGACAT GGTTCATGCCG 750
    GCGGACAACG TTGAGATGAG CGTCAAGC 778
  
```

2) INFORMATION FOR SEQ ID NO: 44

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    20 (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 703 bases
        (B) TYPE: Nucleic acid
        (C) STRANDEDNESS: Double
        (D) TOPOLOGY: Linear

    25 (ii) MOLECULE TYPE: Genomic DNA

        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Corynebacterium xerosis
    30 (B) STRAIN: ATCC 373
  
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44

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    35 CGCAGACCCG TGAGCACGTC CTCCTGGCCC GCCAGGTCGG CGTCCCCTAC 50
    ATCCTCGTCG CCCTGAACAA GTGCGACATG GTCGACGATG AGGAGATCAT 100
    CGAGCTCGTG GAGATGGAGG TGCCTGAGCT TCTCGCCGAG CAGGACTACG 150
    ACCAGGAGGC CCCGATCGTG CACATCTCCG CCCTGGGCGC CCTCAATGGC 200
    GAAGAGAACT GGGTCGACTC CATCGTCGAG CTCATGAACG CCGTCGACGA 250
    GAACGTTCCG GACCCGGTCC GCGAGACCGA CAAGCCGTTT CTGATGCCCCG 300
    40 TCGAGGACAT CTTACCATC ACCGGCCGCG GCACCGTCGC CACCGGTTCG 350
    GTGGAGCGCG GCACCCGTGA GGTCAACGAC GAGGTCGAGA TCCTGGGCAT 400
    CCAGGAGAAG TCCCAGACCA CCACCGTCAC CGGCATCGAG ATGTTCCGCA 450
    AGCTGCTGGA CTCCGCCGAG GCCGGCGACA ACTGTGGCCT GCTGCTCCGC 500
    GGCATCAAGC GCGAGGACAT CGAGCGCGGC CAGATCATCG CGAAGCCGGG 550
    45 CGCCTACACC CCGCACACCG AGTTCGAGGG CTCCGTCTAC ATCCTGGCCA 600
    AGGACGAGGG CGGCCGCCAC ACCCCGTTCT TCGACAATA CCGTCCGCAG 650
    TTCTACTTCC GCACCACCGA CGTCACCGGC GTCGTGAAGC TGCCGGAGGG 700
    CAC 703
  
```

2) INFORMATION FOR SEQ ID NO: 45

```

    55 (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 832 bases
        (B) TYPE: Nucleic acid
        (C) STRANDEDNESS: Double
        (D) TOPOLOGY: Linear

    60 (ii) MOLECULE TYPE: Genomic DNA
  
```

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Coxiella burnetii*
 (B) STRAIN: Nine Mile phase II

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45

	GGAGCGATAT	TGGTGGTGAG	CGCAGCGGAC	GGCCCGATGC	CGCAAACGCG	50
	GGAACACATT	GTATTGGCGA	AGCAAGTGGG	TGTTCCGAAC	ATAGTGGTTT	
10	ACTTGAACAA	AGCGGACATG	GTGGATGACA	AAGAGCTGTT	GGAATTAGTG	100
	GAAATGGAAG	TGAGGGATTT	ATTGAACAGT	TATGATTTCC	CTGGGGATGA	150
	GACGCCGATA	ATAGTGGGGT	CAGCGTTAAA	GGCGTTAGAA	GGTGACAAGA	200
	GTGAGGTTGG	GGAGCCATCG	ATAATCAAAT	TAGTGGAAC	GATGGACACG	250
	TACTTCCCCG	AGCCGGAGCG	AGCGATAGAC	AAACCGTTTT	TAATGCCGAT	300
15	CGAAGATGTG	TTTTTCGATAT	CGGGCCGAGG	GACGGTGGTG	ACGGGACGCG	350
	TAGAGCGAGG	GATCATCAAA	GTGGGCGACG	AGATAGAGAT	TGTGGGGATC	400
	AAGGACACGA	CGAAGACGAC	GTGCACGGGC	GTTGAGATGT	TTCGCAAATT	450
	ATTGGATGAA	GGTCAAGCGG	GTGACAACGT	AGGAATTTTA	TTGAGAGGGA	500
	CGAAACGCGA	AGAAGTGGAG	CGTGGTCAAG	TATTGGCGAA	ACCGGGATCG	550
20	ATCACGCCAC	ACAAGAAATT	TGAGGCGGAG	ATTTATGTGT	TGTCGAAGGA	600
	AGAAGGGGGA	CGCCACACAC	CGTTTTTACA	AGGCTATCGA	CCGCAATTTT	650
	ATTTCCGCAC	GACGGACGTG	ACGGGCCAGT	TATTGAGTTT	ACCGGAGGGG	700
	ATAGAGATGG	TGATGCCGGG	AGATAACGTG	AAAGTGACGG	TTGAATTGAT	750
25	TGCGCCGGTA	GCGATGGATG	AAGGGCTACG	AT		800
						832

2) INFORMATION FOR SEQ ID NO: 46

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 816 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Edwardsiella hoshinae*
 (B) STRAIN: ATCC 33379

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46

	GGCGCTATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCGATGC	CGCAGACCCG	50
45	TGAGCACATC	CTGCTGGGTC	GCCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	100
	TCCTGAACAA	GTGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTT	150
	GAGATGGAAG	TTCGCGAACT	GCTGTCTCAG	TACGATTTCC	CGGGCGACGA	200
	TACGCCGGTA	ATCCGCGGTT	CTGCGCTGAA	AGCGCTGGAA	GGCGAAGCCG	250
50	AGTGGGAAGC	GAAGATCATC	GAAGTGGCTG	AAACGCTGGA	CTCCTACATT	300
	CCGGAACCTG	AGCGTGACAT	CGACAAGCCG	TTCCTGCTGC	CGATCGAAGA	350
	CGTATTCTCA	ATCTCTGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAAGAGC	400
	GCGGTATCAT	CAAGGTAGGC	GACGAAGTTG	AAATCGTAGG	TATCAAGCCG	450
	ACCACCAAGA	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCTGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTACCAAGC	550
55	GTGACGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CACCATCACT	600
	CCGCACACCA	AGTTTCAATC	AGAAGTGTAC	ATCCTGAGCA	AGGATGAAGG	650
	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGTTA	CCGTCCGCAG	TTCTACTTCC	700
	GTACCACTGA	CGTGAAGTGC	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	750
60	GTAATGCCGG	GCGACAACAT	CAAGATGGTT	GTTACCCTGA	TCCACCCGAT	800
	CGCCATGGAC	GATGGT				816

2) INFORMATION FOR SEQ ID NO: 47

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 821 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Edwardsiella tarda*
 (B) STRAIN: ATCC 15947

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47

20	GGCGCGATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCGATGC	CGCAGACCCG	50
	TGAGCACATC	CTGTTGGGTC	GCCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	100
	TCCTGAACAA	GTGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTT	150
	GAGATGGAAG	TTCCGCAACT	GCTGTCTCAG	TACGACTTCC	CGGGCGACGA	200
	CACGCCGGTA	ATCCGCGGTT	CTGCGCTGAA	AGCGCTGGAA	GGCGAAGCCG	250
25	AGTGGGAAGC	GAAGATCATC	GAAGTGGCTG	AAACTCTGGA	CTCCTACATC	300
	CCGGAACCTG	AGCGTGACAT	CGACAAGCCG	TTCCTGCTGC	CGATCGAAGA	350
	CGTATTCTCT	ATCTCTGGCC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAGC	400
	GCGGTATCAT	CAAGGTAGGC	GACGAAGTTG	AAATCGTTGG	TATCAAGCCG	450
	ACCACCAAGA	CCACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
30	CGAAGGCCGT	GCTGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTACTAAGC	550
	GTGACGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CACCATCACT	600
	CCGCACACCA	AGTTCGAATC	TGAAGTGTAC	ATCCTGAGCA	AGGATGAAGG	650
	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	700
	GTACTACTGA	CGTGACTGGT	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	750
35	GTAATGCCGG	GCGACAACAT	CAAGATGGTT	GTTACCCTGA	TCCACCCGAT	800
	CGCCATGGAC	GATGGTCTGC	G			821

2) INFORMATION FOR SEQ ID NO: 48

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Eikenella corrodens*
 (B) STRAIN: ATCC 23834

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48

55	CGGTGCCATC	CTGGTGGTAT	CCGCTGCTGA	CGGCCCCATG	CCTCAGACTC	50
	GCGAACACAT	CCTGTTGGCT	CGTCAGGTAG	GTGTACCCTA	CATCCTCGTA	100
	TTTCATGAACA	AATGCGACAT	GGTAGATGAT	GCCGAGCTGC	TTGAGTTGGT	150
	TGAGATGGAA	ATCCGCGACC	TGCTCTCCAG	CTATGACTTC	CCTGGTGACG	200
60	ACTGCCCGAT	CGTACAAGGT	TCCGCTCTCA	AAGCCCTCGA	AGGCGATGCC	250

	GGTTACAAAG	AAAAAATCTT	CGAACTAGCT	GCTGCTTTGG	ATAGCTACAT	300
	CCCCACTCCT	CAACGTGCTG	TAGACAAACC	CTTCCTGTTG	CCGATCGAAG	350
	ACGTATTCTC	TATCTCCGGC	CGTGGTACCG	TAGTAACCGG	TCGTGTAGAG	400
	CGCGGCATCA	TCAAAGTAGG	TGAAGAGATC	GAAATCGTTG	GTCTGAAGCC	450
5	CACTCAGAAA	ACTACCTGTA	CTGGCGTGGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGTCA	GGCCGGTGAC	AACGTAGGCG	TACTGCTGCG	CGGTACCAAA	550
	CGTGAAGAAG	TTGAGCGTGG	TCAAGTATTG	GCTAAACCCG	GCACCATCAC	600
	TCCGCACACC	AAGTTCAAAG	CCGAAGTATA	CGTATTGAGC	AAAGAAGAAG	650
	GTGGTCGTCA	CACCCCGTTC	TTTGCCAACT	ACCGTCCACA	GTTCTACTTC	700
10	CGTACTACTG	ACGTAACCGG	TGCTGTAGAG	CTGGAGCCTG	GTGTAGAAAT	750
	GTTTATGCCT	GGTGAGAACG	TAACCATCAC	CGTAGAACTG	ATTGCTCCGA	800
	TTGCTATGGA	AGAAGGTCTG	CGCTTTGCGA			830

15

2) INFORMATION FOR SEQ ID NO: 49

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 808 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter aerogenes*
 (B) STRAIN: ATCC 13048

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49

	GGCGCGATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCGATGC	CGCAGACTCG	50
	TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	100
	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTT	150
35	GAGATGGAAG	TTCGTGAACT	GCTGTCTCAG	TACGATTTC	CGGGCGACGA	200
	CACTCCGATC	GTTTCGTGTT	CTGCTCTGAA	AGCGCTGGAA	GGCGACGCAG	250
	AGTGGAAGC	GAAAATCATC	GAAGTGGCTG	GCTTCCTGGA	TTCTTACATC	300
	CCRGAACCAG	AGCGTGCGAT	TGACAAGCCG	TTCCTGCTGC	CGATCGAAGA	350
	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAGC	400
40	GCGGTATCAT	CAAAGTTGGT	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAC	450
	ACCGCGAAAA	CCACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCTGGTGAGA	ACGTAGGYGT	TCTGCTGCGT	GGTATCAAAC	550
	GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CAGCATCAAG	600
	CCGCACACCA	AGTTCGAATC	TGAAGTGATC	ATCCTGTCCA	AAGACGAAGG	650
45	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	700
	GTACTACTGA	CGTGAAGTGG	ACCATCGAAC	TGCCGGAAGG	CGTAGAGRTG	750
	GTAATGCCCG	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TCCACCCGAT	800
	CGCGATGG					808

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2) INFORMATION FOR SEQ ID NO: 50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter agglomerans*
 (B) STRAIN: ATCC 27989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50

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CGGCGCGATC	CTGGTTGTTG	CTGCCACTGA	CGGCCCGATG	CCGCAGACTC	50
GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCGGTA	CATCATCGTG	100
TTCCTGAACA	AATGTGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
TGAAATGGAA	GTTCGTGAAC	TTCTGTCTCA	GTACGATTTC	CCGGGCGACG	200
ATACTCCGAT	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGAMGCW	250
GAGTGGGAAG	CGAAAATCAT	CGARCTGGCT	GGCCACCTGG	ATACCTATAT	300
CCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	GTTCTGCTG	CCGATCGAAG	350
ACGTATTCTC	CATCTCCGGT	CGCGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
CGCGGTATCA	TYAAAGTGGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
TACYGCGAAA	TCAACCTGTA	CCGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
ACGAAGGCCG	TGCTGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTATCAAA	550
CGTGAAGAAA	TGCAACGTGG	TCAGGTACTG	GCTAAGCCGG	GCACCATCAA	600
GCCGCACACC	AAGTTCGAAT	CTGAAGTGTA	CATTCTGTCC	AAAGATGAAG	650
GCGGTTCGTCA	CACTCCGTTT	TTCAAAGGCT	ACCGTCCSCA	GTTCTACTTC	700
CGTACAACCTG	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
GGTAATGCCG	GGCGACAACA	TCAAAATGGT	TGTTACCCTG	ATCCACCCGA	800
TCGCGATGGA	CGACGGTCTG	CGTTCGCA			828

2) INFORMATION FOR SEQ ID NO: 51

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter amnigenus*
 (B) STRAIN: ATCC 33072

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51

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TGGCGCGATC	CTGGTTGTTG	CTGCAACTGA	TGGCCCTATG	CCACAGACGC	50
GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCTTA	CATCATCGTG	100
TTCCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
AGAAATGGAA	GTTCGTGAAC	TTCTGTCTCA	GTACGATTTC	CCAGGTGATG	200
ACACTCCAAT	CATCCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGAAGCA	250
GAGTGGGAAG	CTAAAATCGT	TGAGCTGGCT	GGCTACCTGG	ATTCTTACAT	300
CCCGGAACCA	GAACGTGCTA	TCGATAAGCC	ATTCTGCTG	CCAATCGAAG	350
ACGTATTCTC	TATCTCCGGC	CGTGGTACTG	TTGTAACCGG	TCGTGTAGAG	400
CGCGGTATCG	TTAAAGTTGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
GACTGCTAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
ACGAAGGCCG	TGCTGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTATCAAA	550
CGTGAAGAAA	TGCAACGTGG	TCAGGTACTG	GCTAAGCCAG	GCTCAATCAA	600
GCCGCACACC	AAATTCCGAAT	CTGAAGTTTA	TATTCTGTCC	AAAGATGAAG	650
GCGGCCGTCA	TACTCCGTTT	TTCAAAGGCT	ACCGTCCACA	GTTCTACTTC	700
CGTACAACCTG	ACGTGACCGG	CACCATCGAA	CTGCCAGAAG	GCGTAGAGAT	750
GGTAATGCCA	GGCGACAACA	TTCAGATGGT	TGTTACCCTG	ATCCACCCAA	800
TCGCGATGGA	TGACGGTCTG	CGTTT			825

2) INFORMATION FOR SEQ ID NO: 52

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter asburiae*
 (B) STRAIN: ATCC 35953

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52

20	CGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCAATG	CCTCAGACTC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCTTT	CATCATCGTG	100
	TTCCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	AGAGATGGAA	GTTTCGTGAAC	TGCTGTCTCA	GTACGATTTT	CCGGGCGACG	200
	ATACTCCAAT	CGTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGACGCA	250
25	GAGTGGGAAG	CGAAAATCAT	CGAACTGGCT	GGCTTCCTGG	ATTCTTACAT	300
	CCCAGAACCA	GAGCGTGCGA	TTGACAAGCC	ATTCCTGCTG	CCAATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
	CGCGGTATCA	TCAAAGTTGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	GACTGCTAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
30	ACGAAGGCCG	TGCTGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTTCTG	GCGAAGCCAG	GCTCAATCAA	600
	GCCACACACC	AAGTTCGAAT	CTGAAGTGTA	CATCCTGTCC	AAAGACGAAG	650
	GCGGCCGTCA	TACTCCGTTT	TTCAAAGGCT	ACCGTCCACA	GTTCTACTTC	700
	CGTACAAC TG	ACGTGACCGG	TACCATCGAA	CTGCCAGAAG	GCGTTGAGAT	750
35	GGTAATGCCA	GGCGACAACA	TCAAGATGGT	TGTGACTCTG	ATCCACCCAA	800
	TCGCGATGGA	CGACGGTCTG	CG			822

2) INFORMATION FOR SEQ ID NO: 53

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter cancerogenus*
 (B) STRAIN: ATCC 35317

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53

55	CGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCAATG	CCTCAGACTC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCTTA	CATCATCGTG	100
	TTCCTGAACA	AGTGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	AGAAATGGAA	GTTTCGTGAAC	TGCTGTCTCA	GTACGATTTT	CCAGGCGACG	200
60	AACTCCAAT	CGTTCGTGGT	TCCGCGCTGA	AAGCGCTGGA	AGGCGAAGCT	250

GAGTGGGAAG CAAAAATCAT CGAACTGGCT GGCTTCCTGG ATTCTTACAT 300
 CCCAGAACCA GAGCGTGCGA TTGACAAGCC ATTCCTGCTG CCAATCGAAG 350
 ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAG 400
 CGCGGTATCA TCAAAGTTGG TGAAGAAGTT GAAATCGTTG GTATCAAAGA 450
 5 TACTGCKAAA TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAATGCTGG 500
 ACGAAGGCCG TGCTGGTGAG AACGTTGGTG TTCTGCTGCG TGGTATCAAA 550
 CGCGAAGAAA TCGAACGTGG TCAGGTTCTG GCGAAGCCAG GCTCAATCAA 600
 GCCACACACC AAGTTCGAAT CTGAAGTGTA CATCCTGTCC AAAGACGAAG 650
 GCGGCCGTCA TACTCCGTTT TTCAAAGGCT ACCGTCCACA GTTCTACTTC 700
 10 CGTACAACTG ACGTGACCGG TACCATCGAA CTGCCAGAAG GCGTAGAGAT 750
 GGTAATGCCA GGCGACAACA TCAAGATGGT TGTGACGCTG ATCCACCCAA 800
 TCGCGATGGA CGACGGTCTG CGTTTC 826

15 2) INFORMATION FOR SEQ ID NO: 54

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterobacter cloacae*
 (B) STRAIN: ATCC 13047

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54

GATCCTGGTA GTAGCTGCGA CTGACGGCCC AATGCCTCAG ACTCGTGAGC 50
 ACATCCTGCT GGGTCGTCAG GTAGGCGTTC CTTACATCAT CGTGTTCCCTG 100
 AACAAATGCG ACATGGTTGA TGACGAAGAG CTGCTGGAAC TGGTAGAGAT 150
 35 GGAAGTTCGT GAACTGCTGT CTCAGTACGA TTTCCCAGGC GACGATACCC 200
 CAATCGTTCG TGGTTCTGCT CTGAAAGCGC TGGAAGGCGA CGCAGAGTGG 250
 GAAGMGAAAA TCATCGAACT GGCTGGCTAC CTGGATTCTT ACATCCCAGA 300
 ACCAGAGCGT GCGATTGAYA AGCCATTCTT GCTGCCAATC GAAGACGTAT 350
 TCTCCATCTC CGGTCGTGGT ACCGTTGTTA CCGGTCGTGT AGAGCGCGGT 400
 40 ATCATCAAAG TGGGTGAAGA AGTTGAAATC GTTGGTATCA AAGAGACTGC 450
 GAAGTCTACC TGTACTGGCG TTGAAATGTT CCGCAAACTG CTGGACGAAG 500
 GCCGTGCTGG TGAGAACGTT GGTGTTCTGC TGCCTGGTAT CAAACGTGAA 550
 GAAATCGAAC GTGGTCAGGT TCTGGCGAAG CCAGGCTCAA TCAAGCCACA 600
 CACCAAGTTC GAATCTGAAG TGTACATCCT GTCCAAAGAC GAAGGCGGCC 650
 45 GTCATACTCC GTTCTTCAAA GGCTACCGTC CACAGTTCTA CTTCCGTACA 700
 ACTGACGTGA CCGGTACCAT CGAACTGCCA GAAGGCGTAG AGGTGGTAAT 750
 GCCAGGCGAC AACATCAAGA TGGTTGTGAC TCTGATCCAC CCAATCGCGA 800
 TGGACG 806

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2) INFORMATION FOR SEQ ID NO: 55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter gergoviae*
 (B) STRAIN: ATCC 33028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55

	CGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACCC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	100
10	TTCTTGAACA	AGTGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	AGAGATGGAA	GTTCGTGAAC	TGCTGTCTCA	GTACGATTTC	CCGGGCGACG	200
	ACACCCCGAT	CGTTCGCGGT	TCTGCGCTGA	AAGCGCTGGA	AGGCGACGCA	250
	GAGTGGGAAG	CGAAAATCAT	CGAACTGGCT	GGCCACCTGG	ATACCTAYAT	300
	CCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	GTTCTTGCTG	CCGATCGAAG	350
15	ACGTATTCTC	CATTTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
	CGCGGTATCA	TCAAGGTTGG	TGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	CACCGCGAAA	ACCACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTCGGCG	TTCTGCTGCG	TGGTATCAAG	550
	CGTGAAGAAA	TCGAACGTGG	TCAGGTAAGT	GCTAAGCCGG	GCTCCATCAA	600
20	GCCGACACAC	AAGTTCGAAT	CTGAAGTGTA	CATCCTGTCC	AAAGACGAAG	650
	GCGGCCGTCA	CATCCCGTTC	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACAAGTG	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
	GGTAATGCCG	GGCGACAACA	TCAAGATGGT	TGTTACCCCTG	ATCCACCCGA	800
25	TCGCGATGGA	CGACGGTCTG	CGTTTC			826

2) INFORMATION FOR SEQ ID NO: 56

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter hormaechei*
 (B) STRAIN: ATCC 49162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56

	GGCGCGATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCTATGC	CTCAGACCCG	50
45	TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTCCTTAC	ATCATCGTGT	100
	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTA	150
	GAGATGGAAG	TTCGTGAACT	GCTGTCTCAG	TACGATTTC	CAGGCGACGA	200
	CACCCCAATC	GTTCGTGGTT	CCGCGCTGAA	AGCGCTGGAA	GGCGAMGCAG	250
	AGTGGGAAGM	GAAAATCATC	GARCTGGCTG	GCTTCCTGGA	TTCTTACATC	300
50	CCAGAACCAG	AGCGTGCGAT	TGACAAGCCA	TTCCTGCTGC	CAATCGAAGA	350
	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTWGAGC	400
	GCGGTATCAT	CAAAGTAGGT	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAG	450
	ACTGCGAAGT	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCTGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTATCAAAC	550
55	GTGAAGAAAT	CGAACGTGGT	CAGGTTCTGG	CGAAGCCAGG	CTCAATCAAG	600
	CCACACACCA	AGTTCGAATC	TGAAGTGATC	ATTCTGTCCA	AAGACGAAGG	650
	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700
	GTACAAGTGA	CGTGACCGGT	ACCATCGAAC	TGCCAGAAGG	CGTAGAGATG	750
	GTAATGCCAG	GCGACAACAT	CAAGATGGTT	GTGACGCTGA	TCCACCCAAT	800
60	CGCGATGGAC	GACGGTCTGC	GTTTCGCAA			829

2) INFORMATION FOR SEQ ID NO: 57

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter sakazakii*
 (B) STRAIN: ATCC 29544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57

20	GGCGCTATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCGATGC	CGCAGACCCG	50
	TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	100
	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTT	150
	GAGATGGAAG	TGCGCGAGCT	GCTGTCTCAG	TACGACTTCC	CGGGCGACGA	200
	CACCCCGATC	GTTTCGTGGT	CTGCTCTGAA	AGCGCTGGAA	GGCGACGCTG	250
25	AGTGGGAAGC	GAAAATCATC	GAGCTGGCAG	GTCACCTGGA	TTCTTACATC	300
	CCGGAACCGG	AGCGTGCGAT	TGACAAGCCG	TTCTGCTGTC	CGATCGAAGA	350
	CGTATTCTCC	ATCTCYGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAAGC	400
	GCGGTATCAT	CAAGGTTGGT	GAAGAAGTTG	AAATCGTGGG	CATCAAAGAC	450
	ACCGCGAAAT	CCACCTGTAC	CGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
30	CGAAGGCCGT	GCGGGCGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAAC	550
	GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CTCCATCAAG	600
	CCGCACACCA	AGTTCGAATC	TGAAGTGATC	ATTCTGTCCA	AAGATGAAGG	650
	CGGCCGTCAC	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	700
	GTACRACTGA	CGTGAAGTGC	ACCATCGAAC	TGCCGGAAGG	CGTTGAGATG	750
35	GTAATGCCGG	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TCCACCCGAT	800
	CGCGATGGAC	GACGGTCTGC	GTTTCGCAAT	C		831

40 2) INFORMATION FOR SEQ ID NO: 58

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*
 (B) STRAIN: ATCC 25788

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58

55	CGGCGCGATC	TTAGTAGTAT	CTGCTGCTGA	TGGTCCTATG	CCTCAAACAC	50
	GTGAACACAT	CTTGTTATCA	CGTAACGTTG	GTGTACCATA	CATCGTTGTT	100
	TTCTTAAACA	AAATGGATAT	GGTTGATGAC	GAAGAATTAC	TAGAATTAGT	150
	TGAAATGGAA	GTTTCGTGACT	TATTGTCAGA	ATATGACTTC	CCAGGCGACG	200
60	ATGTTTCCTGT	AATCGCTGGT	TCTGCTTTGA	AAGCTCYTGA	AGGCGATGCT	250

	TCATACGAAG	AAAAAATCAT	GGAATTAATG	GCTGCAGTTG	ACGAATACGT	300
	TCCAACCTCCA	GAACGTGACA	CTGACAAACC	ATTCATGATG	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGA	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
	CGTGGACAAG	TTCGCGTTGG	TGACGAAGTT	GAAATCGTTG	GTATTGCTGA	450
5	AGAAACTGCT	AAAACAACCTG	TAAGTGGTGT	TGAAATGTTT	CGTAAATTGT	500
	TAGACTATGC	TGAAGCAGGG	GATAACATTG	GTGCATTGCT	ACGTGGTGTG	550
	GCTCGTGAAG	ACATCCAACG	TGGACAAGTA	TTGGCTAAAG	CTGGTACAAT	600
	CACACCTCAT	ACAAAATTTA	AAGCTGAAGT	TTACGTTTTA	ACAAAAGAAG	650
	AAGGTGGACG	TCACACACCA	TTCTTCACTA	ACTACCGTCC	TCAGTTCTAC	700
10	TTCCGTACAA	CTGACGTAAC	TGGTGTGTGTT	GAATTACCAG	AAGGAAGTGA	750
	AATGGTTATG	CCTGGTGATA	ACGTAACAAT	CGACGTTGAA	TTGATCCACC	800
	CAATCGCTAT	CGAAGACGGA	ACTCGTTTCT	CAATT		835

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2) INFORMATION FOR SEQ ID NO: 59

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus cecorum*
 (B) STRAIN: ATCC 43198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59

	GGTGCTATCT	TAGTAGTATC	TGCTGCTGAT	GGTCCTATGC	CACAAACTCG	50
	TGAACACATT	CTTTTATCAC	GTAACGTTGG	TGTTCCATAC	ATCGTTGTTT	100
	TCTTAAACAA	AGTTGATATG	GTTGACGACG	AAGAATTATT	AGAATTAGTT	150
35	GAAATGGAAG	TACGTGACTT	ATTAAGTGA	TACGACTTCC	CAGGAGACGA	200
	TGTTCTCTGT	ATCGCTGGTT	CTGCATTAA	AGCTTTAGAA	GGCGACCCAT	250
	CTTACGAAGA	AAAAATCTTA	GAATTAATGG	CTGCAGTTGA	CGAATACATC	300
	CCAAGTCCAG	AACGTGACAA	CGATAAACCA	TTCATGATGC	CAGTCGAAGA	350
	CGTATTTTCA	ATCACTGGTC	GTGGTACTGT	TGCTACAGGT	CGTGTGTAAC	400
40	GTGGACAAGT	ACGTGTTGGT	GACGAAGTTG	AAATAGTTGG	TATCCATGAT	450
	GAAATTTCTA	AAACAACAGT	TACTGGTGTT	GAAATGTTCC	GTAAATTATT	500
	AGATTACGCT	GAAGCTGGAG	ACAACATCGG	TGCATTATTA	CGTGGTGTGG	550
	CTCGTGAAGA	TATCCAACGT	GGTCAAGTAT	TAGCTAAACC	AGGTTCAATC	600
	ACTCCACATA	CAAAATTCAC	TGCTGAAGTG	TACGTTTTAA	CTAAAGAAGA	650
45	AGGTGGACGT	CATACTCCAT	TCTTCACTAA	CTACCGTCCA	CAATTCTACT	700
	TCCGTACAAC	TGACGTTACA	GGTGTAGTTA	ACTTACCAGA	AGGTACTGAA	750
	ATGGTTATGC	CTGGTGATAA	CGTAACATATG	GAAGTTGAAT	TAATCCACCC	800
	AATCGCTATC	GAAGACGGAA	CTCGTT			826

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2) INFORMATION FOR SEQ ID NO: 60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus dispar*

(B) STRAIN: ATCC 51266

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60

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CGGCGCGATC	TTGGTAGTAT	CTGCTGCTGA	TGGTCCTATG	CCTCAAACCTC	50
GTGAACACAT	CCTATTGTCA	CGTAACGTTG	GTGTTCCCTTA	CATCGTCGTT	100
TTCTTTGAACA	AAATGGACAT	GGTTGATGAC	GAAGAATTAT	TAGAATTAGT	150
TGAAATGGAA	GTTTCGTGACT	TATTGTCAGA	ATACGACTTC	CCAGGCGACG	200
ACACTCCAGT	TATCGCAGGT	TCAGCTTTGA	AAGCCTTAGA	AGGCGACGCT	250
TCATATGAAG	AAAAAATCTT	AGAATTAATG	GCTGCAGTTG	ACGAATATAT	300
CCCAACTCCA	GTTTCGTGATA	CTGACAAACC	ATTCATGATG	CCAGTCGAAG	350
ATGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCAACTGG	TCGTGTTGAA	400
CGTGGACAAG	TTCGCGTTGG	TGACGAAGTT	GAAATCGTAG	GTATCGCTGA	450
AGAAACTGCT	AAAACTACTG	TAACAGGTGT	TGAAATGTTT	CGTAAATTGT	500
TGGATTACGC	TGAAGCTGGC	GACAACATTG	GTGCATTATT	ACGTGGTGTG	550
GCTCGTGAAG	ATATCCAACG	TGGTCAAGTA	TTATCAAAAC	CAGGTTCAAT	600
CACTCCACAT	ACAAAATTTG	CGGCAGAAGT	TTACGTTTTA	ACTAAAGAAG	650
AAGGTGGACG	TCATACTCCA	TTCTTCACTA	ACTACCGCCC	ACAATTCTAC	700
TTCCGTACAA	CTGACGTAAC	AGGTGTTGTT	GAATTACCAG	AAGGTACTGA	750
AATGGTTATG	CCTGGCGATA	ACGTTACTAT	GGACGTGAA	TTAATCCACC	800
CAATCGCGAT	CGAAGACGGT	ACTCGTTTCT	CAATC		835

2) INFORMATION FOR SEQ ID NO: 61

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 835 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus durans*

(B) STRAIN: ATCC 19432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61

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CGGAGCTATC	TTAGTAGTTT	CTGCTGCTGA	TGGCCCTATG	CCTCAAACCTC	50
GTGAACATAT	CCTATTATCT	CGTCAAGTTG	GTGTTCCCTTA	CATCGTYGTA	100
TTCTTTGAACA	AAGTAGATAT	GGTCGATGAC	GAAGAATTAC	TAGAATTAGT	150
TGAAATGGAA	GTTTCGTGACT	TATTAACAGA	ATACGAATTC	CCTGGTGACG	200
ATGTTCCCTGT	AATCGCTGGT	TCAGCTTTGA	AAGCTTTAGA	AGGCGACGCT	250
TCATACGAAG	AAAAAATCCT	TGAATTAATG	GCTGCAGTTG	ACGAATATAT	300
CCCAACTCCA	GAACGTGACA	ACGACAAACC	ATTCATGATG	CCAGTTGAAG	350
ATGTATTCTC	RATCACTGGT	CGTGGTACTG	TTGCTACAGG	TCGTGTTGAA	400
CGTGGACAAG	TTCGCGTTGG	TGACGTTGTA	GATATCGTTG	GTATCGCAGA	450
AGAAACAGCT	CAAACAACAG	TTACTGGTGT	TGAAATGTTT	CGTAAATTAT	500
TAGRCTACGC	TGAAGCTGGA	GACAACATTG	GTGCTTTACT	ACGTGGTGTG	550
GCACGTGAAG	ACATCCAACG	TGGACAAGTT	TTAGCTAAAC	CAGGTACAAT	600
CACKCCTCAT	ACAAAATTCT	CTGCAGAAGT	ATACGTGTTG	ACTAAAGAAG	650
AAGGTGGACG	TCATACTCCA	TTCTTCACTA	ACTACCGTCC	ACAATTCTAC	700
TTCCGTACAA	CTGACGTAAC	AGGTGTTGTT	GAATTACCAG	AAGGAACTGA	750
AATGGTTATG	CCTGGCGACA	ACGTAACAAT	GGAAGTTGAA	TTAATCCACC	800
CAATCGCTAT	CGAAAATGGT	ACTAAATTCT	CAATC		835

2) INFORMATION FOR SEQ ID NO: 62

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 680 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
 (B) STRAIN: R610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62

20	AGTAGTTTCT GCTGCTGATG GTCCTATGCC TCAAACACGT GAACATATCT	50
	TATTATCACG TAACGTTGGT GTACCATACA TCGTTGTATT CTTAAACAAA	100
	ATGGATATGG TTGATGACGA AGAATTATTA GAATTAGTAG AAATGGAAGT	150
	TCGTGACTTA TTATCAGAAT ACGATTTCCC AGGCGATGAT GTTCCAGTTA	200
	TCGCAGGTTT TGCTTTGAAA GCTTTAGAAG GCGACGAGTC TTATGAAGAA	250
25	AAAATCTTAG AATTAATGGC TGCAGTTGAC GAATATATCC CAACTCCAGA	300
	ACGTGATACT GACAAACCAT TCATGATGCC AGTCGAAGAC GTATTCTCAA	350
	TCACTGGACG TGGTACTGTT GCTACAGGCC GTGTTGAACG TGGTGAAGTT	400
	CGCGTTGGTG ACGAAGTTGA AATCGTTGGT ATTAAAGACG AAACATCTAA	450
	AACAACGTGT ACAGGTGTTG AAATGTTCCG TAAATTATTA GACTACGCTG	500
30	AAGCAGGCGA CAACATCGGT GCTTTATTAC GTGGTGTAGC ACGTGAAGAT	550
	ATCGAACGTG GACAAGTATT AGCTAAACCA GCTACAATCA CTCCACACAC	600
	AAAATTCAAA GCTGAAGTAT ACGTATTATC AAAAGAAGAA GGCGGACGTC	650
	ACACTCCATT CTTCACTAAC TACCGTCCTC	680

2) INFORMATION FOR SEQ ID NO: 63

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 680 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
 (B) STRAIN: R487

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63

55	AGTAGTTTCT GCTGCTGATG GTCCTATGCC TCAAACACGT GAACATATCT	50
	TATTATCACG TAACGTTGGT GTACCATACA TCGTTGTATT CTTAAACAAA	100
	ATGGATATGG TTGATGACGA AGAATTATTA GAATTAGTAG AAATGGAAGT	150
	TCGTGACTTA TTATCAGAAT ACGATTTCCC AGGCGATGAT GTTCCAGTTA	200
	TCGCAGGTTT TGCTTTGAAA GCTTTAGAAG GCGACGAGTC TTATGAAGAA	250
	AAAATCTTAG AATTAATGGC TGCAGTTGAC GAATATATCC CAACTCCAGA	300
	ACGTGATACT GACAAACCAT TCATGATGCC AGTCGAAGAC GTATTCTCAA	350
60	TCACTGGACG TGGTACTGTT GCTACAGGCC GTGTTGAACG TGGTGAAGTT	400

CGCGTTGGTG ACGAAGTTGA AATCGTTGGT ATTAAAGACG AAACATCTAA 450
 AACAACTGTT ACAGGTGTTG AAATGTTCCG TAAATTATTA GACTACGCTG 500
 AAGCAGGCGA CAACATCGGT GCTTTATTAC GTGGTGTAGC ACGTGAAGAT 550
 ATCGAACGTG GACAAGTATT AGCTAAACCA GCTACAATCA CTCCACACAC 600
 5 AAAATTCAAA GCTGAAGTAT ACGTATTATC AAAAGAAGAA GGCGGACGTC 650
 ACACTCCATT CTTACTAAC TACCGTCCTC 680

10 2) INFORMATION FOR SEQ ID NO: 64

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 685 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: R482

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64

25 AGTAGTTTCT GCTGCTGACG GCCCAATGCC TCAAACCTCGT GAACACATCC 50
 TATTGTCTCG TCAAGTTGGT GTTCCTTACA TCGTTGTATT CTTGAACAAA 100
 GTAGACATGG TTGATGACGA AGAATTACTA GAATTAGTTG AAATGGAAGT 150
 TCGTGACCTA TTAACAGAAAT ACGAATTCCC TGGTGACGAT GTTCCTGTAG 200
 30 TTGCTGGATC AGCTTTGAAA GCTCTAGAAG GCGACGCTTC ATACGAAGAA 250
 AAAATTCTTG AATTAATGGC TGCAGTTGAC GAATACATCC CAACTCCAGA 300
 ACGTGACAAC GACAAACCAT TCATGATGCC AGTTGAAGAC GTGTTCTCAA 350
 TTACTGGACG TGGTACTGTT GCTACAGGTC GTGTTGAACG TGGACAAGTT 400
 CGCGTTGGTG ACGAAGTTGA AGTTGTTGGT ATTGCTGAAG AAACCTTCAA 450
 35 AACAAACAGTT ACTGGTGTG AAATGTTCCG TAAATTGTTA GACTACGCTG 500
 AAGCTGGAGA CAACATTGGT GCTTTACTAC GTGGTGTGTC ACGTGAAGAC 550
 ATCCAACGTG GACAAAGTTT AGCTAAACCA GGTACAATCA CACCTCATAC 600
 AAAATTCTCT GCAGAAGTAT ACGTGTGAC AAAAGAAGAA GGTGGACGTC 650
 ATACTCCATT CTTACTAAC TACCGTCCTC AATTT 685
 40

2) INFORMATION FOR SEQ ID NO: 65

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: *Enterococcus flavescens*
 (B) STRAIN: ATCC 49996

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65

60 CGGCGCGATC TTAGTAGTAT CTGCTGCTGA TGGTCCTAYG CCTCAAACAC 50
 GTGAACACAT CTTGTTATCA CGTAACGTTG GTGTACCATA CATCGTTGTT 100

	TTCTTAAACA	AAATGGATAT	GGTTGATGAC	GAAGAATTAC	TAGAATTAGT	150
	TGAAATGGAA	GTTTCGTGACT	TATTGTCAGA	ATATGACTTC	CCAGGCGACG	200
	ATGTTCTCTGT	AATCGCTGGT	TCTGCTTTGA	AAGCTCTTGA	AGGCGATGCT	250
5	TCATACGAAG	AAAAAATCAT	GGAATTAATG	GCTGCAGTTG	ACGAATACGT	300
	TCCAACCTCCA	GAACGTGACA	CTGACAAACC	ATTCATGATG	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGA	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
	CGTGGACAAG	TTCGCGTTGG	TGACGAAGTT	GAAATCGTTG	GTATTGCTGA	450
	AGAAACTGCT	AAAACAACCTG	TAACCTGGTGT	TGAAATGTTT	CGTAAATTGT	500
	TAGACTATGC	TGAAGCAGGG	GATAACATTG	GTGCATTGCT	ACGTGGGGTT	550
10	GCTCGTGAAG	ACATCCAACG	TGGACAAGTA	TTAGCTAAAG	CTGGTACAAT	600
	CACACCTCAT	ACAAAAATTTA	AAGCTGAAAGT	TTACGTTTTA	ACAAAAGAAG	650
	AAGGTGGACG	TCACACTCCA	TTCTTCACTA	ACTACCGTCC	TCAGTTCTAC	700
	TTCCGTACAA	CTGACGTAAAC	TGGTGTGTGT	GAATTACCAG	AAGGAAGTGA	750
	AATGGTTATG	CCTGGTGATA	AMGTAACAAT	CGACGTTGAA	TTGATCCACC	800
15	CAATCGCTAT	CGAAGACGGA	ACTCG			825

2) INFORMATION FOR SEQ ID NO: 66

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 636 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
 (B) STRAIN: R420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66

35	TCCTATGCCT	CAAACCTCGTG	AACACATCTT	GTTATCACGT	AACGTTGGCG	50
	TACCATACAT	CGTTGTTTTT	TTGAACAAAA	TGGATATGGT	TGATGACGAA	100
	GAATTGCTAG	AATTAGTTGA	AATGGAAGTT	CGTGACCTAT	TGTCTGAGTA	150
	TGACTTCCCA	GGCGACGATG	TTCCTGTAAT	CGCCGGTTCT	GCTTTGAAAG	200
	CTCTTGAAGG	AGATCCTTCA	TACGAAGAAA	AAATCATGGA	ATTGATGGCT	250
40	GCAGTTGACG	AATACGTTCC	AACTCCAGAA	CGTGATACTG	ACAAACCATT	300
	CATGATGCCA	GTCGAAGACG	TATTCTCAAT	CACTGGACGT	GGTACTGTTG	350
	CTACAGGCCG	TGTTGAACGT	GGACAAGTTC	GCGTTGGTGA	TGAAGTAGAA	400
	ATCGTTGGTA	TTGCTGACGA	AACTGCTAAA	ACAACGTGTA	CAGGTGTTGA	450
	AATGTTCCGT	AAATTGTTAG	ACTATGCTGA	AGCAGGGGAT	AACATTGGTG	500
45	CATTGCTACG	TGGGGTTGCT	CGTGAAGACA	TCCAACGTGG	ACAAGTATTG	550
	GCTAAAGCTG	GTACAATCAC	ACCTCATACA	AAATTCAAAG	CTGAAGTTTA	600
	TGTTTTTGACA	AAAGAAGAAG	GTGGACGTCA	CACTCC		636

2) INFORMATION FOR SEQ ID NO: 67

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus hirae*
 (B) STRAIN: ATCC 8043

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67

```

5      CGGAGCTATC TTAGTAGTTT CTGCTGCTGA TGGTCCTATG CCTCAAACCTC      50
      GTGAACATAT CCTAYTATCT CGTCAAGTTG GTGTTCCATA CATCGTTGTA      100
      TTCTTGAACA AAGTAGATAT GGTTGACGAC GAAGAATTAC TAGAATTAGT      150
10     TGAAATGGAA GTTCGTGACT TATTAACAGA ATACGAATTC CCTGGTGACG      200
      ATGTTTCCTGT AGTTGCTGGT YCAGCTTTGA AAGCTTTAGA AGGCGACGCT      250
      TCATACGAAG AAAAAATCCT TGAATTGATG GCTGCAGTTG ACGAATATAT      300
      CCCAACTCCA GAACGTGACA ACGACAAACC ATTCATGATG CCAGTCGAAG      350
      ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG TCGTGTGAA      400
15     CGTGGACAAG TTCGCGTTGG TGACGTTGTA GATATCGTTG GTATCGCAGA      450
      AGAAACAGCT CAAACAACAG TTAAGCTGGT TGAAATGTTT CGTAAATTAT      500
      TAGACTACGC TGAAGCTGGA GACAACATTG GTGCTTTACT ACGTGGTGT      550
      GCACGTGAAG ACATCCAACG TGGACAAGTT TTAGCTAAAC CAGGTACAAT      600
      CACACCTCAT ACAAATTCT CTGCAGAAGT ATACGTGTTG ACAAAGAAG      650
20     AAGGTGGACG TCATACTCCA TTCTTCACTA ACTACCGTCC ACAATTCTAC      700
      TTCCGTACRA CTGACGTAAC AGGTGTTGTT GAATTACCAG AAGGAACTGA      750
      AATGGTTATG CCTGGCGACA ACGTAACAAT GGAAGTTGAA TTAATCCACC      800
      CAATCGCTAT CGAAAACGGT ACTAAATTCT CAATC      835
  
```

25

2) INFORMATION FOR SEQ ID NO: 68

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus mundtii*
 (B) STRAIN: ATCC 43186

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68

```

      CGGAGCAATC TTAGTTGTTT CTGCTGCTGA CGGCCCTATG CCTCAAACCTC      50
      GTGAACACAT CCTATTATCT CGTCAAGTTG GTGTACCATA CATCGTTGTA      100
45     TTCTTGAACA AAGTAGATAT GGTTGATGAC GAAGAATTAC TTGAATTAGT      150
      TGAAATGGAA GTTCGTGACC TATTAACAGA ATACGAATTC CCTGGTGACG      200
      ATGTTTCCTGT AATCGCTGGT TCAGCTTTAA GAGCTTTAGA AGGCGACGCT      250
      KCATACGAAG AAAAAATTCT TGAATTGATG GCTGCAGTTG ACGAATATAT      300
      CCCAACTCCA GAACGTGATA ACGACAAACC ATTCATGATG CCAGTTGAGG      350
50     ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG ACGTGTGAA      400
      CGTGGACAAG YTCGTGTTGG TGACGTTATC GATATCGTTG GTATCGCAGA      450
      AGAAACAGCT CAAACAACCTG TAACCTGGTGT TGAAATGTTT CGTAAATTAT      500
      TAGACTACGC TGAAGCAGGC GATAACATTG GTGCGTTACT ACGTGGTGT      550
      TCACGTGAAG ACATCCAACG TGGTCAAGTT TTAGCTAAAC CAGGTACAAT      600
55     CACACCTCAT ACAAATTCT CTGCAGAAGT ATACGTGTTG ACTAAAGAAG      650
      AAGGTGGACG TCATACTCCA TTCTTCACTA ACTACCGTCC ACAATTCTAC      700
      TTCYGTACGA CTGACGTAAC TRGTGTTGTY GAATTACCAG AAGGAACTGA      750
      AATGGTTATG CCTGGCGACA ACGTAACAAT GGAAGTTGAA TTAATCCACC      800
      CAATCGCTAT CGAAAATGGT ACTAAATTCT CAATC      835
  
```

60

2) INFORMATION FOR SEQ ID NO: 69

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 836 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus pseudoavium*
 (B) STRAIN: ATCC 49372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69

20	CGGAGCTATC	TTAGTAGTAT	CTGCTGCTGA	TGGCCCTATG	CCTCAAACAC	50
	GTGAACACAT	CTTGTTATCT	CGTAACGTTG	GTGTTCCCTA	CATCGYTGTA	100
	TTCTTAAACA	AAATGGATAT	GGTTGATGAC	GAAGAATTAC	TAGAATTAGT	150
	TGAAATGGAA	GTTTCGTGACT	TATTGTCAGA	ATACGATTTT	CCAGGCGACG	200
	ACACTCYAGT	TATCGCTGGT	TCAGCYTTGA	AAGCTTTAGA	AGGCGACCCT	250
	TCATACRAAG	AAAAAATCTT	AGAATTAATG	SCTGCTGTTG	ACGAATACAT	300
25	CCCAACACCA	GTTTCGTGATA	CTGACAAACC	ATTCAATGATG	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCAACTGG	TCGTGTTGAA	400
	CGTGGACAAG	TTCGCGTTGG	TGACGAAGTT	GAAATCGTAG	GTATCGCTGA	450
	AGAAACTGCT	AAAACAACCTG	TTACAGGTGT	TGAAATGTTT	CGTAAATTGT	500
	TAGACTACGC	TGAAGCAGGC	GATAACATCG	GTGCATTATT	ACGTGGTGTG	550
30	GCACGTGAAG	ACATCCAACG	TGGACAAGTA	TTGGCTAAAC	CAGCTTCAAT	600
	CACTCCACAT	ACAAAATTCT	CTGCAGAAGT	TTACGTTTTA	ACTAAAGAAG	650
	AAGGCGGGCG	TCACACTCCG	TTCTTCACTA	ACTACCGTCC	TCAGTTCTAC	700
	TTCCGTACAA	CTGACGTAAC	TGGTGTGTTG	GATCTACCAG	AAGGTACTGA	750
	AATGGTAATG	CCTGGTGATA	ACGTAACAT	GGAAGTTGAA	TTAATCCACC	800
35	CAATCGCGAT	CGAAGACGGA	ACTCGTTTCT	CTATTC		836

2) INFORMATION FOR SEQ ID NO: 70

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus raffinosus*
 (B) STRAIN: ATCC 49427

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70

55	CGGAGCTRTC	TTAGTAGTAT	CTGCTGCTGA	TGGCCCTATG	CCTCAAACCTC	50
	GTGAACACAT	CTTGTTATCT	CGTAACGTTG	GTGTTCCCTA	CATCGTTGTA	100
	TTCTTAAACA	AAATGGATAT	GGTTGACGAT	GAAGAATTAC	TAGAATTAGT	150
	TGAAATGGAA	GTTTCGTGACT	TATTAAGTGA	ATACGACTTC	CCAGGCGACG	200
	ACACTCCAGT	TATCGCAGGT	TCAGCTTTGA	AAGCCTTAGA	AGGCGACGCT	250
60	TCATACGAAG	AAAAAATCTT	AGAATTAATG	GCTGCTGTTG	ATGAATACAT	300

```

    . . .
    CCCAACACCA GTTCGTGATA CTGACAAACC ATTCATGATG CCAGYGGAAG 350
    ACGTAYTCTC AATCACTGGT CGTGGAAGTG TTGCAACTGG TCGTGTTGAA 400
    CGTGGACAAG TTCGCGTTGG TGACGAAGTT GAAATCGTAG GTATTGCTGA 450
    AGAAACTGCT AAAACAACTG TTACAGGTGT TGAAATGTTC CGTAAATTGT 500
    5 TGGATTACGC TGAAGCGGGC GACAACATTG GTGCATTATT ACGTGGTGTT 550
    GCACGTGAAG ACATCCAACG TGGACAAGTA TTGGCTAAAC CAGCTTCAAT 600
    CACTCCACAT ACAAAATTCT CTGCAGAAGT TTACGTTTTA ACTAAAGAAG 650
    AAGGCGGACG TCATACTCCA TTCTTCACTA ACTACCGTCC TCAGTTCTAC 700
    TTCCGTACAA CTGACGTAAC TGGTGTAGTT GATCTACCAG AAGGTACTGA 750
    10 AATGGTAATG CCTGGTGATA ACGTAACTAT GGAAGTTGAA TTAATCCACC 800
    CAATCGCGAT CGAAGACGGA ACTCGTTTCT CTATT 835
  
```

15 2) INFORMATION FOR SEQ ID NO: 71

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus saccharolyticus*
 (B) STRAIN: ATCC 43076

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71

```

    30 CGGCGCGATC TTAGTAGTAT CTGCTGCTGA TGGTCCTATG CCTCAAACCTC 50
    GTGAACACAT CTTGTTATCT CGTAACGTAG GTGTTCCCTTA CATCGTTGTA 100
    TTCTTAAACA AAATGGATAT GGTTGATGAC GAAGAATTAT TAGAATTAGT 150
    AGAAATGGAA GTTCGTGACT TATTATCAGA ATACGATTTT CCAGGCGATG 200
    35 ACACTCCAGT TATTGCAGGT TCTGCTTTGA AAGCTTTAGA AGGCGATCCA 250
    GTTTACGAAG AAAAAATCTT CGAATTAATG GCTGCAGTTG ACGAATATAT 300
    CCCAACTCCA GAACGTGATA CTGAAAAACC ATTCATGATG CCAGTTGAGG 350
    ATGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG TCGTGTTGAA 400
    CGTGGACAAG TTCGCGTTGG TGACGTTGTA GAAATCGTTG GTATCGACGA 450
    40 AGAAACAGCT CAAACTACTG TAACAGGTGT TGAAATGTTC CGTAAATTAT 500
    TAGACTACGC TGAAGCAGGC GATAACATCG GTGCTTTATT ACGTGGGGTT 550
    GCTCGTGAAG ACATCCAACG TGGACAAGTA TTAGCTAAAC CAGGAACAAT 600
    CACTCCTCAT ACAAATTCG TAGCTGAAGT TTACGTTTTA ACTAAAGAAG 650
    AAGGTGGACG TCATACTCCA TTCTTCACTA ACTACCGTCC TCAATTCTAC 700
    45 TTCCGTACAA CTGACGTAAC TGGTGTGTA GAATTACGCG AAGGTACTGA 750
    AATGGTAATG CCTGGTGACA ACGTAACTAT CGACGTTGAA TTAATCCACC 800
    CAATCGCTAT CGAAGACGGA ACTCGTTTCT CTATT 835
  
```

50 2) INFORMATION FOR SEQ ID NO: 72

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus solitarius*
 (B) STRAIN: ATCC 49428

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72

```

GAGCTATCTT GGTAGTTTCT GCAGCTGATG GCCCAATGCC ACAAACCTCGT      50
GAACATATTT TGTTGTCACG TAATGTAGGT GTACCTTACA TCGTTGTGTT      100
CTTGAACAAA ATGGATATGG TTGATGACGA AGAATTACTT GAGTTAGTTG      150
10 AAATGGAAGT ACGTGATCTA TTATCTGAAT ACGACTTCCC AGGAGATGAT      200
ACTCCAGTTA TTCCCGGTTT AGCTTTGAAA GCTTTAGAAG GCGACGAAGA      250
ATATGAACAA AAAATTATGG ACTTAATGGA TGCAGTTGAT GACTACATTC      300
CAACTCCTGA ACGTGACCAT GACAAACCAT TCATGATGCC AATTGAAGAT      350
GTATTTTCAA TTACAGGCCG TGGTACTGTT GCTACAGGAC GTGTTGAACG      400
15 CGGGACTATC AAAGTCGGCG ATGAAGTTGA CATTATTGGT ATTCATGAAG      450
ACGTTAAAAA GACAACAGTT ACTGGTGTAG AAATGTTCCG TAAATTGTTG      500
GACTACGCTG AAGCAGGCCG TAACATTGGT ACTTTGTTAC GTGGTGTGTT      550
TCGTGATGAT ATCGAACGTG GTCAAGTATT AGCTAAACCA GGTTCAATCA      600
20 CACCACATAC AAGATTCTCT GCTGAAGTTT ATGTTTGGAC TAAAGAAGAA      650
GGCGGACGTC ATACTCCATT CTTCTCAAAC TATCGTCCTC AATTCTACTT      700
CCGTACAACG GATATCACTG GTGTCATTGA ATTGCCAGAA GGTACTGAAA      750
TGGTAATGCC AGGTGATAAT GTAACAATGG ATGTTGAATT AATCCACCCA      800
GTCGCTATCG AAGAAGGAAC TCG                                     823
  
```

2) INFORMATION FOR SEQ ID NO: 73

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 665 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*
 (B) STRAIN: ATCC 25788

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73

```

GCAATCTTGG TCGTATCAGC GACAGATGGC CCAATGCCAC AAACACGGGA      50
GCATATTTTG CTTTCTCGTC AAGTGGGTGT GAAACATTTG ATCGTCTTTT      100
45 TGAATAAGAC GGACCTTGTC GATGATGACG AGTTGATCGA TTAGTTGAA      150
ATGGAAGTCA GAGAATTGCT GACTGAATAT GATTTTCCTG GCGACGACAT      200
TCCTGTGATC AAGGGCTCTG CGTTAAAAGC CTTGGAAGGG GACCCAGATG      250
CTGAAGCAGC GATCTTAACG CTGATGGATA CAGTAGATGA ATATATCCCA      300
50 ACGCCAGAAC GTGATACTGA CAAACCATTG TTGTTACCGA TCGAAGATGT      350
CTTTTTCGATC ACAGGACGGG GGACCGTTGC TTCTGGTCCG ATCGATCGCG      400
GCATGGTAAA AGTCGGGGAT GAAGTAGAAA TCGTCGGAAT CAAACCTGAA      450
ACACAAAAAG CAGTCGTGAC AGGGGTAGAA ATGTTCCGCA AAACGATGGA      500
CTTCGGAGAA GCTGGCGATA ACGTAGGGGT ATTGTTACGG GGCATCACCC      550
55 GTGATGAAAT TGAACGTGGC CAAGTGTTAG CAAAACCAGG TTCTATCACA      600
CCGCATACGA AATCCAAGC GGAAGTCTAT GTGTTGACAA AAGAAGAAGG      650
CGGTCGCCAT ACCCC                                     665
  
```

60 2) INFORMATION FOR SEQ ID NO: 74

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 664 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: ATCC 19434

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74

```

15  AATCTTAGTT GTTTCTGCAA CTGACGGTCC GATGCCTCAA ACACGTGAAC      50
    ACATTTTATT GTCACGCCAA GTTGGTGTA AATACCTGAT TGTTTCTTG      100
    AACAAAGTTG ATTTAGTCGA TGATGAAGAA TTGATCGATT TGGTAGAAAT      150
    GGAAGTTCGC GAGTTATTGA GCGAATATGG TTTCCCAGGC GATGACACTC      200
    CTGTGATCAA AGGTTCCGCA TTAAAAGCAT TGCAAGGCGA TCCAGATGCT      250
    GAAGCTGCTA TTATGGAATT GATGGATACA GTAGATGAAT ATATCCCAAC      300
    ACCGAACGT  GATACAGATA AACCATTACT ATTGCCAGTG GAAGACGTCT      350
    TCTCAATTAC AGGTCGAGGA ACTGTTGCCT CAGGTCGTAT TGATCGTGGT      400
    GCTGTTTCGTG TCGGTGATGA GGTAGAGATC GTAGGGATCA AACCTGAAAC      450
    ACAAAAAGCA GTTGTAACAG GTGTAGAAAT GTTCCGTAAA ACGTTAGATT      500
    ACGGGGAAGC TGGGGATAAC GTAGGCGTGT TGTTACGGGG GATCCAACGT      550
    GACGATATCG AACGTGGACA AGTACTTGCT AAACCAGGTT CCATTACTCC      600
    ACATACAAAA TTCAAAGCAG AAGTGTACGT GTTGACAAAA GAAGAAGGTG      650
    CACGTCATAC TCCA                                     664
  
```

2) INFORMATION FOR SEQ ID NO: 75

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 666 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus flavescens*
 (B) STRAIN: ATCC 49996

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75

```

50  GCAATCTTGG TCGTATCAGC GACAGATGGC CCAATGCCAC AAACACGGGA      50
    GCATATTTTG CTTTCTCGTC AAGTGGGTGT GAAACATTTG ATCGTCTTTT      100
    TGAATAAGAC GGACCTTGTC GATGATGACG AGTTGATCGA TTTAGTTGAA      150
    ATGGAAGTCA GAGAATTGCT GACTGAATAT GATTTTCCTG GCGACGACAT      200
    TCCTGTGATC AAGGGCTCTG CGTTAAAAGC CTTGGAAGGG GACCCAGATG      250
    CTGAAGCAGC GATCTTAACG CTGATGGATA CGGTAGATGA ATATATCCCA      300
    ACGCCAGAAC GTGATACTGA CAAACCATTG TTGTTACCGA TCGAAGATGT      350
    CTTTTCGATC ACAGGACGGG GGACCGTTGC TTCTGGTCGG ATCGATCGCG      400
    GCATGGTAAA AGTCGGGGAT GAAGTAGAAA TCGTCGGAAT CAAACCTGAA      450
    ACACAAAAAG CAGTCGTGAC AGGGGTAGAA ATGTTCCGCA AAACGATGGA      500
    CTTCCGAGAA GCTGGCGATA ACGTAGGGGT ATTGTTACGG GGCATCACCC      550
    GTGATGAAAT TGAACGTGGC CAAGTGTTAG CAAAACCAGG TTCTATCACA      600
  
```

CCGCATACGA AATTCCAAGC GGAAGTCTAT GTGTTGACAA AAGAAGAAGG
CGGTCGCCAT ACCCCA

650
666

5

2) INFORMATION FOR SEQ ID NO: 76

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 667 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
(B) STRAIN: ATCC 49573

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76

	TGCGATTTTA GTTGTATCCG CAACAGATGG TCCAATGCCT CAAACCCGGG	50
	AACATATCTT GCTTTCGAGA CAAGTTGGTG TGAAACATCT GATTGTTTTC	100
	TTGAACAAAA TCGATTTAGT CGATGACGAA GAATTGATTG ATTTAGTAGA	150
25	AATGGAAGTA AGAGAACTGC TATCTGAATA TAATTTTCCA GGGGATGACA	200
	TTCTGTATAT CAAAGGTTCG GCATTAATAAG CGTTGGAAGG AGACCCTGAT	250
	GCAGAAGCTG CCATCATGGA ATTAATGGAT ACAGTAGACA GCTATATCCC	300
	AACACCTGAG CGTGATACAG ACAAACCATT ACTCTTGCCA GTTGAAGATG	350
	TCTTTTTCGAT TACTGGACGA GGAACAGTTG CTTCCGGACG GATCGATCGG	400
30	GGAACAGTTC GGGTAGGCCA TGAAGTAGAA ATCGTCGGTA TCAAACCTGA	450
	AACCCAAAAA GCTGTAGTGA CAGGCGTCCA AATGTTCCGC AAGACGATGG	500
	ACTTTGGGGA AGCCGGTGAC AATGTAGGTG TCTTGCTGAG AGGGATCACT	550
	CGTGACGAAA TTGAACGAGG ACAAGTGTTG GCTAAACCAG GTTCGATCAC	600
	ACCACATACA AAATTCCAAG CAGAAGTTTA TGTATTGACG AAAGAAGAAG	650
35	GTGGTCGTCA TACACCA	667

2) INFORMATION FOR SEQ ID NO: 77

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 834 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Ehrlichia canis*
(B) STRAIN: Florida

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77

55	TGCAGCAATA TTAGTAGTGT CTGCAACTGA TGGAGCAATG CCACAAACAA	50
	GAGAACATAT ATTATTAGCA AAGCAAGTAG GTGTAAAAGA TATAGTAGTG	100
	TGGATGAATA AGTGTGATGT TGATAGATGAT GAAGAAATGT TGTCATTAGT	150
	TGAAATGGAA ATAAGGGAAT TGTTATCAAA ATATGGGTAT CCTGGGGATG	200
	ATATAGATGT AGTTAGAGGA TCTGCAGTTA AAGCATTAGA AGAAGAAACA	250
60	GGCTCAGGTG TGTGGAGTGA AAAAATAATG GAATTGATGA ATGCTTTAGA	300

5 AAAAATAAGT TTACCAGTAA GAGAAAAAGA TAAGCCATTT TTAATGTCAA 350
 TAGAAGATGT GTTTTCAATA CCTGGAAGAG GTACAGTAGT AACAGGAAGA 400
 ATAGAAAGAG GAGTAATTAG AGTAGGGGAT AAAATAGAGA TAGTAGGATT 450
 GCGTGAGATA CAAAGTACAG TATGTACAGG TGTGAAATG TTTCATAAAG 500
 CATTAGATGC AGGAGAAGCA GGGGATAATG CTGGAATATT GTTAAGAGGG 550
 ATAAAAAAG AAGATGTAGA AAGAGGGCAA GTATTGAGTG CACCTGGACA 600
 GATACATTCA TATAAGAGAT TTAAGGCAGA GGTATATATA TTGAAAAAAG 650
 AAGAAGGAGG AAGACATACT CCATTTTCT CAAATTACCA GCCGCAATTT 700
 TATGTTAGAA CAACAGATGT AACAGGGAAT ATAAAGTTAC CAGAAGGAGT 750
 10 AGAAATGGTA ATGCCAGGGG ATAATATAAA TATCGAAGTG AGTTTGGATA 800
 AGCCTGTTGC TATTGATCAA GGATTGAGAT TTGC 834

15 2) INFORMATION FOR SEQ ID NO: 78

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: ATCC 23511

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78

30 CGGCGCGATC CTGGTAGTTG CTGCGACTGA CGGCCCGATG CCGCAGACTC 50
 GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG 100
 TTCCTGAACA AATGCGACAT GGTGATGAC GAAGAGCTGC TGGAAGTGGT 150
 TGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGACTTC CCGGGCGACG 200
 35 ACGACTCCGAT CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGACGCA 250
 GAGTGGGAAG CGAAAATCCT GGAAGTGGT GGCTTCCTGG ATTCTTAYAT 300
 TCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG 350
 ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAA 400
 CGCGGTATCA TCAAAGTTGG TGAAGAAGTT GAAATCGTTG GTATCAAAGA 450
 40 GACTCAGAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAAGTGTCTGG 500
 ACGAAGGCCG TGCTGGTGAG AACGTAGGTG TTCTGCTGCG TGGTATCAA 550
 CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCACCATCAA 600
 GCCGCACACC AAGTTCCAAT CTGAAGTGTA CATTCTGTCC AAAGATGAAG 650
 GCGGCCGTCA TACTCCGTTT TTCAAAGGCT ACCGTCCGCA GTTCTACTTC 700
 45 CGTACTACTG ACGTGAAGTGG TACCATCGAA CTGCCGGAAG GCGTAGAGAT 750
 GGTAATGCCG GCGGACAACA TCAAATGGT TGTTACCCTG ATCCACCCGA 800
 TCGCGATGGA CGACGGT 817

50 2) INFORMATION FOR SEQ ID NO: 79

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia fergusonii*
 (B) STRAIN: ATCC 35469

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79

	CGATCCTGGT	AGTTGCTGCG	ACTGACGGCC	CGATGCCGCA	GACTCGTGAG	50
	CACATCCTGC	TGGGTCGTCA	GGTAGGCGTT	CCGTACATCA	TCGTGTTTCCT	100
	GAACAAGTGC	GACATGGTTG	ATGACGAAGA	GCTGCTGGAA	CTGGTTGAAA	150
10	TGGAAGTTTC	TGAACTTCTG	TCTCAGTACG	ACTTCCCGGG	CGACGACACT	200
	CCGATCGTTC	GTGGTTCTGC	TCTGAAAGCG	CTGGAAGGCG	ACGCAGAGTG	250
	GGAAGCGAAA	ATCCTGGAAC	TGGCTGGCTT	CCTGGATTCT	TACATTCCGG	300
	AACCAGAGCG	TGCGATTGAC	AAGCCGTTCC	TGCTGCCGAT	CGAAGACGTG	350
	TTCTCCATCT	CCGGTCGTGG	TACCGTTGTT	ACCGGTCGTG	TAGAACGCGG	400
15	TATCATCAAA	GTTGGTGAAG	AAGTTGAAAT	CGTTGGTATC	AAAGAGACTC	450
	AGAAGTCTAC	CTGTACTGGC	GTTGAAATGT	TCCGCAAAC	GCTGGACGAA	500
	GGCCGTGCTG	GTGAGAACGT	AGGTGTTCTG	CTGCGTGGTA	TCAAACGTGA	550
	AGAAATCGAA	CGTGGTCAGG	TACTGGCTAA	GCCGGGCACC	ATCAAGCCGC	600
	ACACCAAGTT	CGAATCTGAA	GTGTACATTC	TGTCCAAAGA	TGAAGGCGGT	650
20	CGTCATACTC	CGTTCCTTCA	AGGCTACCGT	CCGCAGTTCT	ACTTCCGTAC	700
	TACTGACGTG	ACTGGTACCA	TCGAACTGCC	GGAAGGCGTA	GAGATGGTAA	750
	TGCCGGGCGA	CAACATCAAA	ATGGTTGTTA	CCCTGATCCA	CCCATCGCG	800
	ATGGACGACG	GTCTGCGTTT	CGCAA			825

25

2) INFORMATION FOR SEQ ID NO: 80

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia hermannii*
 (B) STRAIN: ATCC 33650

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80

	GGCGCGATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCGATGC	CGCAGACCCG	50
	TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	100
45	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTT	150
	GAGATGGAAG	TTCGCGAACT	GCTGTCCCAG	TACGATTTC	CGGGCGACGA	200
	CACCCCGATC	GTTTCGTGGT	CCGCGCTGAA	AGCGCTGGAA	GGCGAAGCAG	250
	AGTGGGAAGA	GAAAATCATC	GAAGTGGCTG	GCTACCTGGA	TTCCTATATC	300
	CCGGAACCAG	AGCGTGCGAT	TGACAAGCCG	TTCCTGCTGC	CTATCGAAGA	350
50	CGTATTCTCC	ATCTCCGGCC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAGC	400
	GCGGTATCAT	CAAAGTGGGT	GAAGAAGTTG	AAATCGTGGG	TATCAAAGAT	450
	ACTGCGAAAT	CAACCTGTAC	CGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCGGGCGAGA	ACGTGGGTGT	TCTGCTGCGT	GGTATCAAAC	550
	GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	TTCCATCAAG	600
55	CKKACACCA	AGTTCGAATC	TGAAGTGATC	ATTCTGTCCA	AAGACGAAGG	650
	CGGCCGTCAC	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	700
	GTACAACCTGA	CGTGACTGGC	ACCATCGAAC	TGCCGGAAGG	CGTTGAGATG	750
	GTAATGCCCG	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TCCACCCGAT	800
60	CGCGATGGAC	GACGGTCTGC	GTTTCGCAA			829

2) INFORMATION FOR SEQ ID NO: 81

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 816 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Escherichia vulneris*
 - (B) STRAIN: ATCC 33821

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81

20	CGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACCC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	100
	TTCTTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	TGAGATGGAA	GTGCGTGAAC	TTCTGTCCCA	GTACGACTTC	CCGGGCGACG	200
	ACACCCCGAT	CATTCGTGGT	TCTGCGCTGA	AAGCGCTGGA	AGGCGAAGCT	250
	GAGTGGGAAG	AGAAAATCGT	TGAGCTGGCT	GGCTACCTGG	ATTCTACAT	300
25	CCCGGAACCA	GAGCGTGCGA	TTGACAAGCC	GTTCTGCTG	CCGATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
	CGCGGTATCA	TCAARGTKGG	TGAAGAAGTT	GAAATCGTGG	GTATCAAAGA	450
	TACTGCGAAA	TCTACCTGTA	CCGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGTCG	TGCAGGCGAG	AACTGCGGCG	TTCTGCTGCG	TGGTATCAAG	550
30	CGTGAAGAGA	TCCAGCGTGG	CCAGGTTCTG	GCTAAGCCGG	GCTCAATCAA	600
	GCCGCACACC	AAGTTCGAAT	CCGAAGTGTA	CATCCTGTCC	AAAGACGAAG	650
	GCGGCCGTCA	CACTCCGTTT	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACAACTG	ACGTGACTGG	CACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
	GGTAATGCCG	GGCGACAACA	TCAAATGGT	TGTTACCCTG	ATCCATCCGA	800
35	TCGCGATGGA	CGACGG				816

2) INFORMATION FOR SEQ ID NO: 82

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 828 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Eubacterium lentum*
 - (B) STRAIN: ATCC 43055

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82

55	CGGCGCCTCC	TCGTTATCGC	CGCCACCGAC	GGCCCGATGG	CCCAGACCCG	50
	CGAGCACATC	CTGCTCGCCC	GTCAGGTCGG	CGTGCCCTAC	ATCGTGGTCT	100
	TCCTGAACAA	GTGCGACATG	GTCGACGACG	AGGAGCTCCT	CGAGCTCGTC	150
	GAGATGGAAG	TTGCGGAGCT	GCTCGACTCT	TACGAGTTCC	CGGGCGACGA	200
	CACCCCGATC	ATCCGCGGCT	CCGCTTTGAA	GGCCCTCGAG	GGCGACAAAG	250
60	AGTGGCAGGA	GAAGGTCTGG	GAGCTCATGG	ACGCCGTCGA	CTCCTACATC	300

	CCGACGCCGG	AGCGCATGGT	CGACAAGCCG	TTCCTGATGG	CCGTCGAGGA	350
	CACGATGACC	ATCACCGGCC	GCGGCACCGT	TGCCACCGGT	CGTGTGGAGC	400
	GTGGTACGCT	GCATGTCAAC	GACCCGCTGG	AGATCGTCGG	TATCAAGGAG	450
	ACCCAGAACA	CGGTCTGCAC	CGGTATCGAG	ATGTTCCGCA	AGCTGCTCGA	500
5	CGAGGCTCAG	GCCGGCGACA	ACATCGGCTG	CCTGCTCCGC	GGTGTCAAGC	550
	GCGAGGAGAT	CGTTTCGCGC	CAGGTTCTCT	GCAAGCCCGG	TAGCGTGACC	600
	CCGCACACCG	AGTTTCGAGG	TCAGGTCTAC	ATCCTGACGA	AGGAAGAGGG	650
	CGGCCGCCAC	ACGCCGTTCT	TCGACGGCTA	CCGTCCGCAG	TTCTACTTCC	700
	GCACGACGGA	CGTGACGGGT	GTTGCCACC	TTCCCGAGGG	CACCGAGATG	750
10	GTCATGCCGG	GCGACAACGT	GGAGATCAAG	GGCGAGCTCA	TTCACCCGAT	800
	CGCCAGGAAG	AGGGCTGCGT	TCGCTAAC			828

15 2) INFORMATION FOR SEQ ID NO: 83

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Eubacterium nodatum*
 (B) STRAIN: ATCC 33099

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83

30	GGAGCAATTC	TGGTTTGTGC	AGCAACKGAC	GGACCAATGC	CTCAGACAAG	50
	AGAACATATC	CTTTTGTCAA	GGCAGGTAGG	AGTGCCATAT	ATCATCGTAT	100
	TCCTGAATAA	ATGTGACATG	GTGGATGAYG	AAGAGCTTCT	GGAAGTGGTA	150
	GAGATGGAAG	TAAGAGAACT	TCTCAGTGAG	TATGAATTCC	CGGGAGATGA	200
35	TACCCCGATA	GTAAGAGGTT	CAGCCCTGAA	GGCACTGGAA	GAACCCAATG	250
	GAGAATGGGC	AGACAAGATT	GTAGAGCTGA	TGGAGGAAGT	AGATAAATAC	300
	ATTCCTGAAC	CAAAGAGAGA	TAACGACAAA	CCGTTCTCTGA	TGCCTGTAGA	350
	GGACGTATTC	TCAATAACAG	GAAGAGGAAC	AGTAGCGACA	GGAAGRGTG	400
	AAAGAGGAAT	CCTGAAGGTC	GGTGATGAAG	TAGAAATCGT	GGGAATGAGC	450
40	GAAGAGAGAA	GAAAGGTAGT	AGTAACGGGA	GTTGAAATGT	TCAGAAAGCT	500
	TCTGGATGAA	GCAGAGACAG	GAGACAACAT	CGGAGCACTG	CTGAGAGGAG	550
	TTCAGAGAAC	RGAGATCCAG	AGAGGTCAGG	TATTGGCRGC	ACCTGGAACG	600
	ATCAACCCAC	ATACAAAGTT	CAAGGGTCAG	GTATATGTAC	TGAAGAAGGA	650
	AGAAGGAGGA	AGGCATACGC	CGTTCTTCAA	YGGATACAGW	CCACAGTTCT	700
45	ACTTCAGAAC	AACAGACGTA	ACAGGAGATT	TGCAGCTGCC	GGAAGGARCA	750
	GAGATGTGCA	TGCCGGGAGA	TAATGTGGTA	ATGAACRTCA	GCCTGATCAC	800
	TCCGATTGCT	ATAGAAGAGG	GWCTGAGATT	TGCCA		835

50

2) INFORMATION FOR SEQ ID NO: 84

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Ewingella americana*
 (B) STRAIN: ATCC 33852

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84

```

5      GCGATCCTGG TTGTTGCTGC AACTGATGGC CCTATGCCAC AGACTCGTGA      50
      GCACATCCTG TTGGGTCGYC AGGTTGGCGT TCCATTCATG ATCGTATTCA      100
      TGAACAAATG CGACATGGTT GATGACGAAG AGCTGCTGGA ACTGGTAGAA      150
10     ATGGAAGTTC GYGAAC TTCT GTCTGCTTAC GATTTC CAG GCGACGACAT      200
      CCCAGTTGTT AAAGGTT CAG CGCTGAAAGC ACTGGAAGGC GAAGCAGAGT      250
      GGGAAAGCTAA GATCATCGAG CTGGCTGGCC ACCTGGATAG CTACATCCCA      300
      GAACCAGAGC GTGCGATTGA CAAGCCATTC CTGCTGCCAA TCGAAGACGT      350
      ATTCTCCATC TCCGGTCGTG GTACCGTTGT TACCGGTCGT GTAGAGCGCG      400
15     GTATCATCAA AGTTGGCGAA GAAGTTGAAA TCCGCGAAAC TGCTGGACGA      500
      GTTAAGTCTA CTTGTACTGG CGTTGAAATG TTCCGCAAAC TGCTGGACGA      550
      AGGCCGTGCT GGTGAGAACG TTGGTGTCTT GCTGCGTGGT ATCAAGCGTG      600
      AAGACATCGA ACGTGGTCAG GTTCTGGCTA AACCAGGTTT AATCAAACCA      650
      CACACCACWT TYGACTCAGA AGTTTATATC CTGAGCAAAG ATGAAGGCGG      700
20     CCGTCATACT CCGTCTTCA AAGGCTACCG TCCACAGTTC TACTTCCGTA      750
      CAACTGACGT GACCGGTACC ATCGAACTGC CAGAAGGCGT AGAGATGGTA      800
      ATGCCAGGTG ACAACATCAA CATGRTAGTT ACCCTGATCC ACCCAATCGC      826
      GATGGATGAC GGTCTGCGTT TCGCAA
  
```

25

2) INFORMATION FOR SEQ ID NO: 85

(i) SEQUENCE CHARACTERISTICS:

```

30     (A) LENGTH: 828 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear
  
```

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Francisella tularensis*
 (B) STRAIN: LVS

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85

```

      TGGTGCTATT CTAGTATGTT CTGCTGCGGA TGGTCCTATG CCACAAACTC      50
      GTGAGCACAT TCTGCTTTCT CGTCAAGTTG GTGTACCAA AATCGTTGTT      100
45     TTCTTAAACA AGTGTGACAT GGTTGATGAT GAAGAGTTAT TAGAGCTAGT      150
      TGAGATGGAA GTTCGTGAGC TTTTAGATCA GTATGAGTTC CCAGGTGATG      200
      AACTCCAGT TATTATGGGT TCAGCTCTTA GAGCTATTGA AGGTGACGAA      250
      GCTTACGTTG AGAAAATTGT TGAGCTAGTT CAAGCTATGG ATGACTATAT      300
      TCCTGCTCCT GAGCGTGATA CTGAGAAGCC ATTTATTCTT CCGATCGAAG      350
50     ATGTATTCTC AATTTCAGGT CGTGGTACTG TTGTAAGTGG TCGTATTGAG      400
      CGCGGTGTAG TTAACGTTGG TGATGAAGTT GAAGTTGTTG GTATTTCGTCC      450
      AACTCAAAAA ACTACAGTAA CTGGTGTGGA AATGTTCCGT AAGCTTTTAG      500
      ATAGAGGGGA AGCTGGTGAT AACGTTGGTA TCCTAGTTCG TGGACTTAAG      550
      AGAGATGATG TTGAGCGTGG ACAAGTATTA TGTAAGCCAG GTTCAATTAA      600
      GCCACATACT AAGTTTGAAG CTGAGGTTTA TGTATTATCT AAAGAAGAGG      650
55     GTGGTAGACA TACTCCATTC TTCAAGGGAT ATAGACCACA ATTCTACTTC      700
      CGTACTACAG ACATTACTGG AGCTGTTGAG CTTCAGAGG GTGTAGAAAT      750
      GGTTATGCCT GGTGATAACG TTAAGATGAC TATCACTCTA ATTAACCCAA      800
      TCGCTAGGAT GAAGGGTTAC GTTTTGCA      826
  
```

60

2) INFORMATION FOR SEQ ID NO: 86

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fusobacterium nucleatum* subsp. *polymorphum*
 (B) STRAIN: ATCC 10953

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86

20	CGGTGCTATC ATCGTAGKTG CTGCTACTGA TGGTCCGATG CCTCARACTC	50
	GTGAGCAYAT CYTGCTGGCT CGTCAGGTAA ACGTWCKAG ACTGGTTGTA	100
	TTCATGAACA AGTGYGACAT GGTAGACGAC GCTGAAATGY TGGAACCTCGT	150
	TGAAATGGAA ATGCGTGAAC TGCTTTCAGC YTACGAATTC GAYGGYGACA	200
	ACACTCCKTT CATTACAGGT TCTGCTCTTG GTGCRTTGAA YGGCGTTGAA	250
	AAGTGGGAAG AGAAGGTTAT GGANCTGATG GATGCTTGCG ACACTTGGAT	300
25	TCCTTTGCCT CCGCGTGATA TTGAYAAACC GTTCTTGATG CCGGTTGAAG	350
	ACGTATTCTC AATCACTGGT CGTGGTACTG TAGCTACTGG TCGTATCGAA	400
	GCTGGTGTTA TCCATGTAGG TGACGAAGTT GAAATCCTCG GTTTGGGTGA	450
	AGACAAGAAG TCTGTTGTAA CTGGTGTTGA AATGTTCCGC AAGTTGCTGG	500
	ATCAAGGTGA AGCTGGTGAC AACGTAGGTY TGTTGCTCCG TGGTATCGAC	550
30	AAGAACGAAA TCAAACGTGG TATGGTTCTT TGTAAGCCCG GTCAGATTAA	600
	ACCTCACTCT AAGTTCAAAG CTTCTATCTA CGTTTTGAAG AAAGAAGAAG	650
	GTGGTCGTCA CACTCCGTTT CACAACAAAT ACCGTCCTCA GTTCTATCTG	700
	CGTACTATGG ACTGTACAGG TGAAATCWCT CTTCCGGAAG GAACTGAAAT	750
	GGTAATGCCT GGTGATAACG TAGAAATCAC TGTAGAAGT ATCTACCCGG	800
35	TAGCATTGAA CGTAGGTTTG CGTTTCGCT	829

2) INFORMATION FOR SEQ ID NO: 87

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Gemella haemolysans*
 (B) STRAIN: ATCC 10379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87

55	CTATCTTAGT AATCGCTGCT ACAGATGGAC CAATGGCTCA AACTCGTGAG	50
	CACATCCTAT TATCTCGTAA CGTTGGAGTA CCAAAAATCG TTGTATTCTT	100
	AAACAAATGT GATATGGTTG ATGACGAAGA GTTATTAGAA TTAGTTGAAA	150
	TGGAAGTTTC TGAACATTA TCTGAATACG GATTCGACGG AGATGAACTA	200
	CCAGTAATCA AAGGTTCTGC TCTTAAAGCT CTTGAAGGAG ATGCAGATGC	250
60	AGAAAAAGCT ATCATCGAAT TAATGGAAAC AGTTGACGAA TACATCCCAA	300

CTCCAGAACG TGATAACGCT AAACCATTCA TGATGCCAGT TGAGGACGTA 350
 TTCTCAATCA CAGGTCGTGG TACAGTTGCT ACTGGACGTG TTGAACGTGG 400
 ACAAGTTAAA GTTGGAGACG TAGTAGAAAT CGTTGGATTA ACTGAAGAAC 450
 CAGCTTCAAC TACTGTAAAC GGTGTTGAAA TGTTCCGTAA ATTATTAGAT 500
 5 TACGCTGAAG CAGGAGATAA CATCGGTGCA TTATTACGTG GTGTTGCTCG 550
 TGAAGACATC GAACGTGGAC AAGTTTTCAGC AGCTCCTAAA ACAATCACTC 600
 CACACACTCA ATTCGTAGCT GACGTGTACG TATTATCTAA AGAAGAAGGT 650
 GGACGTCACA CTCCATTCTT CACAACTAC CGTCCTCAAT TCTACTTCCG 700
 TACTACTGAC GTAACGTGGT TAGTTACTTT ACCAGAAGGT ACTGAAATGG 750
 10 TAATGCCTGG GGATAACGTA TCAATCAACG TAGAACTTAT TTCTCCAATC 800
 GCGATCGAAG AAGGAACTCG TTTCTCAA 828

15 2) INFORMATION FOR SEQ ID NO: 88

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Gemella morbillorum*
 (B) STRAIN: ATCC 27824

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88

30 TCTTAGTAAT CGCTGCTACA GATGGTCCTA TGGCTCAAAC TCGTGAACAC 50
 ATCCTATTAT CTCGTAACGT TGGAGTACCT AAAATTGTTG TATTCTTAAA 100
 CAAATGTGAT ATGGTTGATG ACGAAGAGTT ATTAGAATTA GTAGAAATGG 150
 AAGTTTCGTGA ACTATTATCT GAATACGGAT TTGATGGAGA TGAACCTACCA 200
 35 GTAATCAAAG GTTCAGCTCT TAAAGCTCTT GAAGGAGATG CAGATGCTGA 250
 AAAAGCTATC ATCGAATTAA TGGAAACAGT TGACGAGTAC ATCCCAACTC 300
 CAGAACGTGA TAACGCTAAA CCATTATATG TGCCAGTTGA GGACGTGTTT 350
 TCAATCACAG GTCGTGGTAC AGTTGCTACT GGACGTGTTG AACGTGGACA 400
 AGTTAAAGTT GGTGACGTAG TAGAAATCGT TGGATTAATC GAAGAACCAG 450
 40 CTTCAACTAT TGTAACAGGT GTTGAAATGT TCCGTAAATT ATTAGATTAC 500
 GCTGAAGCAG GAGATAACAT CGGTGCATTA TTACGTGGTG TTGCTCGTGA 550
 AGATATCGAA CGTGGACAAG TTTTAGCAGC TCCTAAAACA ATCACTCCAC 600
 ATRACTCAATT CGTAGCTGAT GTGTACGTAT TATCTAAAGA AGAAGGTGGA 650
 CGTCACACTC CATTCTTCAC AAACCTACCT CCACAATTCT ACTCCGTAC 700
 45 TACTGACGTA ACTGGTGTAG TTACTTTACC AGAAGGTACT GAAATGGTAA 750
 TGCCTGGGGA CAACGTATCA ATCAACGTAG AACTTATTTT TCCAATCGCT 800
 ATCGAAGAAG GAACTCGTTT CTC 823

50 2) INFORMATION FOR SEQ ID NO: 89

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 829 bases
 55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Haemophilus actinomycetemcomitans*

(B) STRAIN: ATCC 33384

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89

	GCTATCTTAG	TAGTAGCAGC	AACCGACGGT	CCTATGCCAC	AAACTCGTGA	50
	GCACATCTTA	TTAGGTCGCC	AAGTAGGTGT	TCCTTACATC	ATCGTATTCT	100
	TAAACAAATG	CGACATGGTA	GATGACGAAG	AGTTATTAGA	ATTAGTTGAA	150
10	ATGGAAGTTC	GTGAACTTCT	TTCTCAATAT	GACTTCCCGG	GCGATGACAC	200
	CCCAATCGTA	CGCGGTCTTG	CATTAAAAGC	GCTTGAAGGC	GATGCCGCAT	250
	GGGAAGAAAA	AATCCTTGAA	TTAGCAAACC	ATTTAGATAC	TTACATCCCG	300
	GAACCTGAGC	GTGCTATCGA	CCAACCGTTC	CTTCTTCCAA	TTGAAGATGT	350
	GTTCTCTATC	TCCGGTCGTG	GTACCGTAGT	AACGGGTCGT	GTTGAGCGCG	400
15	GTATCATCCG	TACCGGTGAT	GAAGTTGAAA	TCGTGGGTAT	CAAACCGACT	450
	GCAAAAACCA	CCGTAACCGG	TGTTGAAATG	TTCCGTAAAT	TACTTGACGA	500
	AGGTCGTGCG	GGTGAAAACA	TCGGTGCAAT	ATTGCGTGGT	ACTAAACGTG	550
	AAGAAATCGA	ACGTGGTCAG	GTATTGGCGA	AACCGGGGTC	AATCACCCTG	600
	CACACTGACT	TCGAATCTGA	AGTGTACGTA	TTGTCCAAAG	AAGAAGGTGG	650
20	TCGTCATACT	CCATTCTTCA	AAGGTTACCG	TCCACAATTC	TATTTCCGTA	700
	CAACTGACGT	AACCGGTACT	ATCGAGTTAC	CTGAAGGCGT	GGAAATGGTT	750
	ATGCTGGCG	ATAACATCAA	AATGACCGTA	TCCTTAATTC	ACCCAATTGC	800
	GATGGACCAA	GGTTTACGTT	TCGCTATCG			829

25

2) INFORMATION FOR SEQ ID NO: 90

(i) SEQUENCE CHARACTERISTICS:

30	(A)	LENGTH: 833 bases
	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Haemophilus aphrophilus*

(B) STRAIN: ATCC 33389

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90

	TGGTGCTATC	TTAGTAGTAG	CAGCAACTGA	TGGTCCTATG	CCACAAACTC	50
	GTGAGCACAT	CTTATTAGGT	CGCCAAGTAG	GTGTTCTTA	CATCATCGTA	100
45	TTCTTAAACA	AATGCGACAT	GGTAGATGAC	GAAGAGTTAT	TAGAATTAGT	150
	TGAAATGGAA	GTTTCGTGAAC	TTCTTTCTCA	ATATGACTTC	CCGGGTGATG	200
	ATACACCAAT	CGTACGTGGT	TCTGCATTAC	AAGCGTTAAA	CGGCGTTGCA	250
	GAATGGGAAG	AAAAAATCCT	TGAATTAGCA	AACCACTTAG	ATACTTACAT	300
	TCCTGAGCCA	CAACGTGCTA	TCGACCAACC	GTTCTTCTT	CCAATTGAAG	350
50	ACGTGTTCTC	TATCTCCGGT	CGTGGTACTG	TAGTAACAGG	TCGTGTTGAG	400
	CGTGGTATCA	TCCGTACCGG	TGATGAAGTT	GAAATCGTAG	GTATCAAACC	450
	GACTGCGAAA	ACTACCGTAA	CCGGTGTTGA	AATGTTCCGT	AAATTACTTG	500
	ACGAAGGTCG	TGCAGGTGAA	AACATCGGTG	CATTATTACG	TGGCACTAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAAGTATTG	GCTAAACCGG	GCTCAATCAC	600
55	TCCGCACACT	GATTTTCAAT	CTGAAGTGTA	CGTATTATCC	AAAGAAGAAG	650
	GTGGTTCGTA	TACTCCATTC	TTCAAAGGTT	ACCGTCCACA	ATTCTATTTC	700
	CGTACAACCTG	ACGTAACCGG	TACTATCGAG	TTACCGGAAG	GCGTGGAAT	750
	GGTTATGCCT	GGCGATAACA	TCAAAATGAC	TGTATCCTTA	ATCCACCCAA	800
60	TCGCGATGGA	CCAAGGTTTA	CGTTTCGCTA	TCG		833

2) INFORMATION FOR SEQ ID NO: 91

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 815 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Haemophilus ducreyi*
 - (B) STRAIN: DSM 8925

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91

20	CGGCGCTATC	TTAGTTGTAG	CAGCAACTGA	TGGTCCTATG	CCTCAAACTC	50
	GTGAACACAT	CTTATTAGGC	CGCCAAGTTG	GTGTTCCCTA	CATCATCGTA	100
	TTCTTAAATA	AATGCGATAT	GGTAGATGAT	GAAGAATTAT	TAGAATTAGT	150
	TGAAATGGAA	GTTCGTGAAC	TTCTTTCTCA	ATATGATTTC	CCAGGTGACG	200
	ATACTCCTAT	CGTTCGTGGT	TCAGCATTAC	AAGCATTAAA	TGGTGTGCCT	250
	GAGTGGGAAG	AAAAAATCAT	TGAATTAGCA	CAACACTTAG	ATTCTTATAT	300
25	CCCTGAGCCT	GAGCGTGCGA	TTGATAAACC	TTTCTTATTA	CCAATCGAAG	350
	ACGTATTCTC	AATTTAGGT	CGTGGTACAG	TAGTAACCGG	TCGTGTTGAG	400
	CGTGGTATCA	TCAAATCAGG	TGAAGAAGTT	GAAATCGTAG	GGATTAAAGA	450
	AACGACAAAA	ACAACAGTAA	CCGGTGTTGA	GATGTTCCGT	AAACTATTAG	500
	ACGAAGGTCG	TGCGGGTGAA	AACGTAGGTG	CCTTATTACG	TGGTACTAAA	550
30	CGTGAAGAAA	TGCAACGTGG	TCAAGTATTA	GCGAAACCAG	GTACAATTAC	600
	ACCACACACT	GATTTTGAAT	CAGAAGTTTA	TGTATTATCA	AAAGAAGAAG	650
	GTGGTCGTCA	TACTCCATTC	TTCAAAGGTT	ATCGTCCTCA	GTTCTACTTC	700
	CGYACAACGG	ACGTAACAGG	AACGATTGAA	TTACCTGAAG	ATGTTGAGAT	750
	GGTAATGCCT	GGTGATAATA	TCAAGATGAC	AGTAAGCTTA	ATTCACCCTA	800
35	TCGCGATGGA	CGAAG				815

2) INFORMATION FOR SEQ ID NO: 92

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 830 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Haemophilus haemolyticus*
 - (B) STRAIN: ATCC 33390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92

55	TGGTGCTATC	TTAGTAGTAG	CAGCAACTGA	TGGTCCAATG	CCACAAACTC	50
	GTGAGCACAT	CTTATTAGGT	CGCCAAGTAG	GTGTTCCATA	CATCATCGTA	100
	TTCTTAAACA	AATGCGACAT	GGTAGATGAC	GAAGAGTTAT	TAGAATTAGT	150
	AGAAATGGAA	GTTCCGTGAAC	TTCTTTCTCA	ATATGACTTC	CCAGGTGACG	200
	ATACACCAAT	CGTACGTGGT	TCTGCATTAC	AAGCATTAAA	TGGCGTAGCA	250
60	GAATGGGAAG	AAAAAATCCT	TGAGTTAGCA	AACCACTTAG	ATACTTACAT	300

	CCCAGAACCA	GAGCGTGCAA	TTGACCAACC	GTTCCCTTCTT	CCAATCGAAG	350
	ATGTGTTCTC	AATCTCAGGT	CGTGGTACAG	TAGTAACTGG	TCGTGTAGAA	400
	CGTGGTATCA	TCCGTACTGG	TGATGAAGTA	GAAATCGTAG	GTATCAAAGA	450
	TACAGCAAAA	ACTACTGTAA	CGGGTGTGTA	AATGTTCCGT	AAATTACTTG	500
5	ACGAAGGTCG	TGCAGGTGAA	AACATCGGTG	CATTATTACG	TGGTACCAAA	550
	CGTGAAGAAA	TCGAACGTGG	TCAAGTATTA	GCGAAACCAG	GTTCAATCAC	600
	GCCACACACT	GACTTCGAAT	CAGAAGTTTA	TGTATTATCA	AAAGAAGAAG	650
	GTGGTCGTCA	TACTCCATTG	TTCAAAGGTT	ACCGTCCACA	ATTCTATTTT	700
	CGTACAACTG	ACGTAACCTG	TACTATCGAG	TTACCAGAAG	GCGTAGAAAT	750
10	GGTAATGCCA	GGCGATAACA	TCAAGATGAC	AGTAAGCTTA	ATCCACCCAA	800
	TCGCGATGGA	CCAAGGTTTA	CGTTTCGCAA			830

15 2) INFORMATION FOR SEQ ID NO: 93

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 20 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus parahaemolyticus*
 (B) STRAIN: ATCC 10014

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93

30	TCTTAGTAGT	AGCAGCAACA	GACGGTCCAA	TGCCACAAAC	TCGTGAGCAC	50
	ATCTTATTAG	GTCGCCAAGT	AGGTGTTCCA	TACATCATCG	TATTCTTAAA	100
	CAAATGCGAT	ATGGTTGACG	ATGAAGAATT	ATTAGAATTA	GTTGAAATGG	150
	AAGTGCGTGA	ACTTCTTTCA	CAATATGACT	TCCCAGGTGA	TGACACGCCA	200
35	GTAGTACGTG	GTTTCAGCGTT	ACAAGCGTTA	AACGGCGTAG	CAGAGTGGGA	250
	AGAAAAAATT	CTTGAATTAG	CAAACCACTT	AGATACATAC	ATCCCAGAGC	300
	CAGAGCGTGC	GATTGATAAA	CCATTCTTAT	TACCAATCGA	AGACGTATTC	350
	TCAATCTCAG	GTCGTGGTAC	AGTAGTAACA	GGTCGTGTTG	AGCGTGGTAT	400
	CATCAAAGCG	GGTGAAGAAG	TTGAAATCGT	AGGTATCAAA	GACACTGCCA	450
40	AAACAACAGT	AACGCGCGTG	GAAATGTTCC	GTAAATTATT	AGACGAAGGT	500
	CGTGCGGGTG	AAAACGTTGG	TGCATTATTA	CGTGGTACAA	AACGTGAAGA	550
	AATCGAACGT	GGTCAAGTGT	TAGCGAAACC	AGGTACAATT	ACACCACACA	600
	CAGACTTCGA	ATCAGAAAGT	TACGTATTAT	CAAAAGAAGA	AGGTGGTCGT	650
	CACACTCCAT	TCTTCAAAGG	TTACCGTCCA	CAATTCTACT	TCCGTACAAC	700
45	TGACGTAACT	GGTACTATTG	AATTACCAGA	AGGCGTAGAA	ATGGTAATGC	750
	CAGGCGATAA	CATCAAAATG	ACAGTATCAT	TAATCCACCC	AATCGCGATG	800
	GACGAAGGTT	TACGTTTTGC	GATT			824

50

2) INFORMATION FOR SEQ ID NO: 94

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 bases
 55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus parainfluenzae*
 (B) STRAIN: ATCC 7901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94

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5      TGGTGCTATC TTAGTAGTAG CAGCAACTGA TGGTCCTATG CCACAAACTC      50
      GTGAGCACAT CTTATTAGGT CGCCAAGTAG GTGTTCCCTTA CATCATCGTG      100
      TTCTTAAACA AATGCGACAT GGTAGATGAC GAAGAGTTAT TAGAATTAGT      150
10     TGAAATGGAA GTTCGTGAAC TTCTTTCTCA ATATGACTTC CCGGGTGACG      200
      ATACACCAAT CGTACGTGGT TCTGCATTAC AAGCGTTAAA CGGCGTWGCA      250
      GAATGGGAAG AAAAAATCCT TGAATTAGCT AGCCACTTAG ATTCTTACAT      300
      TCCTGAGCCT CAACGTGCTA TCGACCAACC GTTCCTTCTT CCAATCGAAG      350
      ACGTGTTCTC TATCTCCGGT CGTGGTACAG TAGTAACAGG TCGTGTTGAG      400
15     CGTGGTATCA TCCGTACCGG TGATGAAGTT GAAATCGTAG GTATCAAACC      450
      GACTGCGAAA ACTACCGTAA CCGGTGTTGA AATGTTCCGT AAATTACTTG      500
      ACGAAGGTCG TGCAGGTGAA AACATCGGTG CATTATTACG TGGTACYAAA      550
      CGTGAAGAAA TCGAACGTGG TCAAGTATTG GCTAAACCGG GTTCAATCAC      600
      TCCACACACT GATTTCTGAAT CTGAAGTGTA CGTATTATCC AAAGAAGAAG      650
20     GTGGTCGTCA TACTCCATTC TTCAAAGGTT ACCGTCCACA ATTCTATTTC      700
      CGTACAAC TGACGTAACCGG AACTATCGAA TTACCGGAAG GCGTGGAAT      750
      GGTATGCCT GGTGATAACA TCAAATGAC TGTATCCTTA ATCCACCCAA      800
      TCGCGATGGA CCAAGGTTTA CGTTTCGCTA TCG      833
  
```

2) INFORMATION FOR SEQ ID NO: 95

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus paraphrophilus*
 (B) STRAIN: ATCC 29241

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95

```

45     TGGTGCTATC TTAGTAGTAG CAGCAACTGA TGGTCCTATG CCACAAACTC      50
      GTGAGCACAT CTTATTAGGT CGCCAAGTAG GTGTTCCCTTA CATCATCGTA      100
      TTCTTAAACA AATGCGACAT GGTAGATGAC GAAGAGTTAT TAGAATTAGT      150
      TGAAATGGAA GTTCGTGAAC TTCTTTCTCA ATATGACTTC CCGGGTGACG      200
      ATACGCCAAT CGTACGTGGT TCTGCATTAC AAGCGTTAAA CGGCGTTGCA      250
      GAATGGGAAG AAAAAATCCT TGAATTAGCA AACCCTTGG ATACTTACAT      300
      TCCTGAGCCA CAACGTGCTA TCGACCAACC GTTCCTTCTT CCAATCGAAG      350
50     ACGTGTTCTC TATCTCCGGT CGTGGTACAG TAGTAACAGG TCGTGTTGAG      400
      CGTGGTATCA TCCGTACCGG TGATGAAGTT GAAATCGTAG GTATCAAACC      450
      GACTGCGAAA ACTACCGTAA CCGGTGTTGA AATGTTCCGT AAATTACTTG      500
      ACGAAGGTCG TGCAGGTGAA AACATCGGTG CATTATTACG TGGTACCAA      550
      CGTGAAGAAA TCGAACGTGG TCAAGTATTG GCTAAACCGG GTTCAATCAC      600
55     TCCACACACT GATTTCTGAAT CTGAAGTGTA CGTATTATCC AAAGAAGAAG      650
      GTGGTCGTCA TACTCCATTC TTCAAAGGTT ACCGTCCACA ATTCTATTTC      700
      CGTACAAC TGACGTAACCGG TACTATCGAG TTACCGGAAG GTGTGGAAT      750
      GGTAAATGCCT GGCATAACA TCAAATGAC CGTATCCTTA ATCCACCCAA      800
      TCGCGATGGA CCAAGGTTTA CGTT      824
  
```

2) INFORMATION FOR SEQ ID NO: 96

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 818 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus segnis*
- (B) STRAIN: ATCC 33393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96

	GCTATCTTAG	TAGTAGCAGC	AACTGATGGT	CCTATGCCAC	AAACTCGTGA	50
20	GCACATCTTA	TTAGGTCGCC	AAGTAGGTGT	TCCTTACATC	ATCGTATTCT	100
	TAAACAAATG	CGACATGGTA	GATGACGAAG	AGTTATTAGA	ATTAGTTGAA	150
	ATGGAAGTTC	GTGAACTTCT	TTCTCAATAT	GACTTCCCAG	GTGATGATAC	200
	TCCAATCATT	CGTGGTTCTG	CATTACAAGC	GTAAACGGC	GTAGCAGAAAT	250
	GGGAAGAAAA	AATCCTTGAA	TTAGCTCAAG	CATTAGATAC	TTACATTCCCT	300
25	GAACCTGAGC	GTGCAATCGA	CCAACCGTTC	CTTCTTCCAA	TTGAAGACGT	350
	GTTCTCAATC	TCTGGTCGTG	GTACTGTAGT	AACAGGTCGT	GTAGAGCGTG	400
	GTATCATCCG	TACCGGTGAT	GAAGTTGAAA	TCGTTGGTAT	CAAACCAACT	450
	GCGAAAACAA	CCGTAACCGG	TGTTGAAATG	TTCCGTAAAT	TACTTGACGA	500
	AGGTCGTGCA	GGTGAAAACA	TCGGTGCAAT	ATTACGTGGT	ACTAAACGTG	550
30	AAGAAATCGA	ACGTGGTCAA	GTATTAGCGA	AACCGGGTTC	AATCACTCCA	600
	CACACTGACT	TCGAATCTGA	AGTGTACGTA	TTATCTAAAG	AAGAAGGTGG	650
	TCGTCATACT	CCATTCTTCA	AAGGTTACCG	TCCACAATTC	TATTTCCGTA	700
	CAACTGACGT	AACCGGTACT	ATCGAGTTAC	CGGAAGGCGT	GGAAATGGTT	750
	ATGCCTGGCG	ATAACATCAA	AATGACCGTA	TCCTTAATCC	ACCCAATCGC	800
35	GATGGACCAA	GGTTTACG				818

2) INFORMATION FOR SEQ ID NO: 97

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 763 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Hafnia alvei*
- (B) STRAIN: ATCC 13337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97

55	CGGCGCTATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCTATG	CCTCAGACTC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTTG	GCGTTCCTTW	CATCATCGTR	100
	TTCCCTGAACA	AATGCGACAT	GGTTGATGAT	GAAGAGCTGC	TGGAAGTGGT	150
	AGAAATGGAA	GTTTCGTGAAC	TTCTGTCTCA	GTACGACTTC	CCWGGYGATG	200
	ATACTCCAAT	CATCCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGYGMACCT	250
60	GAGTGGGAAG	CTAAGATCGT	AGAACTGGCT	GAAACTCTGG	ATTCTTACAT	300

YCCACARCCA GAACGTGCTA TCGAYAAGCC ATTCTGCTG CCAATCGAAG 350
 ACGTATTCTC TATCTCTGGC CGTGGTACWG TTGTACCGG TCGTGTAGAG 400
 CGCGGTATCG TTAAAGTTGG TGAAGAAGTT GARATCGTTG GTATCAAAGA 450
 TACCGTTAAA TCAACTTGTA CCGGCGTTGA AATGTTCCGT AAAGTGTCTGG 500
 5 ACGAAGGTCG TGCAGGCGAG AACGTTGGTG TTCTGCTGCG TGGTATCAAG 550
 CGTGAAGACA TCGAACGTGG TCAGGTTCTG GCTAAACCAG GYTCYATCAA 600
 GCCACACACC AAGTTCGAAT CAGAAGTTTA TATTCTGAGC AAAGATGAAG 650
 GCGGYCGTCA TACTCCGTTT TTCAAAGGCT ACCGTCCACA GTTCTACTTC 700
 CGTACAACCTG ACGTGACCGG TACCATCGAA TTGCCAGAAG GCGTGGAAT 750
 10 GGTAAATGCCA GGC 763

2) INFORMATION FOR SEQ ID NO: 98

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 20 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 25 (A) ORGANISM: *Kingella kingae*
 (B) STRAIN: ATCC 23330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98

30 CGGCGCAATC TTGGTATGTT CAGCAGCTGA CGGTCCTATG CCACAAACTC 50
 GCGAACACAT CTTGTTGGCT CGCCAAGTAG GTGTACCTTA TATCATCGTA 100
 TTCATGAACA AATGCGACAT GGTCGATGAT GCTGAGTTGT TGGAATTGGT 150
 TGAAATGGAA ATCCGTGACT TGTTGTCTAG CTACGATTTT CCAGGCGACG 200
 ATTGCCCAAT CGTTCAAGGT TCTGCATTGC GYGCAATTGGA AGGCGACGCT 250
 35 GCATACAAAG AAAAAATCTT TGAATTGGCT GCTGCTTTGG ATAGCTACAT 300
 TCCTACTCCA GAACGTGCTG TTGATAAACC ATTCTTGTG CCAATCGAAG 350
 ATGTATTCTC TATCTCTGGT CGTGGTACAG TAGTTACTGG TCGTGTAGAG 400
 CGCGGTATCA TCAAAGTAGG CGAAGAGATT GAAATCGTTG GTTTGAAAGA 450
 CACGCAAAAA ACCACTTGTA CTGGCGTGGA AATGTTCCGC AAATTGTTGG 500
 40 ACGAAGGTCA AGCTGGTGAT AACGTTGGTG TATTATTGCG TGGTACGAAG 550
 CGTGAAGACG TTGAACGTGG TCAGGTATTG GCTAAACCAG GTTCTATCAC 600
 TCCGCACACT AAATTTGAAG CTGAAGTGTA TGTGTTGAGC AAAGAAGAAG 650
 GTGGCCGTC TACGCCATTC TTCGCTAAT ACCGCCACA ATTCTACTTC 700
 CGTACGACTG ACGTAACTGG TGCAGTTACT TTGTCTGAGG GTGTGGAAAT 750
 45 GGTATGCCA GCGGAAAACG TGAAATCAC TGTGAGTTG ATTGCACCTA 800
 TCGCTAGGAA AACGGTTTGC GTTTTGCG 828

50 2) INFORMATION FOR SEQ ID NO: 99

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 55 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella ornithinolytica*
 (B) STRAIN: ATCC 31898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99

5
 GGCGCGATCC TGGTTGTTGC TGC GACTGAC GGCCCGATGC CGCAGACTCG 50
 TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT 100
 TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAGCTGGTT 150
 GAAATGGAAG TCCGTGAGCT GCTGTCTCAG TACGACTTCC CGGGCGACGA 200
 10 CACGCCGATC GTTCGTGGTT CCGCTCTGAA AGCGCTGGAA GGCGAAGCAG 250
 ACTGGGAAGC GAAAATCATC GAACTGGCTG GCTACCTGGA TTCTTACATC 300
 CCGGAACCAG AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CGATCGAAGA 350
 CGTATTCTCC ATCTCCGGTC GTGGTACCGT TGTTACCGGT CGTGTAGAGC 400
 GCGGTATCAT CAAAGTGGGC GAAGAAGTTG AAATCGTTGG TATCAAAGAG 450
 15 ACTGCGAAGT CTACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA 500
 CGAAGGCCGT GCTGGTGAGA ACGTTGGTGT TCTGCTGCGT GGTATCAAAC 550
 GTGAAGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG CTCTATCAAG 600
 CCGCACACCA AGTTCGAATC TGAAGTGATC ATTCTGTCCA AAGACGAAGG 650
 CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC 700
 20 GTACAACTGA CGTGA CTGGC ACCATCGAAC TGCCGGAAGG CGTAGAGATG 750
 GTCATGCCGG GCGACAACAT CAAAATGGTT GTTACCCTGA TTCACCCGAT 800
 CGCGATGGAC GATGGTCTGC GTTTCGCA 828

25
 2) INFORMATION FOR SEQ ID NO: 100

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 749 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- 35 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Klebsiella oxytoca*
 (B) STRAIN: ATCC 33496

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100

GATGCCGCAG ACTCGTGAGC ACATCCTGCT GGGTCGTCAG GTAGGCGTTC 50
 CGTACATCAT CGTGTTCTCTG AACAAAGTGCG ACATGGTTGA TGACGAAGAG 100
 CTGCTGGAAC TGGTTGAAAT GGAAGTTCTGT GAATTCTGT CTCAGTACGA 150
 45 TTTCCCGGGC GACGACACTC CGATCGTTCTG TGGTCTGCT CTGAAAGCGC 200
 TGGAAGGCGA CGCWGAGTGG GAAKCKAAAA TCATCGAACT GGCTGGCTTC 250
 CTGGATTCTT ACATTCGCGA ACCAGAGCGT GCGATTGACA AGCCGTTCTCT 300
 GCTGCCGATC GAAGACGTAT TCTCCATCTC CGGTCGTGGT ACCGTTGTGA 350
 CCGGTCGTGT AGAGCGCGGT ATCATCAAAG TTGGCGAAGA AGTTGAAATY 400
 50 GTTGGTATYA AAGACACTGC TAAGTCTACC TGTACTGGCG TTGAAATGTT 450
 CCGCAAAC TG GACGAAG GCCGYGCTGG TGAGAACGTT GGTGTTCTGC 500
 TGCGTGGTAT CAAACGTGAA GAAATCGAAC GTGGTCAGGT ACTGGCTAAG 550
 CCGGGCTCTA TCAAGCCGCA CACCAAGTTC GAATCTGAAG TTTATATCCT 600
 GTCCAAAGAC GAAGGCGGCC GTCACACTCC GTTCTTCAA GGCTACCGTC 650
 55 CGCAGTTCTA CTTCCGTACA ACTGACGTGA CTGGCACCAT CGAACTGCCG 700
 GAAGGCGTAG AGATGGTTAT GCCGGGCGAC AACATCAAAA TGTTGTGA 749

60 2) INFORMATION FOR SEQ ID NO: 101

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella planticola*
 (B) STRAIN: ATCC 33531

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101

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15  TGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCCGATG CCGCAGACTC      50
    GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG      100
    TTCCTGAACA AATGCGACAT GGTTGATGAC GAAGAGCTGC TGGAAGTGGT      150
    TGAATGGGAA GTTCGTGAGC TGCTGTCTCA GTACGACTTC CCGGGCGACG      200
20  ACACTCCGAT CGTTCGTGGT TCCGCTCTGA AAGCGCTGGA AGGCGAAGCA      250
    GACTGGGAAG CGAAAATCAT CGAACTGGCT GGCTACCTGG ATTCTTACAT      300
    CCCGGAACCA GAGCGTGC GA TGTACAAGCC GTTCCTGCTG CCTATCGAAG      350
    ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAG      400
    CGCGGTATCA TCAAAGTGGG CGAAGAAGTT CYGGCGTTGA AATGTTCCGC AAAGTGTG      450
25  TACTGCTAAR TCWACCTGTA AATGTTCCGC AAAGTGTG      500
    ACGAAGGCCG TGCTGGTGAG AACGTTGGTG TTCTGCTGCG TGGTATCAAA      550
    CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCTCTATCAA      600
    GCCGCACACC AAGTTCGAAT CTGAAGTGTA CATTCTGTCC AAAGACGAAG      650
    GCGGCCGTCA TACTCCGTTT TTCAAAGGCT ACCGTCCGCA GTTCTACTTC      700
30  CGTACAACCTG ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTAGAGAT      750
    GGTAATGCCG GCGGACAACA TCAAATGGT TGTTACCCTG ATTCACCCRA      800
    TCGCGATGGA CGACGGTCTG CGTTTCGCAA      830
  
```

2) INFORMATION FOR SEQ ID NO: 102

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *ozaenae*
 (B) STRAIN: ATCC 11296

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102

```

50  CCTGGTTGTT GCTGCGACTG ACGGCCCGAT GCCGCAGACT CGTGAGCACA      50
    TCCTGCTGGG TCGTCAGGTA GCGTTCCGT ACATCATCGT GTTCCTGAAC      100
    AAATGCGACA TGGTTGATGA CGAAGAGCTG CTGGAAGTGG TTGAGATGGA      150
55  AGTTCGTGAA CTGCTGTCTC AGTACGATTT CCCGGGCGAC GACACCCCGA      200
    TCGTTTCGTG TTCTGCTCTG AAAGCGCTGG AAGGCGACGC AGAGTGGGAA      250
    GCGAAAATCA TCGAACTGGC TGGCCACCTG GATACCTATA TCCCGGAACC      300
    AGAGCGTGCG ATTGACAAGC CGTTCCTGCT GCCGATCGAA GACGTATTCT      350
    CCATCTCCGG TCGTGGTACC GTTGTTACCG GTCGTGTAGA GCGCGGTATC      400
60  ATCAAAGTAG GTGAAGAAGT TGAAATCGTT GGTATCAAAG AAACCGCGAA      450
  
```

	AACCACCTGT	ACTGGCGTTG	AAATGTTCCG	CAAACCTGCTG	GACGAAGGCC	500
	GTGCTGGTGA	GAACGTAGGT	GTTCTGCTGC	GTGGTATCAA	ACGTGAAGAA	550
	ATCGAACGTG	GTCAGGTACT	GGCTAAGCCG	GGCACCATCA	ACCCGCACAC	600
	CAAGTTCGAA	TCTGAAGTGT	ACATCCTGTC	CAAAGACGAA	GGCGGCCGTC	650
5	ATACTCCGTT	CTTCAAAGGC	TACCGTCCGC	AGTTCTACTT	CCGTACTACT	700
	GACGTGACTG	GCACCATCGA	ACTGCCGGAA	GGCGTAGAGA	TGGTAATGCC	750
	GGGCGACAAC	ATCAAAATGG	TTGTTACCCT	GATCCACCCG	ATCGCGATGG	800
	ACGACG					806

10

2) INFORMATION FOR SEQ ID NO: 103

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 743 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*
 (B) STRAIN: ATCC 13883

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103

	GCAGACTCGT	GAGCACATCC	TGCTGGGTCG	TCAGGTAGGC	GTTCCGTACA	50
	TCATCGTGTT	CCTGAACAAA	TGCGACATGG	TTGATGACGA	AGAGCTGCTG	100
30	GAAGTGGTTG	AGATGGAAGT	TCGTGAACTG	CTGTCTCAGT	ACGATTTCCT	150
	GGGCGACGAC	ACTCCGATCG	TTCGTGGTTC	TGCTCTGAAA	GCGCTGGAAG	200
	CCGACGCAGA	GTGGGAAGCG	AAAATCATCG	AACTGGCTGG	CCACCTGGAT	250
	ACCTATATCC	CGGAACCAGA	GCGTGCGATT	GACAAGCCGT	TCCTGCTGCC	300
	GATCGAAGAC	GTATTCTCCA	TCTCCGGTCG	TGGTACCGTT	GTTACCGGTC	350
35	GTGTAGAGCG	CGGTATCATC	AAAGTAGGTG	AAGAAGTTGA	AATCGTTGGT	400
	ATCAAAGAAA	CCGCGAAAAC	CACCTGTACT	GGCGTTGAAA	TGTTCCGCAA	450
	ACTGCTGGAC	GAAGGCCCGTG	CTGGTGAGAA	CGTAGGTGTT	CTGCTGCGTG	500
	GTATCAAACG	TGAAGAAATC	GAACGTGGTC	AGGTACTGGC	TAAGCCGGGC	550
	ACCATCAACC	CGCACACCAA	GTTCTGAATCT	GAAGTGTACA	TCCTGTCCAA	600
40	AGACGAAGGC	GGCCGTCACA	CTCCGTTCTT	CAAAGGCTAC	CGTCCGCAGT	650
	TCTACTTCCG	TACTACTGAC	GTGACTGGCA	CCATCGAACT	GCCGGAAGGC	700
	GTAGAGATGG	TAATGCCGGG	CGACAACATC	AAAATGGTTG	TTA	743

45

2) INFORMATION FOR SEQ ID NO: 104

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *rhinoscleromatis*
 (B) STRAIN: ATCC 13884

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104

	TGGTTGTTGC	TGCGACTGAC	GGCCCGATGC	CGCAGACTCG	TGAGCACATC	50
	CTGCTGGGTC	GTCAGGTAGG	CGTTCGGTAC	ATCATCGTGT	TCCTGAACAA	100
	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTT	GAGATGGAAG	150
5	TTCGTGAACT	RCTGTCTCAG	TACGATTTCC	CGGGCGACGA	CACCCCGATC	200
	GTTTCGTGGTT	CTGCTCTGAA	AGCGCTGGAA	GGCGACGCAG	AGTGGGAAGC	250
	GAAAATCATC	GAAGTGGCTG	GCCACCTGGA	TACCTATATC	CCGGAACCAG	300
	AGCGTGCGAT	TGACAAGCCG	TTCCTGCTGC	CGATCGAAGA	CGTATTCTCC	350
	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAGC	GCGGTATCAT	400
10	CAAAGTAGGT	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAA	ACCGCGAAAA	450
	CCACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	CGAAGGCCGT	500
	GCTGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAAC	GTGAAGAAAT	550
	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CACCATCAAC	CCGCACACCA	600
	AGTTCGAATC	TGAAGTGTAC	ATCCTGTCCA	AAGACGAAGG	CGGCCGTCAC	650
15	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	GTACTACTGA	700
	CGTGACTGGC	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	GTAATGCCGG	750
	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TCCATCCGAT	CGCGATGGAC	800
	GACGGTCTGC	GTTTCGCAA				819

20

2) INFORMATION FOR SEQ ID NO: 105

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Kluyvera ascorbata*
 (B) STRAIN: ATCC 33433

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105

	CGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	TGGCCCTATG	CCACAGACTC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCTTA	CATCATCGTG	100
40	TTCTTGAACA	AATGYGACAT	GTTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	TGAAATGGAA	GTTTCGTGAAC	TTCTGTCTCA	GTACGATTTT	CCAGGCGACG	200
	ATACTCCAAT	CATCCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGATGCA	250
	GAGTGGGAAG	CGAAAATCAT	CGAAGTGGCT	GGCTTCCTGG	ATTCTTACAT	300
	CCCAGAACCA	GAACGTGCTA	TCGATAAGCC	GTTCTGCTG	CCAATCGAAG	350
45	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAG	400
	CGCGGTATCA	TCAAAGTTGG	YGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	CACCGCTAAG	TCTACCTGTA	CCGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTATCAAA	550
	CGTGAAGAAA	TGAACGTGG	TCAGGTTCTG	GCTAAGCCAG	GCTCTATCAA	600
50	GCCGCACACC	AAGTTCGAAT	CTGAAGTGTA	CATTCTGTCC	AAAGACGAAG	650
	GCGGCCGTCA	TACTCCGTTT	TTCAAAGGCT	ACCGTCCACA	GTTCTACTTC	700
	CGTACTACTG	ACGTGACCGG	TACCATCGAA	CTGCCAGAAG	GCGTTGAGAT	750
	GGTAATGCCA	GGCGACAACA	TCAAGATGGT	TGTGACTCTG	ATCCACCCAA	800
55	TCGCGATGGA	CGACGGCCTG	CGTTTCGCAA	CC		832

2) INFORMATION FOR SEQ ID NO: 106

60 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Kluyvera cryocrescens*
 (B) STRAIN: ATCC 33435

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106

15	TGGCGCGATC CTGGTTGTTG CTGCAACTGA TGGCCCTATG CCACAGACTC	50
	GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCTTA CATCATCGTG	100
	TTCCTGAACA AATGTGACAT GGTGATGAC GAAGAGCTGC TGGAAGTGGT	150
	TGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGATTTC CCAGGCGACG	200
	ACACTCCTAT CGTTCGTGGT TCCGCGCTGA AAGCGCTGGA AGGCGACGCT	250
	GAGTGGGAAG CAAAAATCAT CGAACTGGCT GGCTTCCTGG ATTCTTACAT	300
20	CCCAGAACCA GAGCGTGCGA TTGATAAGCC GTTCCTGCTG CCAATCGAAG	350
	ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAG	400
	CGCGGTATCA TCAAAGTTGG TGAAGAAGTT GAAATCGTGG GTATCAAAGA	450
	CACTGCTAAG TCTACCTGTA CCGCGGTGA AATGTTCCGC AACTGCTGG	500
	ACGAAGGCCG TGCTGGTGAG AACGTTGGTG TTCTGCTGCG TGGTATCAAA	550
25	CGTGAAGAAA TCGAACGTGG TCAGGTTCTG GCTAAGCCAG GCTCCATCAA	600
	GCCGCACACC AAATTCGAAT CTGAAGTTTA CATCCTGTCC AAAGACGAAG	650
	GCGGCCGTCA TACTCCGTTT TTCAAAGGCT ACCGTCCACA GTTCTACTTC	700
	CGTACTACTG ACGTGACTGG TACCATCGAA CTGCCAGAAG GCGTAGAGAT	750
	GGTAATGCCG GGCGACAACA TCAAATGGT TGTTACCCTG ATCCACCCAA	800
30	TCGCGATGGA CGACGGTCTG CGTTTCGCAA	830

2) INFORMATION FOR SEQ ID NO: 107

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Kluyvera georgiana*
 (B) STRAIN: ATCC 51603

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107

50	CGCGATCCTG GTTGTGCTG CGACTGACGG CCCGATGCCG CAGACTCGTG	50
	AGCACATCCT GCTGGGTCGT CAGGTTGGCG TTCCGTACAT CATCGTGTTT	100
	CTGAACAAAT GCGACATGGT TGATGACGAA GAGCTGCTGG AACTGGTTGA	150
	AATGGAAGTT CGTGAAGTTC TGTCTCAGTA CGACTTCCCG GGCGACGACA	200
	CGCCGATCGT TCGTGGTTCT GCTCTGAAAG CGCTGGAAGG CGACGCTGAG	250
55	TGGGAAGCGA AAATCATCGA ACTGGCGGGC TTCCTGGATT CTTACATCCC	300
	GGAACCAAG CGTGCGATTG ACAAGCCGTT CCTGCTGCCG ATCGAAGACG	350
	TATTCCTCCAT CTCGGTCGT GGTACCGTTG TTACCGGTCG TGTAAGACGC	400
	GGTATCATCA AAGTTGGCGA AGAAGTTGAA ATCGTTGGTA TCAAAGACAC	450
	CGCTAAGTCT ACCTGTACTG GCGTTGAAAT GTTCCGCAA CTGCTGGACG	500
60	AAGGCCGTGC TGGTGAGAAC GTTGGTGTTT TGCTGCGTGG TATCAAACGT	550

GAAGAAATCG AACGTGGTCA GGTACTGGCT AAGCCGGGTT CTATCAAGCC 600
 GCACACCAAG TTCGAATCTG AAGTGTACAT TCTGTCCAAA GACGAAGGCG 650
 GCCGTCATAC TCCGTTCTTC AAAGGCTACC GTCCGCAGTT CTACTIONCCGT 700
 ACTACTGACG TGACTIONGAC CATCGAAGTG CCGGAAGGCG TTGAGATGGT 750
 5 AATGCCGGGC GACAACATCA AAATGGTTGT TACCCTGATC CACCCGATCG 800
 CGAAGGACGA AGGTCTGCGT TTCGCA 826

10 2) INFORMATION FOR SEQ ID NO: 108

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 803 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactobacillus casei* subsp. *casei*
 (B) STRAIN: ATCC 393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108

25 GCTGCTGATG GCCCAATGCC ACAAACCTCGT GAACATATCT TACTTTCACG 50
 TCAAGTTGGT GTTCCATACA TCGTTGTATT CATGAACAAA TGTGACATGG 100
 TTGACGATGA AGAATTACTA GAATTAGTTG AAATGGAAAT TCGTGATCTA 150
 TTAAGTGAAT ATGAATTCCC TGGCGATGAC ATTCCCTGTAA TCAAAGGTTT 200
 30 AGCTCTTAAA GCACTTCAAG GTGAAGCTGA CTGGGAAGCT AAAATTGACG 250
 AGTTAATGGA AGCTGTAGAT TCTTACATTC CAACTCCAGA ACGTGATACT 300
 GACAAACCAT TCATGATGCC AGTTGAGGAT GTATTCTCAA TCACTGGTCG 350
 TGGAACAGTT GCAACTGGAC GTGTTGAACG TGGACAAGTT AAAGTTGGTG 400
 ACGAAGTAGA AGTTATCGGT ATTGAAGAAG AGAGCAAAAA AGTAGTAGTA 450
 35 ACTGGAGTAG AAATGTTCCG TAAATYACTA GATTACGCTG AAGCTGGCGA 500
 CAACATTGGC GCACTTCTAC GTGGTGTGTC TCGTGAAGAT ATCCAACGTG 550
 GTCAAGTATT AGCTAAACCA GGTTCGATTA CTCCACACAC TAACTTCAAA 600
 GCTGAAACTT ATGTTTAAAC TAAAGAAGAA GGTGGACGTC ACACTCCATT 650
 CTTCAACAAC TACCGCCAC AATTCTATTT CCGTACTACT GACGTAACTG 700
 40 GTATTGTTAC ACTTCCAGAA GGTACTGAAA TGGTAATGCC TGGTGATAAC 750
 ATTGAGCTTG CAGTTGANCT AATTGCACCA ATCGCTATCG AAGACGGTAC 800
 TAA 803

45 2) INFORMATION FOR SEQ ID NO: 109

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 825 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactococcus lactis* subsp. *lactis*
 (B) STRAIN: ATCC 19435

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109

	CGGTGCAATC	CTCGTTGTTG	CTGCAACTGA	TGGACCAATG	CCACAAACTC	50
	GTGAACACAT	CTTGCTTTCA	CGTCAAGTTG	GTGTTAAATA	CCTTATCGTC	100
	TTCTTTAACA	AGGCTGACCT	TGTTGATGAT	GAAGAATTGA	TGGAACCTCGT	150
5	TGAAATGGAA	GTTCGTGACC	TCTTGAGCGA	ATACGACTTC	CCAGGTGACG	200
	ATATTCTCTG	AATCGCTGGT	TCAGCACTTG	GTGCTTTGAA	CGGTGAACCA	250
	CAATGGGTTG	CTAAAGTTGA	AGAATTGATG	GACATCGTTG	ATGAATACAT	300
	CCCAACTCCA	GAACGCGACA	CTGACAAACC	ACTCCTTCTT	CCAGTCGAAG	350
	ACGTATTCTC	TATCACTGGT	CGTGGTACAG	TTGCTTCAGG	ACGTATCGAA	400
10	CGTGGTACTG	TTAAAGTTGG	TGACGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	AGAAACTAAA	AAAGCTGTTG	TTACTGGTAT	CGAAATGTTC	CGTAAACAC	500
	TTACTGAAGG	TCTTGCTGGT	GATAACGTCG	GTGCACTTCT	CCGTGGTATC	550
	CAACGTGACG	AAATCGAACG	TGGTCAAGTT	ATTGCTAAAC	CAGGTTCAAT	600
	CACTCCACAC	AAACTTTTCG	AAGGTGAAGT	TTACGTATTG	AGCAAAGAAG	650
15	AAGGCGGACG	TCACACTCCA	TTCTTCGACA	ATAACCGTCC	TCAATTCTAC	700
	TTCCACACAA	CTGACGTTAC	TGGTTCAAGT	AAACTTCCAG	AAGGAACTGA	750
	AATGGTAATG	CCTGGTGACA	ACGTGCATAT	CGACGTTGAA	TTGATCCACC	800
	CAGTTGCGAT	CGAACAAGGT	ACTAC			825

20

2) INFORMATION FOR SEQ ID NO: 110

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 824 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leclercia adecarboxylata*

35 (B) STRAIN: ATCC 23216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110

	GGCGCGATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCAATGC	CTCAGACCCG	50
	TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTCCTTTC	ATCATCGTGT	100
40	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAACCTGGTT	150
	GAGATGGAAG	TTCGTGAACT	YCTGTCCAG	TACGACTTCC	CGGGCGACGA	200
	CACCCCAATC	GTTCGTGGTT	CTGCGCTGAA	AGCGCTGGAA	GGCGAAGCAG	250
	AGTGGAAGA	GAAAATCATC	GARCTGGCTG	GCTACCTGGA	TTCTACATC	300
	CCAGAGCCAG	AGCGTGCGAT	TGACAAGCCG	TTCTGCTGCT	CTATCGAAGA	350
45	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAGC	400
	GCGGTATCAT	CAARGTTGGC	GAAGAAGTTG	AAATCGTTGG	TATCAAGGAC	450
	ACTGCTAAGT	CTACCTGTAC	CGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCCGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTATCAAAC	550
	GTGAAGAAAT	CGAACGTGGT	CAGGTTCTGG	CTAAGCCAGG	CTCYATCAAG	600
50	CCGCACACCA	AGTTCGAATC	TGAAGTGATC	ATCCTGTCYA	AAGACGAAGG	650
	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700
	GTACKACTGA	CGTGACCGGT	ACCATCGARC	TGCCAGAAGG	CGTTGAGATG	750
	GTAATGCCAG	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TCCACCCAAT	800
55	CGCAATGGAC	GATGGTCTGC	GTTTC			824

2) INFORMATION FOR SEQ ID NO: 111

60 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 838 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Legionella micdadei*
 (B) STRAIN: ATCC 33218

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111

	CGGAGCGATA	TTAGTAGTAT	CAGCAGCGGA	TGGCCCAATG	CCTCAAACGA	50
	GAGAGCACAT	ACTYTTATCC	CGSCAGGTAG	GTGTTCCCTA	TATAGTAGTG	100
15	TTCTTAAACA	AAGCTGACAT	GGTGGATGAT	GCGGAGTTAT	TAGAATTAGT	150
	TGAAATGGAA	GTACGCGAYT	TGTTGAGCAG	CTATGAATTT	CCAGGAGATG	200
	AGATCCCGAT	TGTAGTTGGT	TCAGCATTAA	AAGCATTGGA	AGGCGATACG	250
	AGTGATATAG	GTGTACCAGC	GATTGAGAAG	TTAGTTGAGA	CGATGGATTC	300
	TTATATACCT	GAGCCGGTAA	GAAACATCGA	TAAAAGTTTC	TTGTTACCGA	350
20	TCGAAGACGT	GTTCTCAATA	TCTGGACGAG	GAACAGTAGT	AACAGGACGT	400
	ATCGAAAGCG	GGATCATCAA	AGTTGGTGAG	GAAGTCGAGA	TTGTTGGTAT	450
	ACGTGACACT	CAAAAGACGA	CATGCACAGG	CGTTGAAATG	TTCCGTAAAT	500
	TACTTGACGA	AGGTCGAGCT	GGAGACAACG	TTGGTATATT	GCTACGTGGT	550
	ACGAAGCGGG	ATGAAGTTGA	ACGCGGACAA	GTATTAGCTA	AGCCGGGAAG	600
25	CATTAAACCG	CATACTAAAT	TTGAAGCTGA	AGTGTATGTG	TTGTCAAAAG	650
	ATGAAGGTGG	ACGTCATACC	CCATTCTTTA	ACGGATATCG	GCCTCAATTT	700
	TACTTCAGGA	CCACAGACGT	AACTGGTTCT	TGTGATTTAC	CTGARGGTAT	750
	AGAAATGGTA	ATGCCAGGTG	ATAACGTCAA	GCTGATTGTT	AGCTTACACT	800
30	CACCGATTGC	TATGGACGAA	GGTTTGCGTT	TTGCAATC		838

2) INFORMATION FOR SEQ ID NO: 112

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 838 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Legionella pneumophila* subsp. *pneumophila*
 (B) STRAIN: ATCC 33152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112

	CGGAGCGATA	CTGGTTGTAT	CAGCAGCTGA	TGGTCCTATG	CCACAAACGA	50
	GGGAACACAT	TCTATTGTCT	CGCCAGGTAG	GTGTTCCATA	TATTGTTGTG	100
	TTCATGAACA	AAGCGGATAT	GGTTGATGAC	CCTGAGTTAT	TAGAGTTAGT	150
	GGAAATGGAA	GTGCGAGATT	TATTAAGCAG	TTACGATTTT	CCAGGGGATG	200
	ACATACCTAT	TGTTGTTGGT	TCAGCTTTGA	AAGCATTGGA	AGGTGAAGAC	250
	AGTGATATAG	GCGTTAAGGC	TATTGAGAAA	TTGGTTGAAA	CAATGGATTC	300
55	ATACATTCCCT	GAGCCAGTTA	GAAACATAGA	CAAGCCATTT	TTGTTGCCGA	350
	TTGAAGACGT	ATTTTCAATT	TCTGGACGCG	GAACAGTGGT	AACTGGTCGT	400
	GTAGAGAGTG	GAATTGTTAA	AGTTGGTGAG	GAAGTTGAAA	TTGTTGGAAT	450
	AAGAGACACC	CAAAAGACGA	CTTGTACGGG	TGTTGAGATG	TTCCGTAAAT	500
60	TACTTGATGA	AGGTCGAGCT	GGTGATAACG	TTGGTGTGTT	ATTACGAGGT	550

ACGAAGCGAG ATGAAGTGGG GCGTGGACAG GTATTGGCGA AGCCAGGAAC 600
 CATCAAGCCA CACACCAAGT TTGAAGCAGA AGTGTATGTA TTATCCAAGG 650
 AAGAAGGCGG ACGTCACACT CCATTCTTTA ATGGATACCG TCCACAATTC 700
 TATTTCAGAA CCACTGACGT GACAGGTACT TGTGACTTGC CATCAGGAGT 750
 5 TGAATGGTA ATGCCTGGAG ATAATGTGCA ATTAGTTGTT AGCTTGCATG 800
 CTCCGATTGC GATGGATGAA GGTTTAAGAT TCGCAATT 838

10 2) INFORMATION FOR SEQ ID NO: 113

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leminorella grimontii*
 (B) STRAIN: ATCC 33999

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113

25 GTGCAATCCT GGTAGTAGCA GCGACTGACG GCCCGATGCC TCAGACTCGC 50
 GAGCACATCC TGCTGGGTCG TCAGGTAGGC GTTCCGTACA TCATCGTATT 100
 CCTGAACAAG TGCGATATGG TTGATGACGA AGAGCTGCTG GAGCTGGTTG 150
 30 ARATGGAAAGT TCGCGAAGT CTGTCTCAGT ACGACTTCCC GGGCGACGAC 200
 ACTCCGGTAG TCCGCGGTTT AGCGCTGAAA GCGCTGGAAG GCGAAGCCGA 250
 GTGGGAARCG AAAATCATCG AGCTGGCAGG CCMTCTGGAT ACTTATATCC 300
 CAGAACCTGA GCGTGCATG GACAAGCCGT TCCTGCTGCC KATCGAAGAC 350
 GTATTCTCTA TCTCCGGCCG TGGTACCGTT GTTACCGGTC GTGTAGAGCG 400
 CGGCATCATC AAAGTCGGTG AAGAAGTGGG AATCGTCGGT ATCAAAGATA 450
 35 CCACCAAGAC CACCTGTACC GGCGTTGAAA TGTTCCGTAA GCTGCTGGAC 500
 GAAGGCCGTG CCGGCGAGAA CGTGGGCGTT CTGCTGCGCG GTACCAAGCG 550
 TGACGAAATC GAACGTGGTC AAGTTCTGGC CAAGCCGGGC ACCATCACTC 600
 CTCACACCCA GTTCGTGTCA GAAGTGTATA TCCTGAGCAA GGATGAAGGC 650
 GGCCGTCATA CTCCGTTCTT CAAAGGCTAC CGTCCTCAGT TCTACTTCCG 700
 40 TACGACTGAC GTGACAGGCA CCATCGAACT GCCGGAAGGC GTAGAGATGG 750
 TAATGCCAGG CGACAACATT CAGATGACCG TAAGTCTGAT TGCGCCGATC 800
 GCAATGGACG AAGGTCTGCG CTTGCGAA 828

45 2) INFORMATION FOR SEQ ID NO: 114

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leminorella richardii*
 (B) STRAIN: ATCC 33998

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114

5 GCTATCCTGG TTGTTGCTGC GACTGACGGC CCAATGCCTC AGACTCGTGA 50
 GCACATCCTG CTGGGTCGCC AGGTAGGCGT TCCTTACATC ATCGTGTTCC 100
 TGAACAAGTG CGACATGGTT GATGACGAAG AGCTGCTGGA ACTGGTAGAA 150
 ATGGAAGTTT GTGAACTTCT GTCTCAATAC GACTTCCCGG GCGACGATAC 200
 GCCGGTTGTT CGCGGTTTCT CGCTGAAAGC GCTGGAAGGT GACGCTGAGT 250
 GCGAARCGAA AATCATTGAA CTGGCGGAAT CCTTRGATAC TTAYATTCCA 300
 GAGCCAGAGC GTGCGATTGA CAAGCCGTTT CTGCTGCCTA TCGAAGACGT 350
 TTTCTCTATC TCTGGCCGTG GTACTGTAGT CACCGGTCGT GTAGAGCGCG 400
 10 GCATCATCAA AGTTGGTGAA GAAGTGGAAA TCGTGGGAAT CAAAGACACC 450
 ACCAAGACCA CCTGTACTGG CGTTGAAATG TTCCGTAAGC TGCTGGACGA 500
 AGGCCGTGCA GGTGAGAACG TTGGTGTCTT GCTGCGYGGT ACTAAGCGTG 550
 ACCGAAATCGA ACGTGGTCAG GTACTGGCTA AGCCAGGCAC CATCACTCCT 600
 CACACAGAAT TCGTGTGAGA AGTGTATATC CTGAGCAAGG ATGAAGGCGG 650
 15 YCGTCATACT CCGTTCTTCA AAGGCTACCG TCCTCAGTTC TACTTCCGTA 700
 CGACTGACGT GACCGGCACC ATCGAACTGC CAGAAGGCGT AGAGATGGTA 750
 ATGCCAGGCG ATAACATCCA GATGGTAGTT ACGCTGATTG CCCCAATCGC 800
 GATGGACGAA GGTCTGCGCT TCGCAA 826

20

2) INFORMATION FOR SEQ ID NO: 115

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 843 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leptospira interrogans*
 (B) STRAIN: ATCC 23581

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115

40 TGCGGCGATT CTTGTAGTAT CCGCAACTGA CGGACCTATG CCACAAACAA 50
 AAGAACATAT CCTTCTTGCT CGTCAGGTAG GTGTTCCATA TGTAATTGTA 100
 TTCATTAACA AAGCAGATAT GCTTGCTGCT GACGAAAGAG CAGAAATGAT 150
 CGAAATGGTT GAGATGGACG TTCGTGAACT TCTCAATAAG TATAGCTTCC 200
 CAGGAGATAC AACTCCTATC GTTCATGGTT CTGCGGTAAA AGCACTTGAG 250
 GGCGATGAAT CTGAAATTGG GATGCCTGCA ATTCTCAAAT TGATGGAAGC 300
 TCTGGATACT TTCGTTCCAA ATCCAAAACG TGTAAATCGAC AAACCTTTCC 350
 45 TTATGCCAGT AGAAGACGTT TTCTCGATCA CTGGTCGTGG AACTGTTGCA 400
 ACTGGAAGAG TGGAACAAGG TGTTTTGAAA GTGAACGACG AAGTTGAAAT 450
 TATCGGTATC CGCCCAACAA CAAAACTGT TGTTACCGGT ATCGAAATGT 500
 TCAGAAAAC TCTCGATCAA GCGGAAGCTG GCGACAACAT CGGCGCTCTT 550
 CTTCGTGGAA CTAAAAAAGA AGAAATCGAA AGAGGGCAAG TTCTTGCGAA 600
 50 GCCAGTTTCT ATCACTCCTC ACAAAAAGTT TGCCGCTGAG GTGTATGTAT 650
 TAACTAAGGA TGAAGGCGGA CGTCATACTC CGTTTATCAA TAACTACCGT 700
 CCTCAGTTTT ACTTTAGAAC AACTGACGTA ACCGGAGTTT GTAACCTTCC 750
 TAATGGTGTC GAAATGGTTA TGCTGGTGA TAACGTTTCT TTGACGGTTG 800
 AATTGATTAG CCCGATCGCA ATGGACAAGG GTCTTAAGTT CGC 843

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2) INFORMATION FOR SEQ ID NO: 116

60 (i) SEQUENCE CHARACTERISTICS:

201

- (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Megamonas hypermegale*
 (B) STRAIN: ATCC 25560

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116

15	CGGTGCTATC	CTCGTTGTTA	GTGCTGCTGA	TGGTCCTATG	CCTCAGACTC	50
	GTGAACACAT	CCTTCTCGCT	CGTCAGGTTG	GTGTTCCAGC	TATCGTTGTA	100
	TTCTCAACA	AAGCTGACCA	GGTTGATGAC	CCTGAACTTC	TCGAACTTGT	150
	TGAAATGGAA	GTTCTGAAC	TTCTTTCCAG	CTATGACTTC	CCAGGCGATG	200
	ACGTTCAGT	AATCACTGGT	TCCGCTCTTC	AGGCTCTCGA	AGGCGACGAA	250
	GAAGCTAAAA	AGAAAATTCT	TGAATTAATG	GATGCTGTTG	ATGATTACAT	300
20	CCCAACTCCA	ACACGTGACA	CTGATAAACC	TTTCTTAATG	CCAGTTGAAG	350
	ACGTATTCAC	AATTACTGGT	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
	CGTGGCGAAC	TTAACTTGG	TGACAGCGTT	GAAATCGTTG	GTCTTTCCGA	450
	TGAAAAGAAA	TCCACTACTG	TAACTGGTAT	CGAAATGTTC	CGCAAAATGC	500
	TTGATAGCGC	TGTTGCTGGT	GATAACATCG	GTGCACTTCT	TCGTGGTATT	550
25	GACCGTAAAG	AAATCGAACG	TGGTCAAGTT	CTTGCTAAAC	CTGGCACAAT	600
	TCATCCACAC	AAAAAATCA	AAGCTCAGGT	TTACGTATTA	ACTAAAGAAG	650
	AAGGTGGACG	TCATACTCCA	TTCTTCTCCA	ACTATCGTCC	ACAGTTCTAT	700
	TTCCGTAATA	CTGACGTTAC	TGGTGTGTTA	ACTCTTCCAG	AAGGTACTGA	750
	AATGGTTATG	CCTGGCGATA	ACATTGAAAT	GAGCATCGAA	CTCATCACTC	800
30	CAATCGCTAT	TGAAAAGGT	CTTCGCTTCG	CT		832

2) INFORMATION FOR SEQ ID NO: 117

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mitsuokella multacida*
 (B) STRAIN: ATCC 27723

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117

50	TGGTGCTATC	CTCGTCGTTT	CCGCTGCTGA	TGGCCCGATG	CCGCAGACGC	50
	GTGAGCACAT	CCTGCTCGCT	CGCCAGGTCG	GTGTTCCGGC	AATCGTTGTC	100
	TTCTCAACA	AGGTTGACCA	GGTTGACGAT	CCGGAGCTCC	TCGAGCTCGT	150
	CGAGATGGAA	GTTTCGCGAGC	TGCTCTCCAG	CTACGACTTC	CCGGGCGATG	200
	ACATCCCTGT	AATCGCTGGT	TCCGCTCTGA	AGGCCCTCGA	AGGCCGACGAA	250
55	GAGCAGAAGA	AGAACATCCT	CAAGCTCATG	GAAGCTGTCG	ATGAGTACAT	300
	CCCAGACGCC	GTCCGCGACA	ACGCTAAGCC	GTTCTTGATG	CCGGTCGAGG	350
	ATGTCTTCAC	GATCACGGGC	CGTGGTACGG	TTGCAACGGG	CCGCGTTGAG	400
	CGTGGTGAGC	TCAAGATGAA	CGATACGGTT	GAGATCGTTG	GTCTGCAGGA	450
	CGAGCCGCGT	CAGACGGTTG	TCACGGGCAT	CGAGATGTTC	CGCAAGATGC	500
60	TTGATTTTCG	TGAGGCTGGC	GATAACATCG	GTGCTCTGCT	CCGTGGTATC	550

5 GACCGCAAGG AGATCGAGCG TGGCCAGGTT CTCGCAAAGC CGGGCACGAT 600
 TCATCCGCAC ACGAAGTTCA AGGCTCAGGT CTATGTCCTG ACGAAAGAAG 650
 AAGGCGGCCG TCATACGCCG TTCTTCACGA ACTATCGCCC GCAGTTCTAC 700
 TTCCGCACGA CGGACGTAAC TGGCGTAGTC AAAGTGCCGG AAGGCACGGA 750
 GATGGTTATG CCTGGCGATA ACGTCGAGAT GGAAGTTGAG CTCATCACCC 800
 CGATCGCTAT CGAGAAGGGC 820

10 2) INFORMATION FOR SEQ ID NO: 118

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mobiluncus curtisii* subsp. *holmesii*
 (B) STRAIN: ATCC 35242

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118

25 CGGCGCTATC CTCGTGGTGG CTGCTACTGA CGGTCCGATG GCTCAGACCA 50
 AGGAACACAT CCTGTTGGCT AAGCAGGTTG GCGTGCCCTC CATCCTGGTC 100
 GCTCTGAACA AGTGCGATTG TTCCGATGTG GACGAAGACA TGCTCGAAAT 150
 CGTCGAGGAC GAAATCCGCG ATGACCTGGA GAAGCAGGGC TTCGATCGTG 200
 30 ACTGCCCCGAT TATCCACGTT TCCGCTCTGA AGGCCCTGGA AGGCGACCCC 250
 GAGTGGACCA AGAAGATTGA AGAGCTCATG GAAGCGGTGCG ATACCTACAT 300
 TCCTGAGCCT GTTCGTGACC TCGACAAGCC GTTCTTGATG CCTATCGAAG 350
 ACGTCTTCAC CATTACTGGT CGCGGTACCG TAGTGACCGG TCGTGTGGAA 400
 CGCGGCAAGC TACCGTTGAA CGCCGAAGTG GAAATCGTAG GTATTCGTCC 450
 35 TACGCAAAAG ACCACCGTTA CCGGTATCGA AATGTTCCAC AAGTCCATGG 500
 ACGAAGCCTA CGCCGGCGAG AACTGTGCTC TGTTGCTGCG TGGCACCAG 550
 CGTGAGGACG TTGAGCGCGG TCAGGTTGTC TGCATTCCCTG GCTCCGTGAC 600
 CCCGCACACC AAGTTCGAGG GCAAGGTCTA CATCTTGAAG AAGGACGAAG 650
 GTGGACGTCA CAAGTCGTTT TACGACGGCT ACCGCCCCGA GTTCTTCTTC 700
 40 CGCACCACCG ACGTGACCGG TGTTATTAC CTGCCCCGAAG GCACCGAAAT 750
 GGTTATGCCT GGCACACCA CCGAAATTAG CGTTGAGCTG ATTCAGCCTA 800
 TCGCTATGGA GGAAGGTCTC GGCTTCGCTA T 831

45 2) INFORMATION FOR SEQ ID NO: 119

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Moellerella wisconsensis*
 (B) STRAIN: ATCC 35017

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119

	GGTGCAATTC	TGGTTGTTGC	TGCAACTGAT	GGCCCTATGC	CACAGACTCG	50
	TGAGCACATC	CTGTTAGGTC	GTCAGGTTGG	CGTTCCATAC	ATCATCGTTT	100
	TCCTGAACAA	ATGTGACATG	GTAGACGACG	AAGAGCTGTT	AGAAGCTGGT	150
5	GAAATGGAAG	TCCGTGAGCT	GCTGTCTCAG	TACGATTTCC	CAGGCGATGA	200
	CACTCCAGTA	ATCCGTGGTT	CAGCGCTGAA	AGCTCTGGAA	GGCGAAGCTG	250
	AGTGGGAAGC	TAAAATCATT	GAAGTGGCAG	AAGCACTGGA	TTCTTATATC	300
	CCAGAGCCAG	AGCGTGACAT	TGATAAGCCA	TTCCTGTTAC	CAATCGAAGA	350
	CGTATTCTCA	ATTTCAAGGC	GTGGTACAGT	TGTTACTGGT	CGTGTGAGC	400
10	GTGGTATCGT	TAAAGTCGGT	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAT	450
	ACCGTGAAAA	CAACATGTAC	TGGCGTTGAA	ATGTTCCGTA	AACTGCTGGA	500
	CGAAGGCCGT	GCTGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTACTAAAC	550
	GTGATGATAT	CGAACGTGGT	CAAGTATTGG	CTAAACCAGG	TTCAATCACT	600
	CCGCATACAA	CTTTTCAATC	AGAAGTTTAC	ATCCTGAGCA	AAGATGAAGG	650
15	TGGCCGTCAT	ACTCCATTCT	TCAAAGGTTA	CCGTCCACAG	TTCTACTTCC	700
	GTACAACTGA	CGTAACCGGT	ACTATCGAAC	TGCCAGAAGG	CGTTGAGATG	750
	GTAATGCCAG	GTGATAACAT	CAAAATGATC	GTTACTCTGA	TCCACCCAAT	800
	TGCAATGGAT	GCAGGTCTGC	GTTTT			825

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2) INFORMATION FOR SEQ ID NO:120

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 827 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Branhamella catarrhalis*
 (B) STRAIN: ATCC 43628

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120

	TGGTGCTATC	TTGGTTGTTT	CTGCAACTGA	TGGTCCTATG	CCACAAACTC	50
	GTGAGCATAT	CCTACTATCT	CGTCAGGTTG	GTGTACCATA	CATCATGGTA	100
40	TTTCATGAACA	AGTGCGATAT	GGTTGATGAT	GAAGAGCTAC	TAGAATTGGT	150
	TGAAATGGAA	GTTTCGTGAAC	TTCTATCTGA	CTATGATTTT	CCTGGTGATG	200
	ATACCCCAAT	CATCAAAGGT	TCAGCACTAG	AAGCATTGAA	TGTTTCTGAT	250
	GGTAAATATG	GCGAGCCTGC	AGTTCTAGAA	CTGCTAGACA	CACTAGACAG	300
	CTATATCCCA	GAGCCTGAGC	GTGATATCGA	TAAGTCATTG	TTGATGCCAA	350
45	TTGAAGATGT	CTTCTCGATC	TCAGGTCGTG	GTACAGTTGT	GAAGTGGTCG	400
	GTTGAATCAG	GTATTATTAA	AGTTGGTGAT	GAAATTGAAA	TCATCGGTAT	450
	CAAACCAACT	GCTAAAACCA	CCTGTACTGG	TGTTGAAATG	TTCCGTAAAC	500
	TGTTAGACGA	AGGTCGTGCA	GGTGAGAACT	GTGGTATCTT	GTTGCGTGGT	550
	ACTAAGCGTG	AAGAAGTTCA	ACGCGGTCAA	GTACTTGCAA	AACCAGGTTT	600
50	AATCACCCCA	CATACTAAGT	TTGATGCTGA	AGTTTATGTA	CTGTCAAAGG	650
	AAGAAGGTGG	TCGTACACCC	CCATTCTTAA	ATGGCTATCG	CCCACAGTTC	700
	TACTTCCGTA	CCACAGATGT	GACTGGTGCC	ATCACTCTAC	AAGAAGGTAC	750
	CGAAATGGTT	ATGCCTGGTG	ACAATGTTGA	GATGAGTGTT	GAGCTTATCC	800
55	ACCCAATCGC	CAGGATAAAG	GTCTACG			827

2) INFORMATION FOR SEQ ID NO: 121

60 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Morganella morganii* subsp. *morganii*
 (B) STRAIN: ATCC 25830

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121

	CGGCGCTATC	CTGGTTGTTG	CTGCAACTGA	TGGCCCTATG	CCACAGACCC	50
	GTGAGCACAT	CCTGTTAGGT	CGTCAGGTTG	GCGTTCCTTA	CATCATCGTA	100
15	TTCCTGAACA	AATGTGACAT	GGTTGATGAT	GAAGAGCTGC	TGGAAGTGGT	150
	TGAAATGGAA	GTTTCGTGAAC	TTCTGTCTCA	GTACGATTTT	CCTGGCGACG	200
	ACACGCCAAT	CGTTCGCGGT	TCAGCGCTGA	AAGCACTGGA	AGGCGAGCCA	250
	GAGTGGGAAG	CTAARATCGT	TGAAGTGGCA	GGTTTCCTGG	ATTCTTACAT	300
20	CCCTGAGCCA	GAGCGTGCAA	TTGACAAGCC	GTTTCCTGCTG	CCAATCGAAG	350
	ACGTATTCTC	AATCTCCGGC	CGTGGTACCG	TTGTTACCGG	TCGTGTTGAG	400
	CGCGGTATCA	TCAAGGTTGG	TGAGGAAGTT	GAAATCGTGG	GTATCAAAGA	450
	TACTGCGAAA	ACCACCTGTA	CCGGTGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCMGGTGAG	AACGTCGGTG	TTCTGCTGCG	TGGTACCAAG	550
25	CGTGAAGAAA	TCGAACGTGG	TCAGGTTCTG	GCTAAACCAG	GTTCAATCAA	600
	ACCACAYACC	AAATTTGAAT	CAGAAGTTTA	TATTCTGAGC	AAAGATGAAG	650
	GTGGTCGTCA	TACTCCATTC	TTCAAAGGYT	ACCGTCCACA	GTTCTACTTC	700
	CGTACCACAG	ACGTAACAGG	TACTATCGAA	CTGCCGGAAG	GCGTTGAAAT	750
	GGTAATGCCG	GGCGACAACA	TCAAAATGAT	CGTCACCCTG	ATCCACCCAA	800
30	TCGCAA					806

2) INFORMATION FOR SEQ ID NO: 122

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*
 (B) STRAIN: TB 299

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122

	GGTGCGATCC	TGGTGGTCGC	CGCCACCGAC	GGCCCGATGC	CCCAGACCCG	50
	CGAGCACGTT	CTGCTGGCGC	GTCAAGTGGG	TGTGCCCTAC	ATCCTGGTAG	100
	CGCTGAACAA	GGCCGACGCA	GTGGACGACG	AGGAGCTGCT	CGAACTCGTC	150
	GAGATGGAGG	TCCGCGAGCT	GCTGGCTGCC	CAGGAATTCG	ACGAGGACGC	200
	CCCGGTTGTG	CGGGTCTCGG	CGCTCAAGGC	GCTCGAGGGT	GACGCGAAGT	250
	GGGTTGCCTC	TGTCGAGGAA	CTGATGAACG	CGGTCGACGA	GTCGATTCGG	300
55	GACCCGGTCC	GCGAGACCGA	CAAGCCGTTT	CTGATGCCCG	TGGAGGACGT	350
	CTTCACCAT	ACCGGCCGCG	GAACCGTGGT	CACCGGACGT	GTGGAGCGCG	400
	CGGTGATCAA	CGTGAACGAG	GAAGTTGAGA	TCGTCCGCAT	TCGCCCATCG	450
	ACCACCAAGA	CCACCGTCAC	CGGTGTGGAG	ATGTTCCGCA	AGCTGCTCGA	500
60	CCAGGGCCAG	GCGGGCGACA	ACGTTGGTTT	GCTGCTGCGG	GCGTCAAGC	550

GCGAGGACGT CGAGCGTGGC CAGGTTGTCA CCAAGCCCGG CACCACCACG 600
 CCGCACACCG AGTTCGAAGG CCAGGTCTAC ATCCTGTCCA AGGACGAGGG 650
 CGGCCGGCAC ACGCCGTTCT TCAACAATA CCGTCCGCAG TTCTACTTCC 700
 GCACCACCGA CGTGACCGGT GTGGTGACAC TGCCCGAGGG CACCGAGATG 750
 5 GTGATGCCCC GTGACAACAC CAACATCTCG GTGAAGTTGA TCCAGCCCCG 800
 CGCCATGGAC GAAGGTCTGC GTTTC 825

10 2) INFORMATION FOR SEQ ID NO: 123

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria cinerea*
 (B) STRAIN: ATCC 14685

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123

25 CCGTGCGATC TTGGTATGTT CCGCAGCTGA CCGTCCTATG CCGCAAATC 50
 GCGAACACAT CCTGTTGGCC CGCCAAGTAG GTGTACCTTA CATCATCGTG 100
 TTCATGAACA AATGCGACAT GGTGACGAT GCCGAGCTGT TGGAGCTGGT 150
 TGAAATGGAA ATCCGTGACT TGCTGTCAAG CTACGACTTC CCAGGTGACG 200
 30 ACTGCCCCGAT CGTACAAGGT TCTGCACTGA AAGCCTTGGA AGGCGACGCA 250
 GCTTACGAAG AAAAAATCTT CGAATTGGCT GCTGCATTGG ACAGCTACAT 300
 CCCAACACCT GAGCGTGCAG TGGACAAACC TTTCTTGTTG CCTATCGAAG 350
 ACGTATTCTC TATTTCCGGT CGCGGTACAG TAGTAACCGG TCGTGTAGAG 400
 CGCGGTATCA TCCACGTTGG TGACGAGATC GAAATCGTAG GTCTGAAAGA 450
 35 AACTCAAAAA ACCACTTGTA CCGGTGTTGA AATGTTCCGC AAATGCTGG 500
 ACGAAGGTCA AGCTGGTGAC AACGTAGGTG TATTGCTGCG TGGTACTAAA 550
 CGTGAAGACG TAGAGCGTGG TCAAGTATTG GCTAAACCGG GTACTATCAC 600
 TCCTCACACC AAGTTCAAAG CAGAAGTATA CGTACTGAGC AAAGAAGAGG 650
 GTGGTTCGTCA CACTCCGTTT TTCGCTAACT ACCGTCCACA ATTCTACTTC 700
 40 CGTACTACCG ACCTAACCGG CGCGGTTACT TTGGAAGAAG GTGTAGAAAT 750
 GGTAAATGCCG GGTGAGAACG TAACCATTAC TGTAGAACTG ATTGCGCCTA 800
 TCGCTA 806

45 2) INFORMATION FOR SEQ ID NO: 124

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria elongata* subsp. *elongata*
 (B) STRAIN: ATCC 25295

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124

5 CCGCGCAATC TTGGTATGTT CCGCTGCTATG CCGTACCTTA CATCATCGTG 50
 GCGAACACAT CCTGTTGGCC CGCCAAGTAG GCGTACCTTA CATCATCGTG 100
 TTCATGAATA AATGCGACAT GGTGAYGAT GCCGAAGTGC TGGAACTGGT 150
 TGAAATGGAA ATCCGTGACT TGCTGTCAAG CTACGACTTC CCAGGCGACG 200
 ACTGCCCCGAT CGTACAAGGT TCCGCACTGA AAGCCTTGGG AGGCGACGCA 250
 GCTTACGAAG AAAAAATCTT CGAACTGGCT GCTGCATTGG ACAGCTACAT 300
 CCCGACACCT GAGCGTGCCG TGGACAAACC GTTCTGTGTT CCTATCGAAG 350
 ACGTATTCTC TATCTCCGGC CGTGGTACAG TAGTAACCGG TCGTGTAGAG 400
 10 CGCGGTATCA TCCACGTCGG TGACGAGATC GAAATCGTAG GTCTGAAAGA 450
 AACCCAAAAA ACCACTTGTA CCGGTGTTGA AATGTCCCG AACTGCTGG 500
 ACGAAGGTCA AGCAGGTGAC AACGTAGGCG TATTGCTGCG CGGTACCAAA 550
 CGTGAAGAAG TGGAACGCGG TCAAGTATTG GCTAAACCGG GTACCATCAC 600
 TCCTCACACC AAATTCAAAG CAGAAGTTTA CGTATTGAGC AAAGAAGAGG 650
 15 GTGGTCGTCA TACTCCGTTT TTCGCTAAGT ACCGTCCACA ATTCTACTTC 700
 CGTACTACCG ACGTAACCGG TCGCGTTACT TTGGAAGAAG GTGTAGAAAT 750
 GGTATGCCT GGTGAGAACG TGGCCATCAC TGTAGAACTG ATTGCACCTA 800
 TCGCTATGGA AGAAGGTCTG CG 822

20

2) INFORMATION FOR SEQ ID NO: 125

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 820 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria flavescens*
 (B) STRAIN: ATCC 13120

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125

40 CCGCGCGACT TGGTATGTTT CGCAGCTGAC GGTCTCTATGC CGCAAACCCG 50
 CGAACACATC CTGTTGGCTC GCCAAGTAGG TGTACCTTAC ATCATCGTAT 100
 TCATGAACAA ATGCGACATG GTAGACGATG CCGAGCTGTT GGAAGTGGTT 150
 GAAATGGAAA TTCGTGACTT GTTGTCAAGC TACGACTTCC CAGGCGACGA 200
 CTGCCCCAATC GTACAAGGTT CTGCACTGAA AGCTTTGGAA GGTGATGCTG 250
 CTTACGAAGA AAAAATCTTC GAATTGGCTG CTGCCCTGGA CAGCTACATC 300
 CCAACACCTG AGCGTGCTGT GGACAAACCT TTCTTGTTGC CTATCGAAGA 350
 45 CGTATTCTCT ATCTCTGGTC GTGGTACAGT AGTAACCGGT CGCGTAGAGC 400
 GCGGTATCAT CCACGTTGGT GACGAGATCG AAATCGTAGG TCTGAAAGAA 450
 ACTCAAAAAA CCACTTGATC CGGCGTTGAA ATGTTCCGCA AACTGCTGGA 500
 CGAAGGTCAA GCAGGTGACA ACGTAGGCGT ATTGCTGCGT GGTACTAAAC 550
 GTGAAGACGT AGAGCGTGGT CAAGTATTGG CTAAACCAGG TACCATCACT 600
 50 CCTCACACCA AATTCAAAGC AGAAGTATAC GTACTGAGCA AAGAAGAGGG 650
 TGGTCGTAC ACTCCATTTT TCGCTAACTA CCGTCCACAA TTCTACTTCC 700
 GTACTACCGA CGTAACTGGT GCAGTTACTT TGGAAGAAGG CGTAGAAATG 750
 GTAATGCCAG GTGAGAACGT AACCATTACT GTAGAACTGA TTGCGCCAAT 800
 55 CGCTATGGAA GAAGTCTGCG 822

2) INFORMATION FOR SEQ ID NO: 126

(i) SEQUENCE CHARACTERISTICS:

60

207

- (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria gonorrhoeae*
 (B) STRAIN: ATCC 49226

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126

15	GGTGCAATCC	TGGTATGTTT	TGCTGCCGAC	GGCCCTATGC	CGCAAACCCG	50
	CGAACACATC	CTGCTGGCCC	GTCAAGTAGG	CGTACCTTAC	ATCATCGTGT	100
	TCATGAACAA	ATGCGACATG	GTCGACGATG	CCGAGCTGTT	GGAAGTGGTT	150
	GAAATGGAAA	TCCGCGACCT	GCTGTCCAGC	TACGACTTCC	CCGGCGACGA	200
	CTGCCCCGATC	GTACAAGGTT	CCGCACTGAA	AGCCTTGGA	GGCGATGCCG	250
	CTTACGAAGA	AAAAATCTTC	GAAGTGGCTA	CCGCATTGGA	CAGCTACATC	300
20	CCGACTCCCG	AGCGTGCCGT	GGACAAACCA	TTCCTGCTGC	CTATCGAAGA	350
	CGTGTCTTCC	ATTTCGCGCC	GCGGTACCGT	AGTCACCGGC	CGTGTAGAGC	400
	GAGGTATCAT	CCACGTTGGT	GACGAGATTG	AAATCGTCGG	TCTGAAAGAA	450
	ACCCAAAAAA	CCACCTGTAC	CGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGTCAG	GCGGGCGACA	ACGTAGGCGT	ATTGCTGCGC	GGTACCAAAC	550
25	GTGAAGACGT	AGAACGCGGT	CAGGTATTGG	CCAAACCGGG	TACTATCACT	600
	CCTCACACCA	AGTTCAAAGC	AGAAGTGTAC	GTATTGAGCA	AAGAAGAGGG	650
	CGGCCGCCAT	ACCCCGTTTT	TCGCCAACTA	CCGTCCCCAA	TTCTACTTCC	700
	GTACCACTGA	CGTAACCGGC	GCGGTTACTT	TGAAAAAAGG	TGTGGAATG	750
	GTAATGCCGG	GTGAGAACGT	AACCATTACT	GTAGAACTGA	TTGCGCCTAT	800
30	CGCTATGGAA	GAAGGTCTGC	GCTTTGCGAT			830

2) INFORMATION FOR SEQ ID NO: 127

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria lactamica*
 (B) STRAIN: ATCC 23970

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127

50	CGGCGCAATC	TTGGTATGTT	CCGCCGCCGA	CGGCCCTATG	CCGCAAACCC	50
	GCGAACACAT	TCTGTTGGCC	CGCCAAGTAG	GTGTACCTTA	CATCATCGTA	100
	TTCATGAACA	AATGCGATAT	GGTCGACGAT	GCCGAGCTGT	TGGAAGTGGT	150
	TGAAATGGAA	ATCCGCGACC	TGCTGTCAAG	CTACGACTTC	CCAGGCGACG	200
	ACTGCCCAAT	CGTACAAGGT	TCCGCACTGA	AAGCTTTGGA	AGGCGATGCC	250
55	GCTTACGAAG	AAAAAATCTT	CGAACTGGCT	GCCGCATTGG	ACAGCTACAT	300
	CCCGACTCCC	GAGCGTGCCG	TGGACAAACC	GTTCTGCTG	CCTATCGAAG	350
	ACGTATTCTC	CATCTCCGGC	CGCGGTACGG	TAGTAACCGG	CCGTGTAGAG	400
	CGCGGTGTCA	TCCACGTTGG	CGACGAGATC	GAAATCGTCG	GTCTGAAAGA	450
	AACCCAAAAA	ACCACCTGTA	CCGGTGTGCA	GATGTTCCGC	AAACTGCTGG	500
60	ACGAAGGTCA	GGCAGGCGAC	AACGTAGGCG	TATTGCTGCG	CGGTACCAAA	550

5 CGTGAAGAAG TGGAACGCGG TCAGGTATTA GCCAAACCGG GTACCATCAC 600
 TCCGCACACC AAGTTCAAAG CAGAAGTGTA TGTATTGAGC AAAGAAGAGG 650
 GCGGTCGTCA CACTCCGTTT TTCGCCAACT ACCGTCCGCA ATTCTACTTC 700
 CGTACCACCG ACGTAACCGG CGCGGTTACT TTGGAAGAAG GCGTGGAAT 750
 GGTAATGCCC GGTGAGAACG TAACCATTAC TGTAGAACTG ATTGCGCCTA 800
 TCGCTATGGA AGAAGG 816

10 2) INFORMATION FOR SEQ ID NO: 128

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria meningitidis*
 (B) STRAIN: ATCC 13077

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128

25 CCGTGCAATC CTGGTATGTT CCGCAGCCGA CCGTCCTATG CCGCAAACCC 50
 CGGAACACAT CCTGCTGGCC CGTCAAGTAG GCGTACCTTA CATCATCGTG 100
 TTCATGAACA AATGCGACAT GGTCGACGAT GCCGAGCTGT TGGAAGTGGT 150
 TGAAATGGAA ATCCGCGACC TGCTGTCCAG CTACGACTTC CCCGGCGACG 200
 30 ACTGCCCCGAT CGTACAAGGT TCCGCACTGA AAGCCTTGGG AGGCGATGCC 250
 GCTTACGAAG AAAAAATCTT CGAATTGGCT GCTGCATTGG ACAGCTACAT 300
 CCCGACTCCC GAGCGTGCCG TGGACAAACC TTTCTTGTG CCTATCGAAG 350
 ACGTATTCTC TATTTCCGGT CGTGGTACAG TAGTAACCGG TCGTGTAGAG 400
 CGCGGTATCA TCCACGTCGG TGACGAGATC GAAATCGTCG GTCTGAAAGA 450
 35 AACTCAAAAA ACCACTTGTA CCGGTGTTGA AATGTTCCGC AAAGTGTGCTGG 500
 ACGAAGGTCA AGCAGGCGAC AACGTAGGCG TATTGCTGCG CCGTACCAAA 550
 CGTGAAGACG TAGAGCGTGG TCAAGTATTG GCTAAACCGG GTACAATCAC 600
 TCCTCACACC AAGTTCAAAG CAGAAGTATA CGTACTGAGC AAAGAAGAGG 650
 GCGGCCGCCA TACCCCGTTC TTCGCCAACT ACCGTCCCCA ATTCTACTTC 700
 40 CGTACCACCG ACGTAACCGG CGCGGTTACT TTGGAAGAAG GTGTGGAAAT 750
 GGTAATGCCG GCGGAGAACG TAACCATCAC CGTAGAACTG ATTGCGCCTA 800
 TCGCTATGGA AGAAGGTTTG CGCTTTGCGA T 831

45 2) INFORMATION FOR SEQ ID NO: 129

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 815 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria mucosa*
 (B) STRAIN: ATCC 19696

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129

	CGGCGCAATC	TTGGTATGTT	CTGCTGCTGAC	CGGTCCTATG	CCGCAAACCC	50
	GYGAACACAT	CCTGTTGGCC	CGTCAAGTAG	GYGTACCTTA	CATCATCGTG	100
	TTCATGAACA	AATGCGACAT	GGTTGACGAT	GCCGAAYTGT	TGGAAGTGGT	150
5	TGAAATGGAA	ATCCGTGACT	TGCTGTCAAG	CTACGACTTC	CCTGGYGACG	200
	ACTGCCCCGAT	TGTACAAGGT	TCTGCACTGA	AAGCCTTGGA	AGGCGATGCC	250
	GCTTACGAAG	AAAAAATCTT	CGAACTGGCT	GCCGCATTGG	ACAGCTACAT	300
	CCCGACTCCC	GAGCGTGCCG	TAGACAAACC	GTTCTGTGTTG	CCTATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACAG	TAGTAACCGG	CCGTGTAGAG	400
10	CGCGGTGTTA	TCCACGTTGG	TGACGAGATC	GAAATCGTAG	GTCTGAAAGA	450
	AACCCAAAAA	ACCACATGTA	CCGGTGTGTA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGTCA	AGCCGGTGAC	AACGTAGGCG	TATTGCTGCG	CGGTACCAAA	550
	CGTGAAGAAG	TGGAACGCGG	TCAAGTATTG	GCTAAACCGG	GTACCATCAC	600
	TCCGCACACC	AAATTCAAAG	CAGAAGTGTA	CGTATTGAGC	AAAGAAGAGG	650
15	GTGGTTCGTC	TACTCCGTTT	TTCGCTAACT	ACCGTCCTCA	ATTCTACTTC	700
	CGTACTACCG	ACGTAACCGG	TGCGGTTACT	TTGGAAGAAG	GTGTAGAAAT	750
	GGTTATGCCT	GGTGAGAAYG	TAGCCATYAC	TGTAGAACTG	ATTGCGCCTA	800
	TYGCTATGGA	AGAAG				815

20

2) INFORMATION FOR SEQ ID NO: 130

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria sicca*
 (B) STRAIN: ATCC 9913

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130

	GGCGCAATCT	TGGTATGTTT	CGCTGCTGAC	GGTCCTATGC	CGCAAACCCG	50
	CGAACACATC	CTGTTGGCCC	GCCAAGTAGG	CGTACCTTAC	ATCATCGTGT	100
40	TCATGAACAA	ATGCGACATG	GTTGACGATG	CCGAGCTGTT	GGAAGTGGTT	150
	GAAATGGAAA	TCCGTGACTT	GCTGTCAAGC	TACGACTTCC	CTGGTGACGA	200
	CTGCCCCGATC	GTACAAGGTT	CTGCACTGAA	AGCCTTGGA	GGCGACGCCG	250
	CTTACGAAGA	AAAAATCTTC	GAAGTGGCTG	CTGCATTGGA	CAGCTACATC	300
	CCGACTCCTG	AGCGTGCCGT	GGACAAACCG	TTCCTGTTGC	CTATTGAAGA	350
45	CGTATTCTCC	ATCTCCGGTC	GCGGTACCGT	AGTAACCGGC	CGTGTAGAGC	400
	GCGGTGTTAT	CCACGTTGGT	GACGAGATTG	AAATCGTAGG	TCTGAAAGAA	450
	ACCCAAAAAA	CCACTTGATC	CGGTGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGTCAA	GCCGGTGACA	ACGTAGGCGT	ATTGCTGCGC	GGTACCAAAC	550
	GTGAAGAAGT	GGAACGCGGT	CAAGTATTGG	CTAAACCGGG	TACCATCACT	600
50	CCTCACACTA	AATTCAAAGC	AGAAGTTTAC	GTATTGAGTA	AAGAAGAGGG	650
	TGTCGTCAT	ACTCCGTTCT	TCGCTAACTA	CCGTCCTCAA	TTCTACTTCC	700
	GTACTACCGA	CGTAACCGGC	GCGGTTACTT	TGGAAGAAGG	TGTAGAAATG	750
	GTTATGCCTG	GTGAGAACGT	AGCCATCACT	GTAGAAGTGA	TTGCACCGAT	800
55	CGCTATGGAA	GAAGGTCTGC	GCTTTGCCA			829

2) INFORMATION FOR SEQ ID NO: 131

60 (i) SEQUENCE CHARACTERISTICS:

210

- (A) LENGTH: 814 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria subflava*
 (B) STRAIN: ATCC 14221

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131

	CGGCGCGACT	TGGTATGTTT	CGCAGCTGAT	GGTCCTATGC	CTCAAACCTCG	50
	CGAACACATC	CTGTTGGCTC	GCCAAGTAGG	TGTACCTTAC	ATCATCGTAT	100
15	TCATGAACAA	ATGCGACATG	GTTGACGATG	CCGAGCTGTT	GGAACCTGGT	150
	GAAATGGAAA	TCCGTGACCT	GTTGTCAAGC	TACGACTTCC	CAGGCGACGA	200
	CTGCCCAATC	GTACAAGGTT	CTGCACTGAA	AGCTTTGGAA	GGTGACGCTG	250
	GTTACGAAGA	GAAAATCTTC	GAATTGGCTG	CTGCTCTGGA	CAGCTACATC	300
20	CCAACACCTG	AGCGTGCTGT	GGACAAACCT	TTCTTGTTGC	CTATCGAAGA	350
	CGTATTCTCT	ATCTCTGGCC	GTGGTACAGT	AGTAACTGGT	CGTGTAGAGC	400
	GCGGTATCAT	CCACGTTGGT	GACGAGATCG	AAATCGTAGG	TCTGAAAGAA	450
	ACCCAAAAAA	CCACTTGATC	CGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGTCAA	AGTGGTGACA	ACGTAGGCGT	ATTGCTGCGT	GGTACCAAAC	550
25	GTGAAGACGT	AGAGCGTGTT	CAAGTATTGG	CTAAACCAGG	TACCATTACT	600
	CCTCACACCA	AATTCAAAGC	AGAAGTATAC	GTACTGAGCA	AAGAAGAGGG	650
	TGGTCGTCAC	ACTCCATTCT	TCGCTAATA	CCGTCCACAA	TTCTACTTCC	700
	GTACTACTGA	CGTAACTGGT	GCAGTTACTT	TGGAAGAAGG	CGTAGAAATG	750
	GTAATGCCAG	GTGAGAACGT	AACCATTACT	GTAGAACTGA	TTGCGCCTAT	800
30	CGCTATGGAA	GAAG				814

2) INFORMATION FOR SEQ ID NO: 132

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria weaveri*
 (B) STRAIN: ATCC 51223

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132

	GCCATCTTGG	TATGTTCTGC	TGCTGACGGT	CCTATGCCGC	AAACCCGTGA	50
	GCACATCCTG	TTGGCTCGTC	AAGTAGGTGT	ACCCTACATC	ATCGTATTCA	100
	TGAACAAATG	CGATATGGTT	GATGATGCAG	AGCTGCTGGA	ATTGGTAGAA	150
	ATGGAAATCC	GTGATCTGCT	GAGCAGCTAC	GATTTCCCTG	GCGATGATTG	200
	YCCAATCGTG	CAAGGTTCTG	CTTTGAAAGC	TTTGGAAGGT	GATGCCGCTT	250
55	ACGAAGAAAA	AATCTTTGAA	TTAGCTGCTG	CATTGGATAG	CTATATTCCA	300
	ACWCCTGAGC	GYGCTGTTGA	TAAACCATTG	CTGTTGCCGA	TTGAAGATGT	350
	ATTCTCAATT	TCAGGTCGTG	GTACAGTAGT	AACTGGTCGT	GTAGAGCGCG	400
	GTATTATTCA	CGTAGGCGAT	GAAATTGAAA	TTGTAGGTTT	GAAAGARACY	450
	CAAAAAACTA	CTTGTAACCG	CGTTGAAATG	TTCCGTAAAT	TGCTGGATSA	500
60	AGGTCAGGCT	GGTGATAACG	TAGGCGTATT	GTTGCGTGGT	ACCAAACGTG	550

AAGACGTTGA	GCGTGGTCAA	GTATTGGCTA	AGCCTGGTWC	TATTACTCCG	600
CAYACCAAAT	TCAAAGCAGA	RGTKTATGTW	TTGAGYAAGG	AAGAAGGCGG	650
TCGTCATACT	CCGTTCTTCG	CTAACTATCG	TCCGCAATTC	TATTTCCGTA	700
CTACAGACGT	TACCGGTGCK	GTRACTTTAG	AAGAAGGTGT	GGAAATGGTA	750
5 ATGCCTGGTG	AGAAYGTTGC	CATTACTGTW	GARYTGATYG	CTCCGATTGC	800
KATGGAAGAA	GGYTGCGT				818

10 2) INFORMATION FOR SEQ ID NO: 133

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 836 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Ochrobactrum anthropi*
 (B) STRAIN: ATCC 49188

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133

25	CGGCGCAATT	CTGGTTGTTT	CGGCCGCTGA	CGGCCCGATG	CCGCAGACCC	50
	GTGAGCACAT	CCTGCTCGCT	CGTCAGGTTG	GCGTTCCGGC	AATCGTCGTG	100
	TTCCTGAACA	AGTGCGACCA	GTTTGACGAT	GCAGAACTGC	TCGAACTGGT	150
	TGAACTGGAA	GTTGCGGAAC	TTCTGTGCGAA	ATACGATTTC	CCGGGCGACG	200
30	AAGTTCGGAT	CATCAAGGGC	TCGGCTCTTG	CTGCTCTGGA	AGATTCTTCG	250
	AAGGAACTGG	GCGAAGACGC	CGTTCGTTTC	CTGATGGCCG	CTGTTGACGA	300
	CTACATTCCG	ACCCCGGAAC	GTCCGATCGA	CCAGCCGTTT	CTGATGCCGA	350
	TCGAAGACGT	TTTCTCGATC	TCGGGCGCGT	GTACGGTTGT	GACGGGTCGC	400
	GTTGAGCGCG	GTATCGTCAA	GGTTGGTGAA	GAAGTTGAAA	TCGTCGGCAT	450
35	CAAGGCGACG	GCGAAGACGA	CGGTAACCGG	CGTTGAAATG	TTCCGCAAGC	500
	TGCTCGAYCA	GGGCCAGGCT	GGCGACAACA	TCGGCGCTCT	GATCCGCGGC	550
	GTTGGCCGTG	AAGACGTTGA	ACGCGGCCAG	GTTCTCTGCA	AGCCGGGTTC	600
	TGTGAAGCCG	CACACCAAGT	TCAAGGCAGA	AGCCTACATT	CTGACCAAGG	650
	ACGAAGGTGG	CCGTCATACG	CCGTTCTTTA	CGAACTACCG	TCCGCAGTTC	700
40	TACTTCCGCA	CGACGGACGT	GACCGGTGTT	GTCACGCTGC	CGGAAGGCAC	750
	GGAAATGGTT	ATGCCTGGCG	ACAACGTCGC	TATGGACGTC	ACCCTGATCG	800
	TGCCGATCGC	CATGGAAGAG	AAGCTCCGCT	TCGCTA		836

45 2) INFORMATION FOR SEQ ID NO: 134

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 805 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pantoea agglomerans*
 (B) STRAIN: ATCC 27155

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134

CCTGGTTGTT GCTGCGACTG ATGGCCCAAT GCCACAGACC CGTGAGCACA 50
 TCCTGCTGGG TCGTCAGGTT GCGGTTTCCTT ACATCATCGT GTTCCTGAAC 100
 AAGTGTGACA TGGTTGATGA TGAAGAGCTG CTGGAACTGG TAGAGATGGA 150
 5 AGTACGTGAC CTGCTGTCAC AGTACGACTT CCCAGGCGAT GACACCCCGA 200
 TCGTTTCGTGG TTCTGCTCTG AAAGCGCTGG AAGGCGTTCC TGAGTGGGAA 250
 GCAAAAATCG TTGAGCTGGC TGAACACCTG GACAACTACA TCCC GGATCC 300
 AGTCCGTGCG ATCGACATGC CGTTCCTGCT GCCAATCGAA GACGTATTCT 350
 CAATCTCTGG CCGTGGTACC GTTGTTACCG GTCGTGTTGA GCGCGGCATC 400
 10 GTTAAAGTCG GCGACGAAGT TGAAATCGTG GGTATCAAAG ATACTGCGAA 450
 ATCAACCTGT ACCGGTGTTG AGATGTTCCG TAAGCTGCTG GACCAGGGTC 500
 AGGCAGGCGA AAAGTGTGGT GTTCTGCTGC GCGGTATCAA GCGTGAAGAC 550
 ATCCAGCGTG GCCAGGTTCT GGCTAAGCCA GGCTCAATCA AGCCGCACAC 600
 CCAGTTCGAG TCAGAAGTTT ACGTTCTGTC TAAAGACGAA GGTGGCCGCC 650
 15 ATACTCCGTT CTTCAAAGGC TATCGTCCAG AGTTCTACTT CCGTACAACT 700
 GATGTAACCG GTTCAGTAGA GCTGCCAGAA GCGGTTGAGA TGGTCATGCC 750
 AGGCGACAAC ATCAAAATGG TTGTTACCCT GATCCACCCA ATCGCAATGG 800
 ACGAA 805

20

2) INFORMATION FOR SEQ ID NO: 135

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pantoea dispersa*
 (B) STRAIN: ATCC 14589

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135

CGCGATCCTG GTTGTGCTG CGACTGATGG CCCAATGCCT CAGACCCGTG 50
 AGCACATCCT GCTGGGCCGT CAGGTTGGCG TTCCTTACAT CATCGTGTTT 100
 40 CTGAACAAGT GTGACATGGT TGATGACGAA GAGCTGCTGG AACTGGTTGA 150
 GATGGAAGTT CGCGATCTGC TGTCTCAGTA CGACTTCCCA GGCGACGATA 200
 CCCCAATCGT ACGCGGTTCT GCGCTGAAAG CGCTGGAAGG CGACGCTGAG 250
 TGGGAAGCGA AAGTCGTTGA GCTGGCTGGT CACCTGGATA CTTACATTCC 300
 AGATCCAGTA CGTGCTATCG ATCTGCCGTT CCTGCTGCCA ATCGAAGACG 350
 45 TATTCTCAAT CTCTGGCCGT GGTACCGTTG TTACCGGTCG TGTGAGCGC 400
 GGCATCGTGA AAGTGGGCGA CGAAGTAGAA ATCGTTGGTA TCAAAGCGAC 450
 TGCCAAGTCT ACCTGTACCG GTGTTGAAAT GTTCCGCAA CTGCTGGACC 500
 AGGGTCAGGC AGGCGAGAAC TGTGGTGTTT TGCTGCGCGG TATCAAGCGT 550
 GAAGAGATCC AGCGTGGTCA GGTTCTGGCT AAGCCAGGCA CCATCAAGCC 600
 50 ACACACCAAG TTCGTATCAG AAGTGTACGT ACTGTCTAAA GACGAAGGCG 650
 GCCGTCATAC TCCGTTCTTC AAAGGCTACC GTCCACAGTT CTACTTCCGT 700
 ACYACTGATG TGACCGGCAM CATMGAACG CCAGAAGGCG TTGAGATGGT 750
 AATGCCAGGC GACAACATCA AAATGRCCGT TGAGCTGATC CACCCAATCG 800
 CGATGGACCA GGGTCTGCGT TTCGC 825

55

2) INFORMATION FOR SEQ ID NO: 136

(i) SEQUENCE CHARACTERISTICS:

60

(A) LENGTH: 762 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pasteurella multocida*
 (B) STRAIN: NCTC 10322

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136

15	CACAAACACG	TGAGCACATC	CTTTTAGGTC	GCCAAGTAGG	CGTTCCTTAC	50
	ATCATCGTAT	TCTTAAACAA	ATGCGACATG	GTGGATGATG	AAGAATTATT	100
	AGAATTAGTT	GAAATGGAAG	TGCGTGAAC	TCTTTCTCAA	TATGATTTC	150
	CAGGTGATGA	TACACCAATC	GTACGTGGTT	CAGCGTTACA	AGCGTTAAAC	200
	GGYGTAGCTG	AGTGGGAAGA	GAAAATTCTT	GAGTTAGCCA	ACCACTTAGA	250
	TACTTACATT	CCAGAGCCAC	AACGTGCAAT	CGACCAACCG	TTCCTTCTTC	300
20	CGATTGAAGA	CGTGTCTCTCA	ATTTCTGGTC	GTGGTACAGT	AGTAACAGGT	350
	CGTGTGAGC	GTGGTATCAT	CCGTACAGGT	GAAGAGGTTG	AAATTGTTGG	400
	TATTAAAGCG	ACAACGAAGA	CCACAGTAAC	AGGTGTTGAG	ATGTTCCGTA	450
	AATTATTAGA	CGAAGGTCGT	GCGGGTGAGA	ACGTTGGTGC	TTTATTACGT	500
	GGTACTAARC	GTGAAGAAAT	CGAACGTGGT	CAAGTGTTAG	CGAAACCGGG	550
25	TTCAATYACG	CCACACACTG	ATTTTGAATC	AGAAGTTTAC	GTGTTATCAA	600
	AAGAAGAAGG	TGGTCGTCAT	ACACCATTCT	TCAAAGGTTA	CCGTCCACAG	650
	TTCTACTTCC	GTACAACGGA	CGTAACAGGT	ACAATCGAAT	TACCGGAAGG	700
	TGTTGAGATG	GTGATGCCTG	GTGATAACAT	CAAGATGACT	GTAAGTTTGA	750
30	TTCACCCAAT	CG				762

2) INFORMATION FOR SEQ ID NO: 137

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Peptostreptococcus anaerobius*
 (B) STRAIN: ATCC 27337

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137

50	TGGAGCTATC	TTAGTTGTAT	CAGCAGCGGA	TGGACCAATG	CCACAAACAA	50
	GAGAACACAT	CTTATTATCA	AGACAAGTAG	GAGTACCATA	TATCGTAGTA	100
	TATTTGAATA	AAGCAGATAT	GGTAGAAGAT	GAAGAATTAT	TAGAATTAGT	150
	AGAAATGGAA	GTAAGAGAAT	TACTATCTGA	ATATGGATTC	CCAGGAGATG	200
	AAATTCCAAT	CATAACAGGA	TCATCCTTAG	GAGCATTAAA	TGGAGAACAA	250
	AAATGGATAG	ATCAAATCAT	GGCATTGATG	AAAGCCGTAG	ATGAATATAT	300
55	TCCAACACCG	GAAAGAGCAG	TAGATCAACC	ATTCTTGATG	CCAATCGAAG	350
	ACGTATTTAC	AATTACAGGA	AGAGGAAGT	TAGTAACAGG	AAGAGTTGAA	400
	AGAGGAGTTG	TAAAAGTWGG	AGAAGAAGT	GAAATCGTAG	GAATCAAAGC	450
	GACAACAAAG	ACAACCTGTA	CYGGAGTAGA	AATGTTCCGA	AAATTATTGG	500
	ATCAAGGACA	AGCAGGAGAT	AACATCGGAG	CTTTATTTRAG	AGGAACCAAG	550
60	AAAGAAGATG	TAGAAAGAGG	ACAAGTATTG	GCAAAACCAG	GAACAATTCA	600

TCCTCATACA AACTTCAGTG GAGAAGTATA TGTATTGACA AAAGAAGAAG 650
 GAGGAAGACA TACTCCATT TTCTCAGGAT ACAGACCACA ATTTTACTTT 700
 AGAACCACAG ATATTACAGG AGCAGTAACA TTACCAGAAG GAGTAGAAAT 750
 GGTAATGCCR GGAGATAATA TCACAATGAC AGTAGAATTG ATTCACCCAA 800
 5 TTGCAATGGA AACAGGATTA CGATTGCAA TT 832

2) INFORMATION FOR SEQ ID NO: 138

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 15 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 20 (A) ORGANISM: *Peptostreptococcus asaccharolyticus*
 (B) STRAIN: LSPQ 2639

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138

25 TAGTATGTTC AGCAGCAGAY GGTCCAATGC CACAAACAAG AGAACACATT 50
 CTACTAGCAA GACAAGTTGG TGTACCAAAG ATAGTAGTAT TCCTAAACAA 100
 AGAAGACCAA GTAGACGATC CAGAACTAAT TGAATTAGTA GAGATGGAAA 150
 TCAGAGACCT ACTATCAGAA TATGACTTCG AYGGAGACAA CACACCAATC 200
 GTAGTAGGAT CAGCATTAAG AGCCCTAGAC GATCCAGACG GAGAATGGGG 250
 30 AGACAAAATC GTAAACTAA TGGAAGMAGT AGACGAATAC ATCCCAACAC 300
 CAGTAAGAGA TACAGAACAC CCATTCTTAA TGCCAATCGA AGACRTATTC 350
 TCAATYACAG GAAGAGGAAC AGTAGCAACA GGAAGAGTAG AACAAAGGTGT 400
 AGTAAAAGTA GGMGACACAG TAGAACTAGT AGGCTTAACA GACGAAAGCA 450
 GACAAGTAGT AGTAACAGGT GTAGAAATGT TTAGAAAACA ACTAGACCTA 500
 35 GCAGAAGCMG GAGACAACAT TGGAGCCCTA CTAAGAGGAG TACAAAGAGA 550
 AGAAATCCAA AGAGGACAAG TACTAGCAGC ACCAGGAACA ATCAAACCAC 600
 ACACAAAATT TGAAGCAGAA GTATACGTAC TAACAAAAGA AGAAGGTGGA 650
 AGACACACAC CATTCTTTAA CGGATACAGA CCACAATTCT ACTTCAGAAC 700
 AACAGACGTA ACAGGAGACA TCCAAC TAGC AGACGGAGTA GAAATGGTAA 750
 40 TGCCAGGAGA CAACTCAACA TTTACAGTAA CACTAATCAC ACCAATCGCA 800
 ATGGACGAAG GACTAAGATT CGC 823

45 2) INFORMATION FOR SEQ ID NO: 139

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 55 (A) ORGANISM: *Peptostreptococcus prevotii*
 (B) STRAIN: ATCC 9321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139

60

CTATCATCGT AGTATCTGCA GCAGACGGTC CAATGCCCAA ACAGAGAGAA 50
 CACATCCTAC TAGCAAGACA AGTAGGCGTT CCAAAAATCG CAGTATTCCT 100
 AAACAAAGAA GACCAAGTAG ACGATCCAGA ACTAATCGAA TTAGTAGAAA 150
 TGGAAATCAG AGACCTACTT TCAGAATACG ACTTCGATGG AGACAACGCT 200
 5 CCAGTAGTAG TAGGATCTGC TCTTAAATCA CTAGAAGAAG GCGGAGAAGG 250
 CCCATGGTCA GACAAAATCC TTGACCTAAT GGCACAAAGTA GACGAATACT 300
 TCGACATCCC AGAAAGAGAC AACGACCAAC CATTCTAAT GCCAGTAGAA 350
 GACGTAATGA CAATCTCAGG ACGTGGAAAC GTAGCAACAG GAAGAGTTGA 400
 AAGAGGAACA CTAAAAGTTG GTGATACAGT AGAAATCGTA GGAATAACAG 450
 10 AAGATACAAA AGAAACAGTA GTAACCTGGAG TAGAAATGTT CCACAAATCM 500
 CTAGACCAAG CAGAATCTGG AGATAACGTA GGAATACTAC TAAGAGGAGT 550
 AACAAAGAGAT CAAATCTCAA GAGGACAAAGT ACTAGCAAAA CCAGGWTCTAG 600
 TAAACCCACA CACAGAATTC GAAGGTCAAG TATACGTAAT AACAAAAGAA 650
 GAAGGTGGAC GTCACACACC ATTCTTCAGT GGATATAGAC CACAATTCTT 700
 15 CTTTAGAACA ACAGACGTAA CAGGAGACAT CGAACTAGAA GAAGGCGTAG 750
 AAATGGTAAT GCCAGGAGAC AACGCAACAT TCAAAATCAC ACTCCAAAAA 800
 CCAATCGCTC TAGAAGAAGG ACTAAGATTC GC 832

20

2) INFORMATION FOR SEQ ID NO: 140

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Porphyromonas asaccharolytica*
 (B) STRAIN: ATCC 25260

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140

CGGTGCTATC ATCGTAGTTG CTGCAACTGA TGGTCCTATG CCTCAGACGC 50
 GTGAGCACAT CCTACTAGCA CGTCAGGTCA ACGTACCTCG TCTAGTTGTC 100
 TTTATGAACA AGTGCGACCT TGTGATGAC GAGGAGATGC TCGAGCTCGT 150
 40 AGATATGGAT ATGCGTGAGC TACTAAGCTT CTATGACTTT GACGGCGACA 200
 AACTCCTGT CATCCGTGGT TCTGCTCTTG GTGCTCTCAA TGGTGAGCCT 250
 AAGTGGGTAG AGAAGGTTAT GGAGCTCATG GAGGCTGTAG AACTTTGGAT 300
 CCCACTACCT GAGCGCGACA TCGACAAGCC TTTCCCTAATG CCTGTAGAGG 350
 ACGTATTCCTC TATCACAGGT CGTGCTACTG TCGCTACTGG TCGTATCGAG 400
 45 ACTGGTGTCG TTAAGGTCAA CGATGAGGTT CAGATCATCG GTCTAGGTGC 450
 TGAGGGTAAG AAGAGCGTCG TAACTGGCGT GGAAATGTTT CGCAAGATCC 500
 TTGATGAGGG TGAAGCTGGT GATAACGTAG GTCTCCTACT CCGTGGTATC 550
 GACAAGGACG AGATCAAGCG CGGTATGGTC CTAGCACACC CAGGTCAGGT 600
 CAAGCCTCAC GATCACTTCA AGGCTGAGGT CTATATCCTG AAGAAGGAAG 650
 50 AGGGTGGTCG TCACACACCA TTCCACAACA AGTACCGTCC TCAGTTCTAC 700
 ATCCGTACGC TAGACGTAAC GGGCGAGATC ACACTCCCAG AGGGTGTAGA 750
 GATGGTTATG CCTGGTGATA ACGTCACCAT CGATGTCAAG CTCATCTCTC 800
 CAGTAGCTTG TAGCGTAGGT CTACGCTTCG C 831

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2) INFORMATION FOR SEQ ID NO: 141

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 818 bases

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*
(B) STRAIN: ATCC 33277

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141

	CGGTGCTATA	ATCGTTGTAG	CAGCTACAGA	CGGTCCTATG	CCTCAGACTC	50
	GCGAGCACAT	CCTTTTGGCT	CGCCAGGTAA	ACGTTCCCTG	TCTGGTTGTT	100
15	TTCATGAACA	AATGTGACAT	GGTAGACGAT	GAAGAGATGC	TCGAGCTTGT	150
	TGAAATGGAC	ATGCGCGAAC	TCCTTTCTTT	CTACGATTTC	GATGGTGACA	200
	ATACCCCTAT	CATCCGTGGT	TCTGCTCTGG	GCGCTTTGAA	TGGAGAGCCT	250
	CAGTGGGAAG	ACAAGGTGAT	GGAGCTTATG	GAAGCTGTTG	ACAACTGGGT	300
	TCCCCTGCCT	GAGCGCGATA	TCGACAAACC	GTTCTTGATG	CCGGTTGAAG	350
20	ACGTGTTCTC	TATCACGGGT	CGTGGTACGG	TCGCTACAGG	ACGTATCGAA	400
	ACCGGTATTG	TGAAGACCGG	TGACGAAGTT	CAAATCATCG	GCCTCGGTGC	450
	AGAAGGAATG	AAGTCGGTTG	TTACGGGTGT	TGAAATGTTT	CGTAAGATTC	500
	TTGACGAAGG	TCAGGCTGGT	GACAACGTTG	GTCTCCTCCT	GCGTGGTATC	550
	GATAAGGATC	AGATCAAGCG	TGGTATGGTT	ATCTCTCACC	CGGGTAAGAT	600
25	TACTCCTCAC	AAGAGATTTA	AGGCCGAGGT	TTATATCTTG	AAGAAAGAAG	650
	AAGGTGGTCG	CCACACTCCT	TTCCACAACA	AATATCGTCC	GCAGTTCTAC	700
	ATCCGTACGC	TTGACGTGAC	CGGTGAAATC	ACTCTTCCCG	AAGGAACAGA	750
	AATGGTTATG	CCCGGTGACA	ACGTAACGAT	CACTGTAGAA	CTCATCTACC	800
30	CGGTTGCATG	TAATGTAG				818

2) INFORMATION FOR SEQ ID NO: 142

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 830 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pragia fontium*
(B) STRAIN: ATCC 49100

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142

	CGGCGCTATT	CTGGTTGTTG	CTGCAACTGA	TGGTCCTATG	CCTCAAATC	50
50	GTGAGCACAT	CCTGTTAGGY	CGCCAGGTTG	GCGTACCATA	CATCATTGTG	100
	TTCCCTGAACA	AGTGTGACAT	GGTTGAYGAT	GAAGAGCTGT	TAGAACTGGT	150
	TGAAATGGAA	GTTTCGTGAGC	TTCTGTCTCA	GTACGATTTC	CCAGGTGATG	200
	ATACTCCAGT	TGTTCTGTTG	TCTGCGCTGA	AAGCGTTTGA	AGGCGAAGCT	250
	GAGTGGGAAG	CTAAATCAT	TGAATTGGCT	GACTCCCTGG	AYAGCTACAT	300
55	TCCACAGCCA	GAGCGTGCAA	TTGATAAGCC	GTTCTGCTG	CCAATCGAAG	350
	ACGTTTTCTC	AATCTCTGGC	CGTGGTACAG	TAGTAACCGG	TCGTGTAGAG	400
	CGCGGTATCG	TTAAAGTTGG	TGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	TACTGTGAAA	ACAACTTGTA	CTGGCGTTGA	AATGTTCCGT	AARTTACTGG	500
	ATGAAGGCCG	TGCGGGTGAG	AACGTTGGTG	TTCTGCTGCC	TGGTACTAAG	550
60	CGTGATGAAA	TCGAACGTGG	TCAAGTATTA	GCAAAACCAG	GTTCAATCAA	600

CCCGCATACT AACTTCGTAT CAGAAGTTTA TATCCTGAGC AAAGATGAAG 650
 GTGGTCGTCA TACTCCATTC TTCAAAGGCT ACCGTCCACA GTTYTACTTC 700
 CGTACAAC TG ACGTGACCGG TACCATCGAA CTGCCAGAAG GCGTAGAGAT 750
 5 GGTAATGCCA GGTGATAACA TTCAGATGAC TGTAACCTCTG ATTGCCCCAA 800
 TCGCGATGGA CGAAGGTTTA CGCTTCGCTA 830

2) INFORMATION FOR SEQ ID NO: 143

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 821 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Prevotella melaninogenica*
 (B) STRAIN: ATCC 25845

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143

25 TGGTGCTATC TTGGTTGTAG CTGCTACTGA TGGTCCTATG CCTCAGACTC 50
 GTGAGCACGT ATTGCTCGCT CGTCAGGTAA ACGTACCTCG CTTGGTTGTA 100
 TTCTTGAACA AGTGTGATAT GGTTGACGAT GCTGAGATGC TTGACCTCGT 150
 TGAGATGGAG GTTCGTGAGA TCCTCGAGCA GTACGGTTAT GAGGAGGATA 200
 CTCCTATTAT TCGTGGTTCT GCACTCGGTG CTTTGAACGG TGTTGAGAAG 250
 30 TGGGTAGACT CTGTAATGGA GCTCATGGAT ACTGTTGACA CTTGGATTGA 300
 AGAGCCAGAG CGTGAGATTG ACAAGCCATT CTTGATGCCT GTTGAGGACG 350
 TATTCTCTAT CACAGGTCGT GGTACTGTAG CTACTGGTCG TATCGAGACT 400
 GGTATCTGTA AGGTAGGTGA TGAGGTTTCAG TTGCTCGGTC TCGGTGAGGA 450
 CAAGAAGTCT GTTATCACTG GTGTTGAGAT GTTCCGTAAG AACCTTCCAA 500
 35 CAGGTCAGGC TGGTGACAAC GTAGGTCTCC TCCTTCGTGG TATCGATAAG 550
 GCTGAGGTTA AGCGTGGTAT GGTTGTTGTG CACCCAGGTG CTATTACTCC 600
 TCACGATCAC TTCAAGGCAT CTATCTATGT ATTGAAGAAG GAAGAGGGTG 650
 GTCGTCATAC TCCATTCGGT AACAAGTATC GTCCACAGTT CTACCTCCGT 700
 40 ACAATGGACT GTACAGGTGA AATCCACCTC CCAGAGGGCG TTGAGATGGT 750
 TATGCCAGGT GACAACGTAG AGATTGAAGT TGTATTGATC TATAAGGTTG 800
 CTTTGAACGA GGGTCTTCGT T 821

2) INFORMATION FOR SEQ ID NO: 144

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Prevotella oralis*
 (B) STRAIN: ATCC 33269

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144

5 TGGTGCTATT CTTGTAGTAG CTGCTACTGA CGGTCCTATG CCTCAAACCTC 50
 GTGAACACGT GCTTCTTGCT CGTCAGGTGA ACGTACCTCG TTTGGTCGTT 100
 TTCTTGAACA AGTGCGATAT GGTGACGAT GAAGAAATGC TTGAGCTCGT 150
 AGAAATGGAG CTTCATGAAC TTCTCGAGCA GTATGAATAT GAGGAGGATA 200
 CTCCTATTGT TCGTGGTTCG GCACTTGGCG CTCTGAATGG AGTAGAGAAG 250
 TGGGTTGACA GCGTGATGAA GTTGATGGAT ACCGTTGATG AATGGATACA 300
 GGAACCACCG CGTGATCTTG ATAAGCCTTT CTTGATGCCG GTAGAGGATG 350
 TATTTTCTAT TACTGGTCGT GGAACGGTTG TTACAGGCCG TATTGAAACT 400
 GGTAAAGGTTA AGGTGGGCGA TGAAGTTCAA CTTCTTGGTC TCGGTGAAGA 450
 10 TAAGAAGTCC GTTGTGACAG GCGTTGAGAT GTTCCGTAAG ATTCTTGACG 500
 AAGGTGAAGC TGGTGATAAT GTAGGCTTGC TGCTTCGTGG TATCGATAAG 550
 ACGGAAGTAA AGCGTGGTAT GGTGTGCGTA CATCCGGGGG CTATTACTCC 600
 TCACGATCAT TTCAAGGCTT CAGTTTACGT ATTGAAGAAA GAAGAAGGCG 650
 GTCGCCATAC TCCGTTTGGT AMCAAGTATC GTCCACAGTT CTATCTTCGT 700
 15 ACCATGGACT GTACTGGTGA AATTACTCTT CCGGAAGGAG TTGAGATGGT 750
 AATGCCGGGT GATAACGTCG AAATTGAAGT TAAGTTGATC TATCCGGTAG 800
 CTTTGAACGA GGGACTTCGT TTCGCTA 827

20 2) INFORMATION FOR SEQ ID NO: 145

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 833 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Propionibacterium acnes*
 (B) STRAIN: ATCC 6919

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145

CGGCGCCATC CTCGTGGTTG CTGCTACCGA CGGCCCGATG CCTCAGACTC 50
 GCGAGCACGT TCTGCTCGCT CGTCAGGTGG GCGTGCCCGC CATCGTCGTC 100
 GCCCTCAACA AGTGCGACAT GGTGACGAT GAGGAGCTCA TTGAGCTCGT 150
 40 CGAGATGGAG GTCCGCGAGC TGCTGACCTC GCAGGAGTTC GACGGCGACA 200
 ACTGCCCTGT CGTTCGCATC TCCGCCTTCC AGGCCCTCCA GGGTGATGAG 250
 AAGTGGACCC AGTCGATCCT CGACCTCATG GACGCCGTGG ACGAGTACAT 300
 CCCGCAGCCT GAGCGCGATC TCGACAAGCC CTTCTTATG CCGATCGAGG 350
 ACGTCTTCAC CATCACCGGC CGTGGCACC GGTGACCCG TCGTGTCGAG 400
 45 CGCGGCGTCG TCAAGACTGG CGAAGAGGTC GAGATCGTCG GTATCCACGA 450
 GAAGACCCAG AAGACCACCG TTACCGGTGT CGAGATGTTT CGCAAGATCC 500
 TCGACGAGGG CCGCGCTGGT GAGAACGTCG GCGTTCTGCT CCGTGGCACC 550
 AAGAAGGAGG ATGTCGTTTC CGGCATGGTC CTCTCCAAGC CTGGTTCCAC 600
 CACCCCCAC ACCGACTTCG AGGGCCAGGT CTACGTCCTC AAGAAGGATG 650
 50 AGGGTGGCCG CCACAAGCCG TTCTTCTCCC ACTACAGCCC CCAGTTCTAC 700
 TTCCGTACCA CGGACGTGAC TGGCACTGTT GAGCTCCCCG AGGGCACCAG 750
 GATGGTCATG CCTGGCGACA ACACCGACAT GACTGTGCAC CTGATTACAC 800
 CGGTTGCCAT GGAGGATCAG CTCAAGTTTC CTA 833

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2) INFORMATION FOR SEQ ID NO: 146

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 745 bases

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Proteus mirabilis*

(B) STRAIN: ATCC 35659

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146

	CACAAACTCG	TGAGCACATC	CTGTTAGGTC	GTCAGGTTGG	TGTTTCCTTAC	50
	ATCATCGTAT	TCCTGAACAA	ATGTGACATG	GATAGATGATG	AAGAGCTGTT	100
15	AGAATTAGTT	GAAATGGAAG	TTCGTGAACT	TCTGTCTCAA	TACGATTTC	150
	CAGGTGATGA	CACTCCAGTA	ATCCGTGGTT	CAGCGCTGAA	AGCACTGGAA	200
	GGCGAAGCAG	AGTGGGAAGC	AAAAATTGTT	GAATTAGCAG	AAGCACTGGA	250
	TTCTTATATC	CCAGAGCCAG	AGCGTGCAAT	TGACAAACCA	TTCCTGTTAC	300
	CAATCGAAGA	TGTATTCTCA	ATCTCAGGCC	GTGGTACAGT	AGTTACTGGT	350
20	CGTGTAGAGC	GTGGTATCAT	CAAAGTAGGT	GATGAAGTTG	AGATTGTTGG	400
	TATCAAAGAA	ACCGCCAAA	CAACTTGATC	TGGCGTTGAA	ATGTTCCGTA	450
	AATTACTTGA	CGAAGGTCGT	GCAGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	500
	GGTACAAAAC	GTGAAGAAAT	CGAACGTGGA	CAAGTACTGG	CRAAACCAGG	550
	CTCAATCAAC	CCACACAACA	AATTTGAATC	AGAAGTTTAT	ATTCTGAGCA	600
25	AAGATGAAGG	TGGTCGTCAC	ACTCCATTCT	TCAAAGGCTA	CCGTCCACAG	650
	TTCTACTTCC	GTACAACTGA	CGTAACTGGT	ACTATCGAAT	TACCAGAAGG	700
	CGTAGAAATG	GTAATGCCAG	GCGACAACGT	GAACATGATC	GTTGA	745

30

2) INFORMATION FOR SEQ ID NO: 147

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 829 bases

35 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Proteus penneri*

(B) STRAIN: ATCC 33519

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147

	GGAGCTATCC	TGGTTGTTGC	TGCGACAGAT	GGCCCAATGC	CACAAACTCG	50
	TGAGCACATC	CTGTTAGGTC	GTCAGGTTGG	TGTTTCCTTAC	ATCATCGTAT	100
	TCCTGAACAA	ATGTGACATG	GATAGATGATG	AAGAGTTACT	GGAATTAGTM	150
50	GAAATGGAAG	TTCGTGAACT	TCTGTCTCAG	TACGATTTC	CAGGTGATGA	200
	CACTCCAGTA	ATCCGTGGTT	CAGCGCTGAA	AGCACTGGAA	GGCGAAGCAG	250
	AGTGGGAAGC	AAAAATTGTT	GAATTAGCAG	AAGCACTGGA	TTCATACATC	300
	CCAGARCCAG	AGCGTGCAAT	TGACAAACCA	TTCCTGTTAC	CAATTGAAGA	350
	CGTATTCTCA	ATTTTCAGGCC	GTGGTACAGT	AGTAACAGGT	CGTGTGAGC	400
55	GTGGCGTAAT	CAAAGTTGGT	GAAGAAGTTG	AAATCGTTGG	TATTAAACCA	450
	ACAGCGAAAA	CAACTTGATC	TGGCGTTGAA	ATGTTCCGTA	AATTACTTGA	500
	CGAAGGTCGT	GCAGGTGAGA	ACGTAGGTGT	TCTTCTGCGT	GGTACTAAAC	550
	GTGAAGAAAT	CGAACGTGGA	CAAGTACTGG	CGAAACCAGG	TTCAATCAAC	600
	CCACACACTA	AATTTGAATC	AGAAGTTTAT	ATTCTGAGCA	AAGATGAAGG	650
60	TGGTCGTCAT	ACTCCATTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700

GTACAACTGA CGTAACTGGT ACTATCGAAT TACCAGAAGG CGTAGAAATG 750
 GTAATGCCAG GTGACAACAT CAACATGATC GTTGAAGTGA TTCACCCAAT 800
 CGCGATGGAC GACGGTTTAC GTTTCGCTA 829

5

2) INFORMATION FOR SEQ ID NO: 148

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Proteus vulgaris*
 (B) STRAIN: ATCC 13315

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148

CGGAGCTATT CTGGTTGTTG CTGCGACTGA TGGCCCAATG CCACAACTC 50
 GTGAGCACAT CCTGTTAGGT CGCCAGGTTG GTGTACCTTA CATCATCGTA 100
 25 TTCCTGAACA AATGTGACAT GGTTGATGAT GAAGAACTGC TGGGAATTAGT 150
 AGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGATTTC CCAGGTGATG 200
 ACACTCCAGT AATCCGTGGT TCAGCGCTGA AAGCACTGGA AGGCGAAGCT 250
 GAGTGGGAAG CAAAAATTGT TGAATTAGCA GAAGCACTGG ATTCTTACAT 300
 CCCAGAACCA GAGCGTGCAA TTGACAAACC ATTCCTGCTG CCTATCGAAG 350
 30 ACGTATTCTC AATCTCTGGT CGTGGTACAG TAGTAACAGG CCGTGTAGAG 400
 CGTGGTGTTG TTAAAGTTGG TGAAGAAGTT GAGATTGTTG GTATTAAAGA 450
 CACAGTTAAA ACAACTTGTA CTGGCGTTGA AATGTTCCGT AAATTACTTG 500
 ACGAAGGTCG TGCAGGTGAG AACGTAGGTG TTCTTCTGCG TGGTACTAAA 550
 CGTGAAGAAA TCGAACGTGG ACAAGTACTG GCTAAACCAG GTTCAATCAA 600
 35 GCCACACACT AAATTCGAAT CAGAAGTTTA TATCCTGAGC AAAGATGAAG 650
 GTGGTCGTCA CACTCCATTC TTCAAAGGTT ACCGTCCACA GTTCTACTTC 700
 CGTACAACCTG ACGTAACTGG TACTATCGAA TTACCAGAAG GCGTAGAAAT 750
 GGTAAATGCCA GGTGACAACA TCAACATGAT CGTTGAAGT ATTACCCCTA 800
 TCGCGTAGGA CGACGGTTTA CGTT 824

40

2) INFORMATION FOR SEQ ID NO: 149

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 745 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: *Providencia alcalifaciens*
 (B) STRAIN: ATCC 9886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149

60 CACAACTCG TGAGCACATC CTGTTAGGTC GCCAAGTAGG TGTTCCCTTAC 50
 ATCATCGTTT TCCTGAACAA ATGTGACATG GTAGACGACG AAGAACTGTT 100

	AGAATTAGTT	GAAATGGAAG	TTCGTGAACT	TCTGTCTCAG	TACGATTTCC	150
	CAGGCGATGA	CACTCCAGTT	GTTGCGGGTT	CAGCACTGAA	AGCGCTGGAA	200
	GGCAACCCAG	AGTGGGAAGC	AAAAATTGTT	GAATTAGCAG	GTTACCTGGA	250
5	TTCTTACATC	CCAGAACCAG	AGCGTGCAAT	TGACAAGCCA	TTCCTGCTGC	300
	CAATCGAAGA	CGTATTCTCA	ATCTCTGGTC	GTGGTACAGT	AGTAACAGGC	350
	CGTGTTGAGC	GTGGTATCAT	CAAAGTTGGT	GAAGAAGTTG	AAATCGTTGG	400
	TATTCAAGCG	ACTGCGAAAA	CAACTTGTAC	TGGCGTTGAA	ATGTTCCGTA	450
	AACTGCTGGA	TGAAGGTCGT	GCGGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	500
	GGTACTAAAC	GTGAAGAAAT	TCAACGTGGT	CAAGTACTGG	CTAAACCAGG	550
10	TTCAATCAAG	CCACACACTC	AATTGCAATC	AGAAGTATAT	ATTCTGAGCA	600
	AAGATGAAGG	TGGTCGTTCAT	ACTCCATTCT	TCAAAGGCTA	CCGTCCACAG	650
	TTCTACTTCC	GTACAACTGA	CGTAACCGGT	ACTATCGAAC	TGCCAGAAGG	700
	CGTAGAGATG	GTAATGCCAG	GCGACAACAT	CAACATGATC	GTGAC	745

15

2) INFORMATION FOR SEQ ID NO: 150

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Providencia rettgeri*
 (B) STRAIN: ATCC 9250

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150

	CGGTGCAATC	CTGGTTGTTG	CTGCGACTGA	TGGCCCAATG	CCACAAACTC	50
	GTGAGCACAT	CCTGTTAGGY	CGCCAAGTAG	GTGTWCCTTA	CATCATCGTT	100
35	TTCCTGAACA	AATGTGACAT	GGTAGACGAC	GAAGAACTGT	TAGAATTAGT	150
	TGAAATGGAA	GTTCGTGAAC	TTCTGTCTCA	ATACGATTTC	CCAGGCGACG	200
	ACACTCCAGT	TGTCCGTGGT	TCAGCTCTGA	AAGCGCTGGA	AGGCAACCCA	250
	GAGTGGAAG	CGAAAATTGT	TGAATTAGCA	GGTCACTTGG	ATTCTTACAT	300
	CCCAGAACCA	GAGCGTGCAA	TTGACAAACC	ATTCTGCTG	CCAATCGAAG	350
40	ACGTATTCTC	AATCTCTGGT	CGTGGTACAG	TAGTAACAGG	CCGTGTTGAG	400
	CGTGGTATCA	TCAAAGTTGG	TGAAGAAGTT	GAAATCGTTG	GTATCCAAGA	450
	CACGGTTAAA	ACAACTTGTA	CTGGCGTTGA	AATGTTCCGT	AAACTGCTGG	500
	ACGAAGGTCG	TGCGGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTACTAAA	550
	CGTGAAGAAA	TTCAACGTGG	TCAAGTACTG	GCAAAACCAG	GTTCAATCAA	600
45	GCCACACACT	AAATTCGAAT	CAGAAGTCTA	TATTCTGAGC	AAAGATGAAG	650
	GTGGTCGTCA	CACTCCATTTC	TTCAAAGGTT	ACCGTCCACA	GTTCTACTTC	700
	CGTACAACCTG	ACGTAACAGG	TACTATCGAA	CTGCCAGAAG	GCGTAGAGAT	750
	GGTAATGCCA	GGTGATAACA	TCAACATGAT	CGTTACCCTG	ATCCACCCAA	800
50	TCGCGATGGA	CGACGGTTTA	CGTTTCGCAA			830

2) INFORMATION FOR SEQ ID NO: 151

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Providencia rustigianii*
(B) STRAIN: ATCC 33673

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151

	CGGTGCAATC	CTGGTTGTTG	CTGCGACTGA	TGGCCCAATG	CCACAAACTC	50
	GTGAGCACAT	CCTGTTAGGT	CGCCAAGTAG	GTGTTTCCTTA	CATCATCGTT	100
10	TTCCTGAACA	AATGTGACAT	GGTTGACGAC	GAAGAACTGT	TAGAATTAGT	150
	TGAAATGGAA	GTTTCGTGAAC	TTCTGTCTCA	GTACGATTTC	CCAGGCGACG	200
	AACTCCAGT	TGTTTCGYGGT	TCAGCACTGA	AAGCGCTGGA	AGGTATCCCT	250
	GAGTGGGAAG	CGAAAATTGT	TGAATTAGCC	GGTTACCTGG	ACAGCTACAT	300
15	CCCAGAACCA	GAGCGCGCAA	TTGACCGTCC	ATTCCTGCTG	CCAATCGAAG	350
	ACGTATTCTC	AATCTCTGGT	CGTGGTACAG	TAGTAACAGG	SCGTGTTGAG	400
	CGTGGTATCG	TTAAAGTTGG	TGAAGAAGTT	GAAATCGTTG	GTATCCAAGA	450
	CACRGTTAAA	ACAACCTTGTA	CTGGCGTTGA	AATGTTCCGT	AAACTGCTTG	500
	ACGAAGGTCG	TGCTGGTGAG	AACGTTGGTG	TTTTACTGCG	TGGTACTAAG	550
20	CGTGAAGAAA	TTCAACGTGG	TCAAGTACTG	GCTAAACCAG	GTTCAATCAA	600
	GCCACACACT	ACTTTTGAAT	CAGAAGTTTA	TATTCTGAGC	AAAGATGAAG	650
	GTGGTCGTCA	TACTCCATTG	TTCAAAGGCT	ACCGTCCACA	GTTCTACTTC	700
	CGTACAACCTG	ACGTAACCGG	TACTATCGAA	CTGCCAGAAG	GCGTAGAGAT	750
	GGTAATGCCA	GGCGACAACA	TCAACATGAT	CGTGACACTG	ATTCACCCAA	800
25	TCGCGATGGA	TGATGGTTTA	CGTTTC			826

2) INFORMATION FOR SEQ ID NO: 152

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 830 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Providencia stuartii*
(B) STRAIN: ATCC 33672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152

45	CGGTGCAATC	CTAGTTGTTG	CGGCAACAGA	TGGCCCAATG	CCACAAACTC	50
	GTGAGCACAT	CCTGTTAGGT	CGTCAGGTTG	GCGTTCCTTA	CATCATCGTG	100
	TTCCTGAACA	AATGTGACAT	GGTAGACGAC	GAAGAGCTGC	TGGAAGTGGT	150
	TGAAATGGAA	GTTTCGTGAAC	TTCTGTCTCA	ATACGATTTC	CCAGGTGATG	200
	AACTCCAGT	TATCCGTGGT	TCAGCGCTGA	AAGCGTTGGA	AGGCAACCCA	250
50	GAGTGGGAAG	CGAAAATCGT	TGAAGTAGCA	GAAGCACTGG	ACAGCTACAT	300
	CCCAGAGCCA	GAGCGTGCAA	TTGACAAGCC	ATTCCTGCTG	CCAATCGAAG	350
	ACGTATTCTC	AATCTCAGGT	CGTGGTACAG	TAGTCACAGG	CCGTGTTGAG	400
	CGTGGTATCA	TCAAAGTTGG	TGAAGAAGTT	GAAATCGTAG	GTATCAAAGA	450
	GACTGCGAAA	ACCACTTGTA	CTGGCGTTGA	AATGTTCCGT	AAACTGCTGG	500
55	ACGAAGGCCG	TGCGGGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTACTAAG	550
	CGTGAAGAAA	TGCAACGTGG	TCAAGTTCTG	GCGAAACCAG	GTTCAATCAA	600
	GCCACACACA	ACTTTTGAAT	CAGAAGTTTA	TATTCTGAGC	AAAGATGAAG	650
	GTGGTCGTCA	CACGCCATTG	TTCAAAGGYT	ACCGTCCACA	GTTCTACTTC	700
	CGTACAACCTG	ACGTAACAGG	TACTATCGAA	CTGCCAGAAG	GCGTAGAGAT	750
60	GGTAATGCCA	GGCGACAACG	TGAACATGAA	AGTAACTCTG	ATTCACCCAA	800

TCGCGATGGA CGATGGTTTG CGTTTCGCAA

830

5 2) INFORMATION FOR SEQ ID NO: 153

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas aeruginosa*
 (B) STRAIN: ATCC 35554

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153

20 CCTGGTTTGC TCGGCTGCCG ACGGCCCAT GCCGAGACC CGCGAGCACA 50
 TCCTGCTGTC CCGCCAGGTA GCGTTCCTT ACATCGTCGT GTTCCTGAAC 100
 AAAGCCGACA TGGTCGACGA CGCCGAGCTG CTGGAACTGG TCGAGATGGA 150
 25 AGTTCGCGAT CTGCTGAACA CCTACGACTT CCCGGGCGAC GACACTCCGA 200
 TCATCATCGG TTCCGCGCTG ATGGCGCTGG AAGGCAAGGA TGACAACGGC 250
 ATCGGCGTAA GCGCCGTGCA GAAGCTGGTA GAGACCCTGG ACTCCTACAT 300
 TCCGGAGCCG GTTCGTGCCA TCGACCAGCC GTTCCTCATG CCGATCGAAG 350
 ACGTGTCTC GATCTCCGGT CGCGGTACCG TGGTAACCGG TCGTGTAGAG 400
 CGCGGCATCA TCAAGGTCCA CCGGCGTTGA AATGTTCCGC AAGCTGCTCG 450
 30 GACCACCAAG ACCACCTGCA CCGGCGTTGA AATGTTCCGC AAGCTGCTCG 500
 ACGAAGGTCG TGCTGGTGAG AACGTTGGTA TCCTGCTGCG TGGCACCAAG 550
 CGTGAAGACG TAGAGCGTGG CCAGGTACTG GCCAAGCCGG GCACCATCAA 600
 GCCGCACACC AAGTTCGAGT GCGAAGTGTA CGTGCTGTCC AAGGAAGAAG 650
 GTGGTCGTCA CACCCCGTTC TTCAAGGGCT ACCGTCCGCA GTTCTACTTC 700
 35 CGTACCACKG ACGTGACCGG TAMCTGCGAG CTGCCGGAAG GCGTAGAGAT 750
 GGTAATGCCG GCGGACAACA TCAAGATGGT TGTACCCTG ATCGCTCCGA 800
 TCGCCATGGA AGATGGCTGC GTTCGCG 827

40 2) INFORMATION FOR SEQ ID NO: 154

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 841 bases
 45 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas fluorescens*
 (B) STRAIN: ATCC 13525

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154

55 CGGCGCAATC CTGGTTTGCT CGGCCGCTGA TGGTCCGATG CCACAAACCC 50
 GTGAACACAT CCTGCTGTCC CGTCAGGTTG GCGTTCGTA CATCGTGGTT 100
 TACCTGAACA AGGCTGACCT GGTAGACGAC GCTGAGCTGC TGGAAGTGGT 150
 60 TGAGATGGAA GTGCGCGATC TGCTGAGCAC TTACGACTTC CCAGGCGACG 200

5 ACACTCCGAT CATCATCGGT TCTGCTCGTA TGGCTCTGGA AGGCAAAGAC 250
 GACAACGAAA TGGGCACCAC GTCCGTTCGT AAACCTCTGGA 300
 CAGCTACATC CCAGATCCAG TTCGTGTTAT CGACAAGCCG TTCCTGATGC 350
 CAATCGAAGA CGTGTTCTCG ATCTCCGGTC GCGGTACTGT TGTGACTGGT 400
 CGTATCGAGC GCGGTATCGT TAAGGTTCAA GATCCACTGG AAATCGTTGG 450
 TCTGCGTGAC ACTACCGTCA CCACCTGCAC CCGTGTTGAA ATGTTCCGTA 500
 AGCTGCTCGA CGAAGGTCGT GCTGGCGAGA ACTGCGGCGT TCTGCTGCGT 550
 GGTACCAAGC GTGACGACGT TGAGCGTGCG CAGGTTCTGG TTAAGCCAGG 600
 TTCGGTTAAG CCGCACACCA AGTTCGAAGC TGAAGTCTAC GTACTGAGCA 650
 10 AAGAAGAAGG CGGTCGTCAC ACTCCGTTCT TCAAAGGCTA CCGTCCACAG 700
 TTCTACTTCC GTACTACTGA CGTGACTGGT AACTGCGAGC TGCCGGAAGG 750
 CGTTGAAATG GTTATGCCAG GCGACAACAT CAAATGGTT GTTACCCTGA 800
 TCAAAACCAT CGCAATGGAA GACGGTCTGC GTTTCGCTAT T 841

15 2) INFORMATION FOR SEQ ID NO: 155

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 841 bases
 20 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

 (ii) MOLECULE TYPE: Genomic DNA

 25 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Pseudomonas stutzeri*
 (B) STRAIN: ATCC 17588

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155

CGGCGCGATC CTGGTCTGCT CGGCTGCTGA CGGCCCCATG CCGCAGACTC 50
 GCGAGCACAT CCTGCTGTCC CGTCAGGTTG GTGTTCCGTA CATCGTCGTG 100
 TTCCTGAACA AGGCCGACAT GGTTGATGAC GCCGAGCTGC TCGAGCTGGT 150
 35 CGAGATGGAA GTTCGYGACC TGCTGTGCGAC CTACGACTTC CCGGGTGAYG 200
 ACACTCCGAT CATCATCGGC TCCGCGCTGA TGGCGCTGAA CGGCGAAGAC 250
 GACAACGAGC TCGGCACCAC TGCGGTGAAG AAGCTGGTCG AGACCCTGGA 300
 CAGCTACATT CCCGAGCCCG TTCGTGCCAT CGACAAGCCG TTCCTGATGC 350
 CGATCGAAGA CGTGTTCTCG ATCTCCGGTC GCGGCACSGT GGTAACCGGT 400
 40 CGCGTAGAGC GCGGCATCGT CAAGGTTTCA GAAGAGATCG AGATCGTCGG 450
 TCTGCGTCCG ACCACCAAGA CTACCTGCAC CCGCGTTGAG ATGTTCCGCA 500
 AGCTGCTCGA YGARGGTCGT GCTGGCGAGA ACTGCGGYGT GCTGCTGCGT 550
 GGCACCAAGC GTGACGAAGT GGAGCGTGTT CAGGTTCTGG CCAAGCCGGG 600
 CACCATCAAG CCGCACACCA AGTTCGAAGC CGAAGTGATC GTGCTGTCCA 650
 45 AGGAAGAAGG TGGTCGTCAC ACCCCGTTCT TYAAGGGCTA CCGTCCKCAG 700
 TTCTACTTCC GTACCACTGA YGTGACYGGW TCGTGCGARC TGCCGGAAGG 750
 CGTCGAGATG GTAATGCCGG GCGACAACGT GAAGATGGTT GTCACCCTGA 800
 TCAAGCCGAT CGCCATGGAA GACGGCCTGC GCTTCGCGAT T 841

50

2) INFORMATION FOR SEQ ID NO: 156

- (i) SEQUENCE CHARACTERISTICS:
 55 (A) LENGTH: 833 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

 60 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Psychrobacter phenylpyruvicus*
 (B) STRAIN: ATCC 23333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156

```

5      GCTATTCTAG TAGTATCAGC AACTGACGGT CCAATGCCAC AAACACGTGA      50
      GCACATTCTA TTATCACGTC AGGTTGGTGT ACCATACATC ATCGTATTCA      100
10     TGAACAAATG TGACATGGTA GATGACGAAG AGTTACTAGA GCTAGTAGAA      150
      ATGGAAGTGC GTGAATTACT TTCAGACTAC GACTTCCCAG GTGATGACAC      200
      TCCAATCATC AAAGGTTTCAG CTTTAGAAGC GTTAAATGGT AACGACGGTA      250
      AGTACGGTGA GCCAGCAGTT ATCGAACTAC TAAACACTCT AGACACTTAC      300
      ATTCCAGAGC CAGAGCGTGA CATCGATAAG CCATTCTCTAA TGCCAATCGA      350
15     AGACGTATTG TCAATCTCAG GTCGTGGTAC AGTAGTAACA GGCCGTGTTG      400
      AATCTGGTAT CATCAAAGTT GGTGACGAAA TCGAAATCGT TGGTATCAAA      450
      GACACAGTTA AAACAACTTG TACTGGTATC GAGATGTTCC GTAAGTTACT      500
      AGACGAAGGT CGTGCTGGTG AGAACTGTGG TGTACTATTA CGTGGTACTA      550
      AGCGTGAAGA CGTACAACGT GGTCAAGTAC TTGCTAAGCC AGGTTCAATC      600
20     ACTCCACACA CCAACTTCGA CGCAGAAGTA TACGTACTAT CAAAAGAAGA      650
      AGGTGGTCGT CACACTCCAT TCTTAAATGG TTACCGTCCA CAGTTCTACT      700
      TCCGTACTAC TGACGTAACA GGTGCAATCA CGTTACAAGA AGGTACTGAA      750
      ATGGTAATGC CAGGCGATAA CGTTGAGATG AGCGTAGAGC TAATCCACCC      800
25     AATCGCTAGG ACAAAGGTTT ACGTTTCGCA ATC                        833
  
```

2) INFORMATION FOR SEQ ID NO: 157

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Rahnella aquatilis*
 (B) STRAIN: ATCC 33071

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157

```

45     GGCGCTATCC TGGTTGTTGC TGCAACTGAC GGCCCTATGC CTCAGACTCG      50
      TGAGCACATC CTGCTGGGTC GCCAGGTTGG CGTTCCATAC ATGATCGTGT      100
      TCATGAACAA ATGCGACATG GTAGATGACG AAGAGCTGCT GGAAGTGGTA      150
      GAAATGGAAG TTCGCGAACT TCTGTCTGCT TACGAATTCC CAGGCGACGA      200
      CATCCCGGTC ATCAAAGGTT CAGCGCTGAA AGCACTGGAA GGCGATGCTA      250
      CTTGGGAAGC GAAAATCATC GAACTGGCAG AAGCACTGGA CAGCTACATT      300
50     CCATTGCCAG AGCGTGCTAT CGATAAGCCA TTCCTGCTGC CAATCGAAGA      350
      CGTATTCTCC ATCTCCGGTC GTGGTACAGT GGTTACCGGT CGTGTAGAGC      400
      GCGGTATCGT TAAAGTGGGC GAAGAAGTTG AAATCGTCGG TATCAAGGAC      450
      ACTGTTAAGT CTACTTGTA TGGCGTTGAA ATGTTCCGCA AACTGCTGGA      500
      CGAAGGCCGT GCGGGCGAGA ACGTGGGTGT TCTGCTGCGT GGTATCAAGC      550
55     GTGAAGACAT CGAACGTGGT CAGGTTCTGG CTAAACCAGG TTCAATCAAA      600
      CCACACACCA AGTTTGATTG CGAAGTGTA ATCCTGAGCA AAGATGAAGG      650
      TGGTCGTCAC ACTCCATTCT TCAAAGGCTA CCGTCCACAG TTCTACTTCC      700
      GTACAACTGA CGTGACCGGT ACTATCGAAC TGCCAGAAGG CGTTGAGATG      750
      GTTATGCCTG GTGACAACGT GAACATGGTT GTTACCCTGA TCCACCCAAT      800
60     CGCGATGGAT GACGGTCTGC GTTTC                        825
  
```

2) INFORMATION FOR SEQ ID NO: 158

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *arizonae*
 (B) STRAIN: ATCC 13314

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158

```

20  CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCCGATG CCGCAGACCC      50
    GTGAGCACAT CCTGCTGGGC CGTCAGGTAG GCGTTCCGTA CATCATCGTG      100
    TTCCTGAACA AATGCGACAT GGTTGATGAC GAAGAGCTGC TGGAAGTGGT      150
    TGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGACTTC CCGGGCGACG      200
    ATACGCCGAT CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGACGCA      250
25  GAGTGGGAAG CGAAAATCAT CGAACTGGCT GGCTTCCTGG ACTCTTACAT      300
    CCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG      350
    ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAA      400
    CGCGGTATCA TCAAAGTGGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA      450
    GACTCAGAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAAC TGCTGG      500
30  ACGAAGGCCG TGCCGGTGAG AACGTAGGTG TTCTGCTGCG TGGTATCAAA      550
    CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCACCATCAA      600
    GCCGCACACC AAGTTCGAAT CTGAAGTGTA CATTCTGTCC AAAGATGAAG      650
    GCGGCCGTCA TACTCGTTC TTCAAAGGCT ACCGTCCGCA GTTCTACTTC      700
    CGTACTACTG ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTGGAGAT      750
35  GGTAATGCCG GGCGACAACA TCAAATGGT TGTTACCCTG ATCCACCCGA      800
    TCGCGATGGA CGACGGTCTG CGTTTCGCAA      830

```

2) INFORMATION FOR SEQ ID NO: 159

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype *choleraesuis*
 (B) STRAIN: ATCC 7001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159

```

60  CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGYCCGATG CCGCAGACCC      50
    GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG      100
    TTCCTGAACA AATGCGACAT GGTTGATGAC GAAGAGCTGC TGGAAGTGGT      150
    TGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGACTTC CCGGGCGACG      200

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ACACGCCGAT CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGTGACGCA 250
GAGTGGGAAG CGAAAATCAT CGAACTGGCT GGCTTCCTGG ATTCTTACAT 300
TCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG 350
ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAG 400
5 CGCGGTATCA TCAAAGTGGG YGAAGAAGTT GAAATCGTTG GTATCAAAGA 450
GACTCAGAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAACGTGTTG 500
ACGAAGGCCG TGCCGGTGAG AACGTAGGTG TTCTGCTGCG TGGTATCAAA 550
CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCACCATCAA 600
GCCGCACACC AAGTTCGAAT CTGAAGTGTA CATTCTGTCC AAAGATGAAG 650
10 GCGGCCGTCA TACTCCGTTT TTCAAAGGCT ACCGTCCGCA GTTCTACTTC 700
CGTACTACTG ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTAGAGAT 750
GGTAATGCCG GGCGACAACA TCAAATGGT TGTTACCCTG ATCCACCCGA 800
TCGCAATGGA CGACGGTCTG CGTTTCGCAA TC 832

```

15

2) INFORMATION FOR SEQ ID NO: 160

(i) SEQUENCE CHARACTERISTICS:

```

20 (A) LENGTH: 807 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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    (A) ORGANISM: Salmonella choleraesuis subsp. diarizonae
    (B) STRAIN: ATCC 43973

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30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160

```

CCTGGTTGTT GCTGCGACTG ACGGCCCGAT GCCGCAGACC CGTGAGCACA 50
TCCTGCTGGG TCGTCAGGTA GGCGTTCCGT ACATTATCGT GTTCCTGAAC 100
35 AAATGCGACA TGGTTGATGA CGAAGAGCTG CTGGAAGTGG TAGAAATGGA 150
AGTTCGTGAA CTTCTGTCTC AGTACGACTT CCCGGGCGAC GACACGCCAA 200
TCGTTTCGTG TTCTGCTCTG AAAGCGCTGG AAGGCGACGC AGAGTGGGAA 250
GCGAAAATCA TCGAACTGGC TGGCTTCCTG GATTCTTACA TCCCGGAACC 300
AGAGCGTGCG ATTGACAAGC CGTTCCTGCT GCCGATCGAA GACGTATTCT 350
40 CCATCTCCGG TCGTGGTACC GTTGTTACCG GTCGTGTAGA GCGCGGTATC 400
ATCAAAGTGG GCGAAGAAGT TGAAATCGTT GGTATCAAAG AGACTCAGAA 450
GTCTACCTGT ACTGGCGTTG AAATGTTCCG CAARCTGCTG GACGAAGGCC 500
GTGCWGGTGA GAACGTAGGT GTTCTGCTGC GTGGTATCAA ACGTGAAGAA 550
ATCGAACGTG GTCAGGTACT GGCTAAGCCG GGCACCATCA AGCCGCACAC 600
45 CAAGTTCGAA TCTGAAGTGT ATATTCTGTC CAAAGATGAA GGCGGCCGTC 650
ATACTCCGTT CTTCAAAGGC TACCGTCCGC AGTTCTACTT CCGTACCACT 700
GACGTGACTG GCACCATCGA ACTGCCGGAA GGCGTGGAGA TGGTAATGCC 750
GGGCGACAAC ATCAAATGG TTGTTACCCT GATCCACCCG ATCGCGATGG 800
ACGACGG 807
50

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2) INFORMATION FOR SEQ ID NO: 161

(i) SEQUENCE CHARACTERISTICS:

```

55 (A) LENGTH: 832 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*

serotype heidelberg

(B) STRAIN: ATCC 8326

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161

10	CGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACCC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	100
	TTCCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	TGAAATGGAA	GTTTCGTGAAC	TTCTGTCTCA	GTACGACTTC	CCGGGCGACG	200
	ACACTCCGAT	CGTTTCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGACGCA	250
15	GAGTGGGAAG	CGAAAATCAT	CGAACTGGCT	GGCTTCCTGG	ATTCTTACAT	300
	CCCGGAACCA	GAGCGTGCGA	TTGACAAAGCC	GTTCTCTGCTG	CCGATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTAGAA	400
	CGCGGTATCA	TCAAAGTGGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	GACTCAGAAG	TCTACCTGTA	CTGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
20	ACGAAGGCCG	TGCCGGTGAG	AACGTAGGTG	TTCTGCTGCG	TGGTATCAAA	550
	GCTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCTAAGCCCG	GCACCATCAA	600
	GCCGCACACC	AAGTTCGAAT	CTGAAGTGTA	CATTCTGTCC	AAAGATGAAG	650
	GCGGCCGTCA	YACTCCGTTC	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACTACTG	ACGTGACTGG	CACCATCGAA	TTGCCGGAAG	GCGTAGAGAT	750
25	GGTAATGCCG	GGCGACAACA	TCAAATGGT	TGTTACCCTG	ATCCACCCGA	800
	TCCGATGGA	CGACGGTCTG	CGTTTCGCAA	TC		832

30 2) INFORMATION FOR SEQ ID NO: 162

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 807 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Salmonella choleraesuis* subsp. *houtenae*

(B) STRAIN: ATCC 43974

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162

45	CCTGGTTGTT	GCTGCGACTG	ACGGCCCGAT	GCCGCAGACC	CGTGAGCACA	50
	TCCTGCTGGG	TCGTCAGGTA	GGCGTTCCGT	ACATCATCGT	GTTCTGAAC	100
	AAATGCGACA	TGGTTGATGA	CGAAGAGCTG	CTGGAAGTGG	TAGAAATGGA	150
	AGTTCGTGAA	CTTCTGTCTC	AGTACGATTT	CCCGGGCGAC	GACACGCCGA	200
50	TCGTGCGTGG	TTCTGCTCTG	AAAGCGCTGG	AAGGCGACGC	AGAATGGGAA	250
	GCGAAAATCA	TCGAACTGGC	TGGCTACCTG	GATTCTTACA	TCCCGGAACC	300
	AGAGCGTGCG	ATTGACAAAC	CGTTCCTGCT	GCCGATCGAA	GACGTATTCT	350
	CTATCTCCGG	TCGTGGTACC	GTTGTTACCG	GTCGTGTAGA	GCGCGGTATC	400
	ATCAAAGTGG	GCGAAGAAGT	TGAAATCGTT	GGTATCAAAG	AGACTCAGAA	450
55	GTCGACCTGT	ACTGGCGTTG	AAATGTTCCG	CAAAGTCTG	GACGAAGGCC	500
	GTGCTGGCGA	GAACGTAGGT	GTTCTGCTGC	GTGGTATCAA	ACGTGAAGAA	550
	ATCGAACGTG	GTCAGGTACT	GGCTAAGCCG	GGCACCATCA	AGCCGCACAC	600
	CAAGTTCGAA	TCTGAAGTGT	ACATTCTGTC	CAAAGATGAA	GGCGGCCGTC	650
	ATACTCCGTT	CTTCAAAGGC	TACCGTCCG	AATTCTACTT	CCGTACGACT	700
60	GACGTGACTG	GCACCATCGA	ACTGCCGGAA	GGCGTGGA	TGGTAATGCC	750

GGGCGACAAC ATCAAAATGG TTGTTACCCT GATCCACCCG ATCGCGATGG 800
ACGACGG 807

5

2) INFORMATION FOR SEQ ID NO: 163

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 827 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *indica*
(B) STRAIN: ATCC 43976

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163

CGCGATCCTG GTTGTGCTG CGACTGACGG CCCGATGCCG CAGACCCGTG 50
AGCACATCCT GCTGGGTCGT CAGGTAGGCG TTCCGTACAT CATCGTGTTT 100
CTGAACAAAT GCGACATGGT TGATGACGAA GAGCTGCTGG AACTGGTTGA 150
25 AATGGAAGTT CGTGAAC TTC TCTCAGTA CGACTTCCCG GGTGACGACA 200
CGCCGATCGT GCGTGGTTCT GCTCTGAAAG CGCTGGAAGG CGACGCAGAG 250
TGGGAAGCGA AAATCATCGA ACTGGCTGGC TTCCTGGATT CTTACATTCC 300
GGAACCAGAG CGTGCGATTG ACAAGCCGTT CCTGCTGCCG ATCGAAGACG 350
TATTCTCCAT CTCCGGTCGT GGTACYGTTG TTACCGGTCG TGTAGAGCGC 400
30 GGATATCATCA AAGTGGGCGA AGAAGTTGAA ATCGTTGGTA TCAAAGAGAC 450
TCAGAACTCT ACCTGTACTG GCGTTGAAAT GTTCCGCAA CTGCTGGACG 500
AAGGCCGTGC CGGTGAGAAC GTAGGTGTTT TGCTGCGTGG TATCAAACGT 550
GAAGAAATCG AACGTGGTCA GGTACTGGCT AAGCCGGGCA CCATCAAGCC 600
GCACACCAAG TTCGAATCTG AAGTGTACAT TCTGTCCAA GATGAAGGCG 650
35 GCCGTCATAC TCCGTTCTTC AAAGGCTACC GTCCGCAGTT CTAATTCCGT 700
ACTACTGACG TGACTGGCAC CATCGAACTG CCGGAAGGCG TAGAGATGGT 750
AATGCCGGGC GACAACATCA AAATGGTTGT TACCCTGATC CATCCGATCG 800
CRATGGACGA CGGTCTGCGT TTCGCAA 827

40

2) INFORMATION FOR SEQ ID NO: 164

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 807 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *salamae*
(B) STRAIN: ATCC 43972

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164

CCTGGTTGTT GCTGCGACTG ACGGCCCGAT GCCGCAGACC CGTGAGCACA 50
TCCTGCTGGG TCGTCAGGTA GCGTTCCGT ACATCATCGT GTTCTGAAC 100
60 AAATGCGACA TGGTTGATGA CGAAGAGCTG CTGGAAGTGG TAGAAATGGA 150

AGTTTCGTGAA CTTCTGTCTC AGTACGACTT CCCGGGCGAC GACACGCCGA 200
 TCGTGCGTGG TTCCGCTCTG AAAGCGCTGG AAGGCGAMGC TGAGTGGGAA 250
 GMGAAAATCA TCGAACTGGC TGGCTWCCTG GATTCTTACA TTCCGGAACC 300
 AGAGCGTGCG ATTGACAAGC CGTTCCTGCT GCCGATCGAA GACGTATTCT 350
 5 CCATCTCCGG TCGTGGTACC GTTGTATTCCG GTCGTGTAGA GCGCGGTATC 400
 ATCAAAGTGG GCGAAGAAGT TGAAATCGTT GGTATCAAAG AGACTCAGAA 450
 GTCTACCTGT ACTGGCGTTG AAATGTTCCG CAAACTGCTG GACGAAGGCC 500
 GTGCCGGTGA GAACGTAGGT GTTCTGCTGC GTGGTATCAA ACGTGAAGAA 550
 ATCGAACGTG GTCAGGTACT GGCTAAGCCG GGCACCATCA AGCCGCACAC 600
 10 CAAGTTCGAA TCTGAAGTGT ACATCTGTTC CAAAGATGAA GGCGGCCGTC 650
 ATACTCCGTT CTTCAAAGGC TACCGTCCGC AGTTCTACTT CCGTACCACT 700
 GACGTGACTG GCACCATCGA ACTGCCGGAA GCGGTGGAGA TGGTAATGCC 750
 GGGCGACAAC ATCAAATGG TTGTTACCCT GATCCACCCG ATCGCGATGG 800
 ACGACGG 807
 15

2) INFORMATION FOR SEQ ID NO: 165

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

30 (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype typhi
 (B) STRAIN: ATCC 10749

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165

35 CGGCGCGATC CTGGTTGTTG CTGCGACTGA CGGCCCGATG CCGCAGACCC 50
 GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG 100
 TTCCTGAACA AATGCGACAT GGTGTATGAC GAAGAGCTGC TGGAAGTGGT 150
 TGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGACTTC CCGGGCGACG 200
 ACACGCCGAT CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGACGCA 250
 40 GAGTGGGAAG CGAAATCAT CGAACTGGCT GGCTTCCTGG ATTCTTACAT 300
 CCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCTGCTG CCGATCGAAG 350
 ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAA 400
 CGCGGTATCA TCAAAGTGGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA 450
 GACTCAGAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAAGTGTCTG 500
 45 ACGAAGGCCG TGCNGGTGAG AACGTAGGTG TTCTGCTGCG TGGTATCAA 550
 CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCACCATCAA 600
 GCCGCACACY AAGTTCGAAT CTGAAGTGTA CATTCTGTCC AAAGATGAAG 650
 GCGGCCGTC TACTCCGTTT TTCAAAGGCT ACCGTCCGCA GTTCTACTTC 700
 CGTACTACTG ACGTGAAGT CACCATCGAA CTGCCGGAAG GCGTAGAGAT 750
 50 GGTAATGCCG GGCGACAACA TCAAATGGT TGTTACCCTG ATCCACCCGA 800
 TCGCAATGGA CGACGGTCTG CGTTTCGCAA TC 832

55 2) INFORMATION FOR SEQ ID NO: 166

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 60 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Serratia fonticola*
 (B) STRAIN: DSM 4576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166

10	CGGCGCTATC CTGGTTGTAG CTGCGACTGA CGGCCCTATG CCTCAGACTC	50
	GTGAGCACAT CCTGCTGGGT CGTCAGGTTG GCGTTCCTTA CATCATCGTA	100
	TTCATGAACA AATGCGACAT GGTTGATGAT GAAGAGCTGC TGGAACTGGT	150
15	AGAAATGGAA GTTCGTGAAC TTCTGTCTGC TTATGACTTC CCTGGTGATG	200
	ACCTGCCGGT TGTTCTGTTG TCAGCGCTGA AAGCACTGGA AGGCGAAGCT	250
	GAGTGGGAAG CTAAAATCAT CGAGCTGGCC GGTACCTGG ATTCCTACAT	300
	CCCAGAACCA GAGCGTGCTA TCGATCAGCC GTTCCTGCTG CCAATCGAAG	350
	ACGTATTCTC CATCTCCGGT CGTGGTACCG TAGTTACCGG TCGTGTTGAG	400
20	CGCGGTATCG TTAAAGTTGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA	450
	CACCGTTAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAATGCTGG	500
	ACGAAGGCCG TGCTGGTGAG AACGTTGGTG TTCTGCTGCG TGGTATCAAG	550
	CGTGAAGACA TCGAACGTGG TCAGTACTG GCTAAACCAG GTTCCATCAA	600
	GCCGCACACT CAGTTCGATT CAGAAGTGA TATCCTGAGC AAAGAAGAAG	650
25	GTGGTCGTCA TACTCCATTC TTCAAAGGCT ACCGTCCACA GTTCTACTTC	700
	CGTACAACCTG ACGTGACCGG TACCATCGAA CTGCCAGAAG GCGTAGAGAT	750
	GGTAATGCCA GCGGATAACG TGAACATGGT TGTTACCCTG ATCCACCCAA	800
	TCGCTATGGA CCAAGGC	817

2) INFORMATION FOR SEQ ID NO: 167

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 787 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Serratia liquefaciens*
 (B) STRAIN: ATCC 27592

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167

10	GCTGCGACTG ACGGCCCAAT GCCTCAGACC CGTGAGCACA TCCTGCTGGG	50
	TCGTCAGGTT GCGGTTTCCTT TCATCATCGT ATTCATGAAC AAATGCGACA	100
	TGGTTGATGA TGAAGAGCTG CTGGAAGTGG TAGAAATGGA AGTTCGTGAA	150
	CTTCTGTCTG CTTACGACTT CCCTGGTGAT GACCTGCCGG TTGTTCTGTTG	200
	TTCAGCGCTG AAAGCACTGG AAGGCGAAGC TGAGTGGGAA GCTAAAATCA	250
	TCGAGCTGGC CGGTTACCTG GATTCTTACA TCCCAGAACC AGAGCGTGCT	300
	ATCGACAAGC CGTTCCTGCT GCCAATCGAA GACGTCTTCT CCATCTCCGG	350
	TCGTGGTACC GTTGTACCG GTGATCAAAG ACACCGTTAA GTCTACCTGT	400
	GCGAAGAAGT TGAAATCGTT GGTATCAAAG GACGAAGGCC GTGCTGGTGA	450
	ACTGGCGTTG AAATGTTCCG CAAACTGCTG GCGTGAAGAC ATCGAACGTG	500
	GAACGTTGGT GTTCTGCTGC GTGGTATCAA AGCCACACAC CAAGTTCGAC	550
	GTCAGGTACT GGCTAAACCA GGTTCATCA GGTGGTCGTC ATACTCCATT	600
	TCAGAAGTGT ACATCCTGAG CAAAGAAGAA CCGTACAAC TACGTGACCG	650
5	CTTCAAAGGC TACCGTCCAC AGTTCTACTT CCGTACAAC	700

GTACCATCGA ACTGCCAGAA GGC GTTGA AAA TGGTAATGCC AGGTGACAAC
GTGAACATGG TTGTTACCT GATCCACCA ATCGCGA

750
787

5

2) INFORMATION FOR SEQ ID NO: 168

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 745 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia marcescens*
(B) STRAIN: ATCC 13880

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168

25	GCCTCAGACT	CGTGAGCACA	TCCTGCTGGG	TCGTCAGGTT	GGCGTTCCTT	50
	TCATCATCGT	ATT CATGAAC	AAATGCGACA	TGTTGATGA	TGAAGAGCTG	100
	YTGGAACTGG	TAGAAATGGA	AGTTCGCGAA	CTGCTGTCCG	CTTACGACTT	150
	CCCTGGCGAC	GACCTGCCGG	TAATCCGCGG	TTCCGCGCTG	AAAGCGCTGG	200
	AAGGCGAAGC	TGAGTGGGAA	GCGAAAATCA	TGGAAGTGGC	CGAAGCCCTG	250
	GACAGCTACA	TCCCAGAGCC	AGAGCGTGCT	ATCGACAAGC	CGTTCCTGCT	300
	GCCAAATCGAA	GACGTATTCT	CCATCTCCGG	TCGTGGTACC	GTTGTTACCG	350
	GTCGTGTTGA	GCGCGGCATC	ATCAAAGTTG	GCGAAGAAGT	TGAAATCGTT	400
30	GGTATCAAAG	ACACCGTTAA	GTCTACCTGT	ACTGGCGTTG	AAATGTTCCG	450
	CAAAGTCTG	GACGAAGGCC	GTGCTGGTGA	GAACGTAGGT	GTTCTGCTGC	500
	GTGGTATCAA	ACGTGAAGAA	ATCGAACGTG	GTCAGGTACT	GGCTAAGCCA	550
	GGCTCCATCA	AGCCGCACAC	CCAGTTTCGAA	TCTGAAGTGT	ACATCCTGAG	600
	CAAAGATGAA	GGTGGTCGTC	ACACKCCATT	CTTCAAAGGC	TACCGTCCAC	650
35	AGTTCTACTT	CCGTACCACT	GACGTGACCG	GTACCATCGA	ACTGCCAGAA	700
	GGCGTAGAGA	TGGTAATGCC	AGGCGACAAC	GTGAACATGG	TTGTA	745

40 2) INFORMATION FOR SEQ ID NO: 169

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 829 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia odorifera*
(B) STRAIN: ATCC 33077

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169

55	GGCGCAATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCTATGC	CTCAGACCCG	50
	TGAGCACATC	CTGCTGGGTC	GCCAGGTTGG	CGTTCCTTTC	ATCATCGTGT	100
	TCATGAACAA	ATGTGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTA	150
	GAAATGGAAG	TTCGCGAGCT	GCTGTCTGCT	TACGATTTC	CTGGCGACGA	200
60	CCTGCCAGTA	ATCCGCGGTT	CTGCGCTGAA	AGCGCTGGAA	GGCGAAGCAG	250

	AGTGGGAAGC	TAAGATTGTA	GAAGTGGCTG	AAGCGCTGGA	TTCTTACATC	300
	CCAGAACCCAG	AGCGTGCTAT	CGACAAGCCG	TTCCTGCTGC	CAATCGAAGA	350
	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTGAGC	400
5	GCGGTATCAT	CAAAGTTGGC	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAC	450
	ACCGTTAAGT	CTACCTGTAC	CGGTGTAGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCTGGTGAGA	ACGTTGGTGT	TCTGCTGCGT	GGTATCAAGC	550
	GTGAAGACAT	CGAACGTGGT	CAGGTTCTGT	CTAAACCAGG	TTCTATCAAG	600
	CCGCACACCA	AATTCGACTC	AGAAGTGATC	ATCCTGAGCA	AAGAAGAAGG	650
	TGGTCGTCAC	ACGCCATTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700
10	GTAATGCCAG	GCGATAACGT	GAACATGGTT	TGCCAGAAGG	CGTAGAGATG	750
	CGCAATGGAC	GACGGTCTGC	GTTTCGCAA	GTTACCCTGA	TTCACCCAAT	800
						829

15

2) INFORMATION FOR SEQ ID NO: 170

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia plymuthica*
 (B) STRAIN: DSM 4540

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170

	CGGCGCAATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCAATG	CCTCAGACCC	50
	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTTG	GCGTTCCTTT	CATCATCGTA	100
35	TTCATGAACA	AATGCGACAT	GGTTGATGAT	GAAGAGCTGC	TGGAAGTGGT	150
	AGAAATGGAA	GTTCGTGAAC	TTCTGTCTGC	TTACGACTTC	CCTGGTGATG	200
	ACCTGCCGGT	TGTTGCTGGT	TCAGCGCTGA	AAGCACTGGA	AGGCGAACCA	250
	GAGTGGGAAG	CTAAAATCAT	CGAGCTGGCT	GGTTTCCTGG	ATTCTTACAT	300
	CCCAGAACCA	GAGCGTGCTA	TCGACAAGCC	GTTTCCTGCTG	CCAATCGAAG	350
40	ACGTATTCTC	CATCTCCGGT	CGTGGTACCG	TTGTTACCGG	TCGTGTTGAG	400
	CGCGGTATCG	TTAAAGTTGG	CGAAGAAGTT	GAAATCGTGG	GTATCAAAGA	450
	CACCGTTAAG	TCTACCTGTA	CCGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTGGGTG	TTCTGCTGCG	TGGTATCAAG	550
	CGCGAAGATA	TCGAACGTGG	TCAGGTCCCTG	GCTAAACCAG	GTTCAATCAA	600
	GCCACACACC	AAGTTTGACT	CAGAAGTGTA	CATCCTGAGC	AAAGAAGAAG	650
45	GTGGTCGTCA	TACTCCATTCT	TTCAAAGGCT	ACCGTCCACA	GTTCTACTTC	700
	CGTACAACCTG	ACGTGACCGG	TACCATCGAA	CTGCCAGAAG	GCGTAGAGAT	750
	GGTAATGCCA	GGTGACAACG	TGAACATGGT	TGTAACCCTG	ATCCACCCAA	800
	TCGCGATGGA	CGACGGCCTG	CGTTTCGCAA			830

50

2) INFORMATION FOR SEQ ID NO: 171

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia rubidaea*
 (B) STRAIN: ATCC 27593

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171

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5      GCGCAATCC TGGTAGTAGC AGCGACTGAC GGCCCAATGC CTCAGACCCG      50
      TGAGCACATC CTGCTGGGCC GCCAGGTAGG CGTACCTTAC ATCATCGTAT      100
10     TCATGAACAA ATGCGACATG GTAGATGATG AAGAGCTGCT GGAAGTGGTA      150
      GAGATGGAAG TTCGCGAACT GCTGTCTGCT TACGACTTCC CAGGCGACGA      200
      CCTGCCGGTA ATCCGTGGTT CCGCGCTGAA AGCGCTGGAA GGCGAAGCCG      250
      AGTGGGAAGC GAAAATCGTT GAGCTGGCAG AAGCGCTGGA CAGCTACATC      300
      CCAGAGCCAG AGCGTGCTGT AGACAAGCCG TTCCTGCTGC CAATCGAAGA      350
15     CGTATTCTCC ATCTCCGGTC GTGGTACCGT TGTTACCGGT CGTGTAGAGC      400
      GCGGTATCAT CAAAGTTGGT GAAGAAGTAG AAATCGTAGG TATCAAAGAC      450
      ACCGTTAAGT CTACCTGTAC TGGCGTAGAA ATGTTCCGCA AACTGCTGGA      500
      CGAAGGCCGT GCTGGTGAGA ACGTAGGTGT TCTGCTGCGT GGTATCAAGC      550
      GTGAAGAAAT CGAACGTGGT CAGGTACTGG CGAAGCCAGG TTCAATCAAG      600
20     CCGCACACCC AGTTCGAATC TGAAGTGTAC ATTCTGTCCA AAGACGAAGG      650
      CCGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCACAG TTCTACTTCC      700
      GTACAACTGA CGTGACCGGT ACCATCGAAC TGCCAGAAGG CGTAGAGATG      750
      GTAATGCCAG GCGACAACGT GAACATGAAA GTTACTCTGA TTCACCCAAT      800
      CGCAATGGAC GACGGTCTGC GTTTCGCAA      829
25
  
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2) INFORMATION FOR SEQ ID NO: 172

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shigella boydii*
 (B) STRAIN: ATCC 9207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172

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45     CCGCGCGATC YTGGTAGTTG CTGCGACTGA CGGCCCGATG CCGCAGACTC      50
      GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCCGTA CATCATCGTG      100
      TTCCTGAACA AATGCGACAT GGTGATGAC GAAGAGCTGC TGGAAGTGGT      150
      TGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGACTTC CCGGCGCAGC      200
      ACACTCCGAT CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGACGCA      250
      GAGTGGGAAG CGAAAATCCT GGAAGTGGCT GGCTTCCTGG ATTCTTACAT      300
50     TCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG      350
      ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAA      400
      CGCGGTATCA TCAAAGTTGG TGAAGAAGTT GAAATCGTTG GTATCAAAGA      450
      GACTCAGAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAAGTCTGG      500
      ACGAAGGCCG TGCTGGTGAG AACGTAGGTG TTCTGCTGCG TGGTATCAAA      550
      CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCACCATCAA      600
55     GCCGCACACC AAGTTCGAAT CTGAAGTGTA CATTCTGTCC AAAGATGAAG      650
      GCGGCCGTCA TACTCCGTTT TTCAAAGGCT ACCGTCCGCA GTTCTACTTC      700
      CGTACTACTG ACGTGACTGG TACCATCGAA CTGCCGGAAG GCGTAGAGAT      750
      GGTAATGCCG GCGACAACA TCAAATGGT TGTTACCCTG ATCCACCCGA      800
      TCGCGATGGA CGACGGTCTG CGTTTC      826
60
  
```

2) INFORMATION FOR SEQ ID NO: 173

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shigella dysenteriae*
 (B) STRAIN: ATCC 11835

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173

20	TGGTAGTTGC	TGCGACTGAC	GGCCCCGATGC	CGCAGACTCG	TGAGCACATC	50
	CTGCTGGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	TCCTGAACAA	100
	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTT	GAAATGGAAG	150
	TTCGTGAACT	TCTGTCTCAG	TACGACTTCC	CGGGCGACGA	CACTCCGATC	200
	GTTTCGTGTT	CTGCTCTGAA	AGCGCTGGAA	GGCGACGCAG	AGTGGGAAGC	250
25	GAAAATCCTG	GAAGTGGCTG	GCTTCCTGGA	TTCYTAYATT	CCGGAACCAG	300
	AGCGTGCGAT	TGACAAGCCG	TTCCTGCTGC	CGATCGAAGA	CGTATTCTCC	350
	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAAC	GCGGTATCAT	400
	CAAAGTTGGT	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAG	ACYCAGAAGT	450
	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	CGAAGGCCGT	500
30	GCTGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAAC	GTGAAGAAAT	550
	CGAACGTGGT	CAGGTACTGG	CGAAGCCRGG	CACCATCAAG	CCGCACACCA	600
	AGTTCGAATC	TGAAGTGTAC	ATTCTGTCCA	AAGATGAAGG	CGGCCGTCAT	650
	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	GTACTACTGA	700
	CGTGACTGGT	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	GTAATGCCGG	750
35	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TCCACCCGAT	CGCGATGGAC	800
	GACGGTCTGC	GTTTCGCA				818

2) INFORMATION FOR SEQ ID NO: 174

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shigella flexneri*
 (B) STRAIN: ATCC 12022

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174

55	CCTGGTAGTT	GCTGCGACTG	ACGGCCCCGAT	GCCGCAGACT	CGTGAGCACA	50
	TCCTGCTGGG	TCGTCAGGTA	GGCGTTCCGT	ACATCATCGT	GTTCTGAAC	100
	AAATGCGACA	TGGTTGATGA	CGAAGAGCTG	CTGGAAGTGG	TTGAAATGGA	150
	AGTTTCGTGAA	CTTCTGTCTC	AGTACGACTT	CCCGGGCGAC	GACACTCCGA	200
60	TCGTTTCGTGG	TTCTGCTCTG	AAAGCGCTGG	AAGCGACGC	AGAGTGGGAA	250

```

    GCGAAAATCC TGGAAGTGGC TGGCTTCCTG GATTCTTACA TTCCGGAACC 300
    AGAGCGTGCG ATTGACAAGC CGTTCCTGCT GCCGATCGAA GACGTATTCT 350
    CCATCTCCGG TCGTGGTACC GTTGTTACCG GTCGTGTAGA ACGCGGTATC 400
    ATCAAAGTTG GTGAAGAAGT TGAAATCGTT GGTATCAAAG AGACTCAGAA 450
    5 GTCTACCTGT ACTGGCGTTG AAATGTTCCG CAAACTGCTG GACGAAGGCC 500
    GTGCTGGTGA GAACGTAGGT GTTCTGCTGC GTGGTATCAA ACGTGAAGAA 550
    ATCGAACGTG GTCAGGTACT GGCTAAGCCG GGCACCATCA AGCCGCACAC 600
    CAAGTTCGAA TCTGAAGTGT ACATTCTGTC CAAAGATGAA GGCGGMCCTC 650
    TACTCCGTT CTTCAAAGGC TACCGTCCGC AGTTCTACTT CCGTACTACT 700
    10 GACGTGACTG GTACCATCGA ACTGCCGGAA GGCGTAGAGA TGGTAATGCC 750
    GGGCGACAAC ATCAAATGG TTGTTACCCT GATCCACCCG ATCGCGATGG 800
    ACGACG 806

```

15 2) INFORMATION FOR SEQ ID NO: 175

```

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 832 bases
        (B) TYPE: Nucleic acid
    20 (C) STRANDEDNESS: Double
        (D) TOPOLOGY: Linear

    (ii) MOLECULE TYPE: Genomic DNA

    25 (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Shigella sonnei
        (B) STRAIN: ATCC 29930

```

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175

```

    CGGCGCGATC CTGGTAGTTG CTGCGACTGA CGGCCCGATG CCGCAGACTC 50
    GTGAGCACAT CCTGCTGGGT CGTCAGGTAG GCGTTCGGTA CATCATCGTG 100
    TTCCTGAACA AATGCGACAT GGTTGATGAC GAAGAGCTGC TGGAAGTGGT 150
    35 TGAAATGGAA GTTCGTGAAC TTCTGTCTCA GTACGACTTC CCGGGCGACG 200
    ACACTCCGAT CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGACGCA 250
    GAGTGGGAAG CGAAAATCCT GGAAGTGGCT GGCTTCCTGG ATTCTTACAT 300
    TCCGGAACCA GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG 350
    ACGTATTCTC CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAA 400
    CGCGGTATCA TCAAAGTTGG TGAAGAAGTT GAAATCGTTG GTATCAAAGA 450
    40 GACTCAGAAG TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAAGTCTGCTG 500
    ACGAAGGCCG TGCTGGTGAG AACGTAGGTG TTCTGCTGCG TGGTATCAAA 550
    CGTGAAGAAA TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCACCATCAA 600
    GCCGCACACC AAGTTCGAAT CTGAAGTGTA CATTCTGTCC AAAGATGAAG 650
    45 GCGGYCGTCA TACTCCGTTT TCAAAGGCT ACCGTCCGCA GTTCTACTTC 700
    CGTACTACTG ACGTGACTGG TACCATCGAA CTGCCGGAAG GCGTAGAGAT 750
    GGTAATGCCG GGCAGACAAC TCAAATGGT TGTACCCTG ATCCACCCGA 800
    TCGCGATGGA CGACGGTCTG CGTTTCGCAA TC 832

```

50

2) INFORMATION FOR SEQ ID NO: 176

```

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 716 bases
    55 (B) TYPE: Nucleic acid
        (C) STRANDEDNESS: Double
        (D) TOPOLOGY: Linear

```

60 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: ATCC 13301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176

```

TCTGCTGCTG ACGGTCCAAT GCCACAACT CGTGAACACA TTCTTTTATC      50
ACGTAACGTT GGTGTACCAG CATTAGTAGT ATTCTTAAAC AAAGTTGACA      100
10 TGGTTGACGA TGAAGAATTA TTAGAATTAG TAGAAATGGA AGTTCGTGAC      150
TTATTAAGCG AATATGACTT CCCAGGTGAC GATGTACCTG TAATCGCTGG      200
TTCAGCATT AAGCTTTAG AAGGCGATGC TCAATACGAA GAAAAAATCT      250
TAGAATTAAT GGAAGCTGTA GATACTTACA TTCCAACCTCC AGAACGTGAT      300
TCTGACAAAC CATTATGAT GCCAGTTGAG GACGTATTCT CAATCACTGG      350
15 TCGTGGTACT GTTGCTACAG GCCGTGTTGA ACGTGGTCAA ATCAAAGTTG      400
GTGAAGAAGT TGAAATCATC GGTTTACATG ACACATCTAA AACAACTGTT      450
ACAGGTGTTG AAATGTTCCG TAAATTATTA GACTACGCTG AAGCTGGTGA      500
CAACATTGGT GCATTATTAC GTGGTGTTCG TCGTGAAGAC GTACAACGTG      550
20 GTCAAGTATT AGCTGCTCCT GGTTCGAATTA CACCACATAC TGAATTCAAA      600
GCAGAAGTAT ACGTATTATC AAAAGACGAA GGTGGACGTC ACACTCCATT      650
CTTCTCAAAC TATCGTCCAC AATTCTATTT CCGTACTACT GACGTAACGT      700
GTGTTGTTCA CTTACC                                     716

```

2) INFORMATION FOR SEQ ID NO: 177

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 719 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: ATCC 29247

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177

```

TTCTTTTATC ACGTAACGTT GGTGTACCAG CATTAGTAGT ATTCTTAAAC      50
AAAGTTGACA TGGTTGACGA TGAAGAATTA TTAGAATTAG TAGAAATGGA      100
45 AGTTCGTGAC TTATTAAGCG AATATGACTT CCCAGGTGAC GATGTACCTG      150
TAATCGCTGG TTCAGCATT AAGCTTTAG AAGGCGATGC TCAATACGAA      200
GAAAAAATCT TAGAATTAAT GGAAGCTGTA GATACTTACA TTCCAACCTCC      250
AGAACGTGAT TCTGACAAAC CATTATGAT GCCAGTTGAG GACGTATTCT      300
CAATCACTGG TCGTGGTACT GTTGCTACAG GCCGTGTTGA ACGTGGTCAA      350
ATCAAAGTTG GTGAAGAAGT TGAAATCATC GGTTTACATG ACACATCTAA      400
50 AACAACTGTT ACAGGTGTTG AAATGTTCCG TAAATTATTA GACTACGCTG      450
AAGCTGGTGA CAACATTGGT GCATTATTAC GTGGTGTTCG TCGTGAAGAC      500
GTACAACGTG GTCAAGTATT AGCTGCTCCT GGTTCGAATTA CACCACATAC      550
TGAATTCAAA GCAGAAGTAT ACGTATTATC AAAAGACGAA GGTGGACGTC      600
ACACTCCATT CTTCTCAAAC TATCGTCCAC AATTCTATTT CCGTACTACT      650
55 GACGTAACGT GTGTTGTTCA CTTACCAGAA GGTMCTGAAA TGGAATGCG      700
TGGTGATAAC GTTGAAATG                                     719

```

2) INFORMATION FOR SEQ ID NO: 178

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 625 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: ATCC 33591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178

15	GTGAACACAT	TCTTTTATCA	CGTAACGTTG	GTGTACCAGC	ATTAGTAGTA	50
	TTCTTAAACA	AAGTTGACAT	GGTTGACGAT	GAAGAATTAT	TAGAATTAGT	100
	AGAAATGGAA	GTTTCGTGACT	TATTAAGCGA	ATATGACTTC	CCAGGTGACG	150
	ATGTACCTGT	AATCGCTGGT	TCAGCATTAA	AAGCTTTAGA	AGGCGATGCT	200
	CAATACGAAG	AAAAAATCTT	AGAATTAATG	GAAGCTGTAG	ATACTTACAT	250
20	TCCAACTCCA	GAACGTGATT	CTGACAAACC	ATTCATGATG	CCAGTTGAGG	300
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	350
	CGTGGTCAAA	TCAAAGTTGG	TGAAGAAGTT	GAAATCATCG	GTTTACATGA	400
	CACATCTAAA	ACAACGTGTA	CAGGTGTTGA	AATGTTCCGT	AAATTATTAG	450
	ACTACGCTGA	AGCTGGTGAC	AACATTGGTG	CATTATTACG	TGGTGTTGCT	500
25	CGTGAAGACG	TACAACGTGG	TCAAGTATTA	GCTGCTCCTG	GTTCAATTAC	550
	ACCACATACT	GAATTCAAAG	CAGAAGTATA	CGTATTATCA	AAAGACGAAG	600
	GTGGACGTCA	CACTCCATTCT	TTCTC			625

2) INFORMATION FOR SEQ ID NO: 179

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 704 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: ATCC 43300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179

	GTTGGTGTAC	CAGCATTAGT	AGTATTCTTA	AACAAAGTTG	ACATGGTTGA	50
	CGATGAAGAA	TTATTAGAAT	TAGTAGAAAT	GGAAGTTCGT	GACTTATTAA	100
	GCGAATATGA	CTTCCCAGGT	GACGATGTAC	CTGTAATCGC	TGGTTCAGCA	150
50	TTAAAAGCTT	TAGAAGGCGA	TGCTCAATAC	GAAGAAAAAA	TCTTAGAATT	200
	AATGGAAGCT	GTAGATACTT	ACATTCCAAC	TCCAGAACGT	GATTCTGACA	250
	AACCATTTCAT	GATGCCAGTT	GAGGACGTAT	TCTCAATCAC	TGGTCGTGGT	300
	ACTGTTGCTA	CAGGCCGTGT	TGAACGTGGT	CAAATCAAAG	TTGGTGAAGA	350
55	AGTTGAAATC	ATCGGTTTAC	ATGACACATC	TAAAACAAC	GTTACAGGTG	400
	TTGAAATGTT	CCGTAAATTA	TTAGACTACG	CTGAAGCTGG	TGACAACATT	450
	GGTGCATTAT	TACGTGGTGT	TGCTCGTGAA	GACGTACAAC	GTGGTCAAGT	500
	ATTAGCTGCT	CCTGGTTCAA	TTACACCACA	TACTGAATTC	AAAGCAGAAG	550
	TATACGTATT	ATCAAAAGAC	GAAGGTGGAC	GTCACACTCC	ATTCTTCTCA	600
60	AACTATCGTC	CACAATTCTA	TTTCCGTACT	ACTGACGTAA	CTGGTGTGTT	650

TCACCTTACCA GAAGGTACTG AAATGGTAAT GCCTGGTGAT AACGTTGAAA
TGAC

700

704

5

2) INFORMATION FOR SEQ ID NO: 180

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 730 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus* subsp. *aureus*
(B) STRAIN: ATCC 6538

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180

	GTGAACACAT	TCTTTTATCA	CGTAACGTTG	GTGTACCAGC	ATTAGTAGTA	50
	TTCTTAAACA	AAGTTGACAT	GGTTGACGAT	GAAGAATTAT	TAGAATTAGT	100
	AGAAATGGAA	GTTTCGTGACT	TATTAAGCGA	ATATGACTTC	CCAGGTGACG	150
25	ATGTACCTGT	AATCGCTGGT	TCAGCATTA	AAGCTTTAGA	AGGCGATGCT	200
	CAATACGAAG	AAAAAATCTT	AGAATTAATG	GAAGCTGTAG	ATACTTACAT	250
	TCCAACCTCA	GAACGTGATT	CTGACAAACC	ATTCATGATG	CCAGTTGAGG	300
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	350
	CGTGGTCAAA	TCAAAGTTGG	TGAAGAAGTT	GAAATCATCG	GTTTACATGA	400
30	CACATCTAAA	ACAACGTGTA	CAGGTGTTGA	AATGTTCCGT	AAATTATTAG	450
	ACTACGCTGA	AGCTGGTGAC	AACATTGGTG	CATTATTACG	TGGTGTGCT	500
	CGTGAAGACG	TACAACGTGG	TCAAGTATTA	GCTGCTCCTG	GTTCAATTAC	550
	ACCACATACT	GAATTCAAAG	CAGAAGTATA	CGTATTATCA	AAAGACGAAG	600
	GTGGACGTCA	CACTCCATTC	TTCTCAAAC	ATCGTCCACA	ATTCTATTTT	650
35	CGTACTACTG	ACGTAACCTG	TGTTGTTTAC	TTACCAGAAG	GTACTGAAAT	700
	GGTAATGCCT	GGTGATAACG	TTGAAATGAC			730

40 2) INFORMATION FOR SEQ ID NO: 181

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus auricularis*
(B) STRAIN: ATCC 33753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181

55	CGGTGCGATC	TTAGTTGTAT	CTGCAGCTGA	TGGTCCAATG	CCACAAACTC	50
	GTGAACACAT	CTTATTATCA	CGTAACGTTG	GTGTACCAGC	ATTAGTTGTA	100
	TTCTTAAACA	AAGTTGACCA	AGTTGACGAC	GAAGAATTAT	TAGAATTAGT	150
	AGAAATGGAA	GTTTCGTGACT	TATTAAGCGA	ATACGACTAC	CCAGGTGACG	200
60	ATGTACCTGT	AATCTCTGGT	TCTGCGTTGA	AAGCATTAGA	AGGCGACAAA	250


```

GAATACGAAC AAAAAATCTT AGACTTAATG CAACAAGTTG ACGATTACAT 300
TCCAAC TCCA GAACGTGACT CTGATAAACC ATTCATGATG CCAGTTGAAG 350
ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCAACAGG CCGTGTGAA 400
CGTGGTCAAA TCAAAGTCGG TGAAGAAGTT GAAATCATCG GTATGAAAGA 450
5 CCGTTCACAA AAAACAACAG TTACTGGTGT AGAAATGTTC CGTAAATTAT 500
TAGACTACGC TGAAGCTGGT GACAACATCG GTGCTTTATT ACGTGGTATT 550
TCACGTGAAG AAGTACAACG TGGTCAAGTT TTAGCTGCTC CTGGTTCAAT 600
TACACCACAC ACTAAATTCA CTGCAGAAGT TTACGTATTA TCTAAAGATG 650
AAGGTGGACG TCACACTCCA TTCTTCTCTA ACTACCGTCC ACAATTCTAT 700
10 TTCCGTACTA CTGACGTAAC AGGTGTTGTT ACTTTACCAG AAGGTACAGA 750
AATGGTAATG CCTGGCGATA ACGTTAAAAT GGAAGTTGAA TTAATTTCTC 800
CAATCGCTAT CGAAGACGGT ACTCGTTTCT CAAT 834

```

15

2) INFORMATION FOR SEQ ID NO: 182

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus capitis* subsp. *capitis*
 (B) STRAIN: ATCC 27840

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182

```

CGGCGGTATC TTAGTAGTAT CTGCTGCTGA CCGTCCAATG CCACAAACTC 50
GTGAACACAT CTTATTATCA CGTAACGTTG GTGTACCAGC ATTAGTTGTA 100
TTCTTAAACA AAGTTGACAT GGTAGACGAC GAAGAATTAT TAGAATTAGT 150
35 TGAAATGGAA GTTCGTGACT TATTAAGCGA ATATGACTTC CCAGGTGATG 200
ATGTACCTGT AATCGCTGGT TCAGCATTAA AAGCTTTAGA AGGCGATGCT 250
CAATACGAAG AAAAAATCTT AGAATTAATG CAAGCAGTTG ATGATTACAT 300
TCCAAC TCCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG 350
ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTGAA 400
40 CCGTGGTCAAA TCAAAGTTGG TGAAGAAGTT GAAATCATCG GTATCCACGA 450
AACTTCTAAA ACAACTGTTA CTGGTGTAGA AATGTTCCGT AAATTATTAG 500
ACTACGCTGA AGCTGGTGAC AACATCGGTG CTTTATTACG TGGTGTGCT 550
CGTGAAGACG TACAACGTGG TCAAGTATTA GCTGCTCCTG GTTCAATCAC 600
ACCACACACT AAATTCAAAG CGGAAGTTTA CGTTTTATCT AAAGACGAAG 650
45 GTGGACGTCA CACTCCATTG TTCAGTAACT ACCGCCACA ATTCTATTTC 700
CGTACTACTG ACGTAACTGG TGTGTTAAC TTACCAGAAG GTACTGAAAT 750
GGTTATGCCT GGCACAAACG TTGAAATGAC AGTTGAATTA ATCGCTCCTA 800
TCGCTATTGA AGACGGTACT CGTTTCTCAA TCGGA 835

```

50

2) INFORMATION FOR SEQ ID NO: 183

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 804 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus caseolyticus*
 (B) STRAIN: ATCC 13548

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183

```

5      GTATCTTAGT AGTATCTGCT GCTGACGGTC CAATGCCACA AACTCGTGAA      50
      CACATCCTTT TATCACGTAA CGTTGGTGTA CCAGCATTAG TAGTATTCTT      100
10     GAACAAAGTT GACATGGTTG ACGATGAAGA ATTATTAGAA TTAGTTGAAA      150
      TGGAAGTTTCG TGAATTATTA TCTGAATATG ACTTCCCTGG TGACGATGTA      200
      CCTGTAATCG CTGGATCTGC TTATAAAGCA TTAGAAGGCG TTGAAGAATA      250
      CGAAGACAAA ATCATGGAAT TAATGGACGC AGTTGATGAG TACATCCCAA      300
      CTCCAGAACG TGATTCTGAC AAACCATTCA TGATGCCAGT TGAGGACGTA      350
15     TTCTCAATCA CTGGTCGTGG TACAGTTGCA ACTGGACGTG TTGAGCGTGG      400
      ACAAGTAAAA GTTGGTGAAG AAGTTGAAAT CATTGGTTTA ACTGAAGAAC      450
      CAGCAAAAAC TACAGTTACA GGTGTAGAAA TGTTCCGTAA ATTATTAGAT      500
      TACGCTGAAG CTGGAGATAA CATCGGTGCT TTATTACGTG GTGTTTCTCG      550
      TGAAGACGTA CAACGTGGAC AAGTATTAGC TAAACCAGGT TCAATTACTC      600
20     CACATACTAA ATTCAAAGCT GAAGTTTACG TATTATCTAA AGAAGAAGGT      650
      GGACGTCATA CTCCATTCTT CACTAACTAC CGCCCTCAGT TCTACTTCCG      700
      TACAACGTGAC GTAACGGTGT TAGTTAACTT ACCAGAAGGT ACTGAAATGG      750
      TAATGCCTGG AGATAACATC GAAATGAACG TTGAATTAAT TTCTCCAATC      800
25     GCGA
                                         804
  
```

2) INFORMATION FOR SEQ ID NO: 184

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus cohnii*
 (B) STRAIN: DSM 20260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184

```

45     CGGAGCTATC TTAGTAGTAT CTGCTGCTGA TGGCCCAATG CCACAACTC      50
      GTGAACATAT CCTTTTATCA CGTAACGTTG GTGTTCCAGC ATTAGTTGTA      100
      TTCTTAAACA AAGTTGACAT GGTGACGAT GAAGAATTAT TAGAATTAGT      150
      AGAAATGGAA GTTCGTGACT TATTAAGCGA ATATGACTTC CCAGGTGACG      200
      ATGTACCTGT AATCTCTGGT TCAGCATTAA AAGCTCTTGA AGGCGACGCT      250
      GACTATGAGC AAAAAATCTT AGACTTAATG CAAGCTGTTG ATGACTTCAT      300
50     TCCAACACCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG      350
      ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG GCGTGTGAA      400
      CGTGGTCAAA TCAAAGTCGG TGAAGAAGTT GAAATCATCG GTATGCAAGA      450
      AGATTCAAGC AAAACAACCTG TTAAGTGGTGT AGAAATGTTT CGTAAATTAT      500
      TAGACTACGC TGAAGCTGGT GACAACATTG GTGCGTTATT ACGTGGTGT      550
55     GCACGTGAAG ACATCCAACG TGGTCAAGTT TTAGCTGCTC CTGGTTCAAT      600
      TACACCACAC ACAAACTTTA AAGCGGAAGT TTACGTTTTA TCAAAAGATG      650
      AAGGTGGCCG TCATACGCCA TTCTTCAGTA ACTATCGCCC ACAATTCTAT      700
      TTCCGTACTA CTGACGTAAC AGGTGTTGTT ACTTTACCAG AAGGTACTGA      750
      AATGGTTATG CCTGGCGACA ACGTAGAAAT GGAAGTTGAA CTAATTTCTC      800
60     CAATCGCTAT CGAAGACGGT ACACGTTTCT CT
                                         832
  
```

5 2) INFORMATION FOR SEQ ID NO: 185

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 699 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 15 (A) ORGANISM: *Staphylococcus epidermidis*
 (B) STRAIN: CSG 269

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185

20 ATCTGCTGCT GACGGTCCAA TGCCACAAAC TCGTGAACAC ATCTTATTAT 50
 CACGTAACGT TGGTGTACCA GCATTAGTTG TATTCTTAAA CAAAGTTGAC 100
 ATGGTAGACG ACGAAGAATT ATTAGAATTA GTTGAAATGG AAGTTCGTGA 150
 CTTATTAAGC GAATATGACT TCCCAGGTGA CGATGTACCT GTAATCGCTG 200
 25 GTTCTGCATT AAAAGCATTG GAAGGCGATG CTGAATACGA ACAAAAAATC 250
 TTAGACTTAA TGCAAGCAGT TGATGATTAC ATTCCAATC CAGAACGTGA 300
 TTCTGACAAA CCATTCATGA TGCCAGTTGA GGACGTATTC TCAATCACTG 350
 GTCGTGGTAC TGTTGCTACA GGCCGTGTTG AACGTGGTCA AATCAAAGTT 400
 GGTGAAGAAG TTGAAATCAT CGGTATGCAC GAAACTTCTA AAACAACTGT 450
 30 TACTGGTGTA GAAATGTTCC GTAAATTATT AGACTACGCT GAAGCTGGTG 500
 ACAACATCGG TGCTTTATTA CGTGGTGTG CACGTGAAGA CGTACAACGT 550
 GGTCAGGTAT TAGCTGCTCC TGGTTCTATT ACACCACACA CAAAATTCAT 600
 AGCTGAAGTA TACGTATTAT CTAAAGATGA AGGTGGACGT CACACTCCAT 650
 TCTTCACTAA CTATCGCCCA CAATTCTATT TCCGTACTAC TGACGTAAC 699
 35

2) INFORMATION FOR SEQ ID NO: 186

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Staphylococcus haemolyticus*
 (B) STRAIN: ATCC 29970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186

55 CGGCGGTATC TTAGTAGTAT CTGCTGCTGA CGGTCCAATG CCACAACTC 50
 GTGAACACAT TCTTTTATCA CGTAACGTTG GTGTACCAGC ATTAGTAGTA 100
 TTCTTAAATA AAGTTGACAT GGTGACGAT GAAGAATTAT TAGAATTAGT 150
 TGAAATGGAA GTACGTGACT TATTATCTGA ATACGACTTC CCAGGTGACG 200
 ATGTACCTGT AATCGCTGGT TCAGCATTAA AAGCTTTAGA AGGCGATGCT 250
 CAATACGAAG AAAAAATCTT AGAATTAATG CAAGCAGTTG ATGACTACAT 300
 60 TCCAACCTCA GAACGTGATT CTGACAAACC ATTATGATG CCAGTTGAGG 350

	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
	CGTGGGCAAA	TCAAAGTTGG	TGAAGAAGTT	GAAATCATTG	GTATCCATGA	450
	CACTTCTAAA	ACAACTGTGA	CTGGTGTAGA	AATGTTCCGT	AAATTATTAG	500
	ACTACGCTGA	AGCTGGTGAC	AACATCGGTG	CATTATTACG	TGGTGTGCT	550
5	CGTGAAGACG	TACAACGTGG	TCAAGTATTA	GCTGCTCCAG	GTTCAATCAC	600
	ACCTCACACA	AAATTTAAAG	CAGACGTATA	CGTTTTATCT	AAAGACGAAG	650
	GTGGACGTCA	CACTCCATTC	TTCACAAACT	ATCGTCCACA	ATTCTATTTT	700
	CGTACTACTG	ACGTAACTGG	TGTTGTTAAC	TTACCAGAAG	GTAAGTAAAT	750
	GGTTATGCCT	GGCGACAACG	TTGAAATGAC	AGTAGAATTA	ATCGCTCCTA	800
10	TCGCGATTGA	AGACGGTACT	CGTTTCTCA			829

2) INFORMATION FOR SEQ ID NO: 187

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 705 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus warneri*
 (B) STRAIN: CSG 123

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187

30	CACAAACTCG	TGAACACATT	CTTTTATCAC	GTAACGTTGG	TGTACCAGCT	50
	TTAGTTGTAT	TCTTAAACAA	AGTTGATATG	GTAGACGACG	AAGAATTATT	100
	AGAATTAGTA	GAAATGGAAG	TTCGTGACTT	ATTATCTGAA	TATGACTTCC	150
	CAGGTGACGA	CGTACCTGTA	ATCGCTGGTT	CAGCATTAAG	AGCTTTAGAA	200
	GGCGACGAAA	AATACGAAGA	AAAAATCTTA	GAATTAATGC	AAGCAGTTGA	250
35	TGACTACATT	CCAACTCCAG	AACGTGATTC	TGACAAACCA	TTCATGATGC	300
	CAGTTGAGGA	CGTATTCTCA	ATCACTGGTC	GTGGTACTGT	TGCTACAGGC	350
	CGTGTGGAAC	GTGGTCAAAT	CAAAGTTGGT	GAAGAAGTTG	AAATCATCGG	400
	TTTACATGAC	ACTTCTAAAA	CAACTGTTAC	TGGTGTAGAA	ATGTTCCGTA	450
	AGTTATTAGA	CTACGCTGAA	GCTGGTGACA	ACATCGGTGC	TTTATTACGT	500
40	GGTGTGCTC	GTGAAGACGT	ACAACGTGGT	CAAGTATTAG	CTGCTCCTGG	550
	TTCAATTACA	CCACATACAA	AATTCAAAGC	GGAAGTTTAC	GTTTTATCTA	600
	AAGACGAAGG	TGGACGTCAC	ACTCCATTCT	TCAGTAACTA	CCGCCCACAA	650
	TTCTATTTCC	GTACTACTGA	CGTAACTGGC	GTTGTTCAAT	TACCAGAAGG	700
45	TACTG					705

2) INFORMATION FOR SEQ ID NO: 188

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 678 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus haemolyticus*
 (B) STRAIN: CSG 23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188

	TTTTATCACG	TAACGTTGGT	GTACCAGCAT	TAGTAGTATT	CTTAAACAAA	50
	GTTGACATGG	TTGACGATGA	AGAATTATTA	GAATTAGTTG	AAATGGAAGT	100
5	ACGTGACTTA	TTATCTGAAT	ACGACTTCCC	AGGTGACGAC	GTACCTGTAA	150
	TCGCTGGTTC	AGCTTTAAAA	GCTTTAGAAG	GCGATGCTCA	ATACGAAGAA	200
	AAAATCTTAG	AATTAATGCA	AGCAGTTGAT	GATTACATTC	CAACTCCAGA	250
	ACGTGACTCT	GATAAACCAT	TCATGATGCC	AGTTGAGGAC	GTATTCTCAA	300
10	TCACTGGTCG	TGGTACTGTT	GCTACAGGTC	GTGTTGAACG	TGGTCAAATC	350
	AAAGTTGGTG	AAGAAGTTGA	AATTATTGGT	ATCAAAGAAA	CTTCTAAAAC	400
	AACTGTTACT	GGTGTAGAAA	TGTTCCGTAA	ATTATTAGAC	TACGCTGAAG	450
	CTGGTGACAA	CATCGGTGCT	TTATTACGTG	GTGTTGCTCG	TGAAGATGTA	500
	CAACGTGGTC	AAGTATTAGC	TGCTCCAGGT	TCAATTACAC	CTCACACAAA	550
15	ATTCAAAGCA	GACGTATACG	TTTTATCAAA	AGATGAAGGT	GGACGTCATA	600
	CTCCATTCTT	CACTAACTAT	CGTCCACAAT	TCTATTTCCG	TACTACTGAC	650
	GTAAGTGGTG	TTGTTAACTT	ACCAGAAG			678

20

2) INFORMATION FOR SEQ ID NO: 189

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 668 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus haemolyticus*
 (B) STRAIN: CSG 33

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189

	ACCAGCATT	A	GTAGTATTCT	TAAATAAAGT	TGACATGGTT	GACGATGAAG	50
	AATTATTAGA	A	ATTAGTTGAA	ATGGAAGTAC	GTGACTTATT	ATCTGAATAC	100
	GACTTCCCAG	G	TGACGATGT	ACCTGTAATC	GCTGGTTCAG	CATTAAAAGC	150
40	TTTAGAAGGC	G	ATGCTCAAT	ACGAAGAAAA	AATCTTAGAA	TTAATGCAAG	200
	CAGTTGATGA	C	TACATTCCA	ACTCCAGAAC	GTGATTCTGA	CAAACCATTC	250
	ATGATGCCAG	T	TGAGGACGT	ATTCTCAATC	ACTGGTCGTG	GTACTGTTGC	300
	TACAGGCCGT	G	TGGAACGTG	GTCAAATCAA	AGTTGGTGAA	GAAGTTGAAA	350
	TCATTGGTAT	C	CATGACACT	TCTAAAACAA	CTGTTACTGG	TGTAGAAATG	400
45	TTCCGTAAAT	T	ATTAGACTA	CGCTGAAGCT	GGTGACAACA	TCGGTGCAAT	450
	ATTACGTGGT	G	TTGCTCGTG	AAGACGTACA	ACGTGGTCAA	GTATTAGCTG	500
	CTCCAGGTTT	A	ATCACACCT	CACACAAAAT	TTAAAGCAGA	CGTATACGTT	550
	TTATCTAAAG	A	CGAAGGTGG	ACGTCAACT	CCATTCTTCA	CAAACTATCG	600
	TCCACAATTC	T	ATTTCGGTA	CTACTGACGT	AACTGGTGTT	GTTAACTTAC	650
50	CAGAAGGTAC	T	GAAATGG				668

55

2) INFORMATION FOR SEQ ID NO: 190

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 593 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Staphylococcus haemolyticus*
(B) STRAIN: CSG 8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190

10	AAAGTTGACA	TGGTTGACGA	TGAAGAATTA	TTAGAATTAG	TTGAAATGGA	50
	AGTACGTGAC	TTATTATCTG	AATACGACTT	CCCAGGTGAC	GATGTACCTG	100
	TAATCGCTGG	TTCAGCATT	AAAGCTTTAG	AAGGCGATGC	TCAATACGAA	150
	GAAAAAATCT	TAGAATTAAT	GCAAGCAGTT	GATGATTACA	TTCCAAGTCC	200
	AGAACGTGAT	TCTGACAAAC	CATTCTATGAT	GCCAGTTGAG	GACGTATTCT	250
15	CAATCACTGG	TCGTGGTACT	GTTGCTACAG	GCCGTGTTGA	ACGTGGTCAA	300
	ATCAAAGTTG	GTGAAGAAAGT	TGAAATCATT	GGTATCCATG	ACACTTCTAA	350
	AACAAGTGT	ACTGGTGTAG	AAATGTTCCG	TAAATTATTA	GACTACGCTG	400
	AAGCTGGTGA	CAACATTGGT	GCATTATTAC	GTGGTGTTC	TCGTGAAGAC	450
	GTACAACGTG	GTCAAGTATT	AGCTGCTCCA	GGTTCAATCA	CACCTCACAC	500
20	AAAATTTAAA	GCAGACGTAT	ACGTTTTATC	TAAAGACGAA	GGTGGACGTC	550
	ACACTCCATT	CTTCACAAAC	TATCGTCCAC	AATTCTATTT	CCG	593

25 2) INFORMATION FOR SEQ ID NO: 191

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 828 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus hominis* subsp. *hominis*
(B) STRAIN: ATCC 27844

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191

40	CGGCGCTATC	TTAGTAGTAT	CTGCTGCTGA	TGGTCCAATG	CCACAAACTC	50
	GTGAACACAT	TCTTTTATCA	CGTAACGTTG	GTGTACCAGC	ATTAGTAGTA	100
	TTCTTAAACA	AAGTTGACAT	GGTTGACGAT	GAAGAATTAT	TAGAATTAGT	150
	TGAAATGGAA	GTACGTGACT	TATTATCTGA	ATACGACTTC	CCAGGTGACG	200
45	ACGTACCTGT	AATCGCTGGT	TCAGCTTTAA	AAGCTTTAGA	AGGCGATGCT	250
	CAATACGAAG	AAAAAATCTT	AGAATTAATG	CAAGCAGTTG	ATGATTATAT	300
	TCCAAGTCCA	GAACGTGACT	CTGATAAACC	ATTCATGATG	CCAGTTGAGG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
	CGTGGTCAAA	TCAAAGTTGG	TGAAGAAGTT	GAAATTATTG	GTATCAAAGA	450
50	AACTTCTAAA	ACAACTGTTA	CTGGTGTAGA	AATGTTCCGT	AAATTATTAG	500
	ACTACGCTGA	AGCTGGTGAC	AACATCGGTG	CTTTATTACG	TGGTGTGCT	550
	CGTGAAGATG	TACAACGTGG	TCAAGTATTA	GCTGCTCCAG	GTTCAATTAC	600
	ACCTCACACA	AAATTCAAAG	CAGACGTATA	CGTTTTATCA	AAAGATGAAG	650
	GTGGACGTCA	TACTCCATTC	TTCTCTAACT	ATCGTCCACA	ATTCTATTTT	700
55	CGTACTACTG	ACGTAACTGG	TGTTGTTAAC	TTACCAGAAG	GTAAGTAAAT	750
	GGTAATGCCT	GGTGACAACG	TTGAAATGAC	AGTAGAATTA	ATCGCTCCTA	800
	TCGCGATTGA	AGACGGTACT	CGTTTCTC			828

60

2) INFORMATION FOR SEQ ID NO: 192

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus warneri*
 (B) STRAIN: ATCC 35982

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192

```

ATGGTCCAAT GCCACAAACT CGTGAACACA TTCTTTTATC ACGTAACGTT      50
GGTGTACCAG CTTTAGTTGT ATTCTTAAAC AAAGTTGATA TGGTAGACGA      100
CGAAGAATTA TTAGAATTAG TAGAAATGGA AGTTCGTGAC TTATTATCTG      150
AATATGACTT CCCAGGTGAC GACGTACCTG TAATCGCTGG TTCAGCATTG      200
AAAGCTTTAG AAGGCGACGA AAAATACGAA GAAAAAATCT TAGAATTAAT      250
GCAAGCAGTT GATGACTACA TTCCAACCTCC AGAACGTGAT TCTGACAAAC      300
CATTGATGAT GCCAGTTGAG GACGTATTCT CAATCACTGG TCGTGGTACT      350
GTTGCTACAG GCCGTGTTGA ACGTGGTCAA ATCAAAGTTG GTGAAGAAGT      400
TGAAATCATC GGTTTACATG ACACTTCTAA AACAACTGTT ACTGGTGTAG      450
AAATGTTCCG TAAGTTATTA GACTACGCTG AAGCTGGTGA CAACATCGGT      500
GCTTTATTAC GTGGTGTGTC TCGTGAAGAC GTACAACGTG GTCAAGTATT      550
AGCTGCTCCT GGTTC AATTA CACCACATAC AAAATTCAA GCGGAAGTTT      600
ACGTTTTATC TAAAGACGAA

```

2) INFORMATION FOR SEQ ID NO: 193

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 692 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus hominis*
 (B) STRAIN: CSG 170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193

```

CCAGCATTAG TAGTATTCTT AAACAAAGTT GACATGGTTG ACGATGAAGA      50
ATTATTAGAA TTAGTTGAAA TGGAAGTACG TGACTTATTA TCTGAATACG      100
ACTTCCCAGG TGACGACGTA CCTGTAATCG CTGGTTCAGC TTTAAAAGCT      150
TTAGAAGGCG ATGCTCAATA CGAAGAAAAA ATCTTAGAAT TAATGCAAGC      200
AGTTGATGAT TATATTCCAA CTCCAGAACG TGACTCTGAT AAACCATTCG      250
TGATGCCAGT TGAGGACGTA TTCTCAATCA CTGGTCGTGG TACTGTTGCT      300
ACAGGCCGTG TTGAACGTGG TCAAATCAAA GTTGGTGAAG AAGTTGAAAT      350
TATTGGTATC AAAGAACTT CTAAAACAAC TGTTACTGGT GTAGAAATGT      400
TCCGTAAATT ATTAGACTAC GCTGAAGCTG GTGACAACAT CCGTGCTTTA      450
TTACGTGGTG TTGCTCGTGA AGATGTACAA CGTGGTCAAG TATTAGCTGC      500
TCCAGGTTCA ATTACACCTC ACACAAAATT CAAAGCAGAC GTATACGTTT      550
TATCAAAAGA TGAAGGTGGA CGTCATACTC CATTCTTCTC TAACTATCGT      600

```

CCACAATTCT ATTTCCGTAC TACTGACGTA ACTGGTGTTG TTAACCTACC 650
AGAAGGTACT GAAATGGTAA TGCCTGGTGA CAACGTTGAA AT 692

5

2) INFORMATION FOR SEQ ID NO: 194

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 684 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus hominis*
(B) STRAIN: CSG 36

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194

CATTCTTTTA TCACGTAACG TTGGTGTACC AGCATTAGTA GTATTCTTAA 50
ACAAAGTTGA CATGGTTGAC GATGAAGAAT TATTAGAATT AGTTGAAATG 100
GAAGTACGTG ACTTATTATC TGAATACGAC TTCCCAGGTG ACGACGTACC 150
25 TGTAATCGCT GGTTCAGCTT TAAAAGCTTT AGAAGGCGAT GCTCAATACG 200
AAGAAAAAAT CTTAGAATTA ATGCAAGCAG TTGATGATTA TATTCCAAC 250
CCAGAACGTG ACTCTGATAA ACCATTTCATG ATGCCAGTTG AGGACGTATT 300
CTCAATCACT GGTTCGTGGTA CTGTTGCTAC AGGCCGTGTT GAACGTGGTC 350
AAATCAAAGT TGGTGAAGAA GTTGAAATTA TTGGTATCAA AGAACTTCT 400
30 AAAACAAC 450
TGAAGCTGGT GACAACATCG GTGCTTTATT ACGTGGTGT GCTCGTGAAG 500
ATGTACAACG TGGTCAAGTA TTAGCTGCTC CAGGTTCAAT TACACCTCAC 550
ACAAAATTCA AAGCAGACGT ATACGTTTTA TCAAAAGATG AAGGTGGACG 600
TCATACTCCA TTCTTCTCTA ACTATCGTCC ACAATTCTAT TTCCGTACTA 650
35 CTGACGTAAC TGGTGTGTTT AACTTACCAG AAGG 684

2) INFORMATION FOR SEQ ID NO: 195

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 685 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
45 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Staphylococcus hominis*
(B) STRAIN: CSG 6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195

55 ACCAGCATTG TAGTATTCT TAAACAAAGT TGACATGGTT GACGATGAAG 50
AATTATTAGA ATTAGTTGAA ATGGAAGTAC GTGACTTATT ATCTGAATAC 100
GACTTCCAG GTGACGACGT ACCTGTAATC GCTGGTTCAG CTTTAAAAGC 150
TTTAGAAGGC GATGCTCAAT ACGAAGAAAA AATCTTAGAA TTAATGCAAG 200
CAGTTGATGA TTACATTCCA ACTCCAGAAC GTGACTCTGA TAAACCATTC 250
60 ATGATGCCAG TTGAGGACGT ATTCTCAATC ACTGGTCGTG GTACTGTTGC 300

TACAGGCCGT GTTGAACGTG GTCAAATCAA AGTTGGTGAA GAAGTTGAAA 350
 TTATTGGTAT CAAAGAAACT TCTAAAACAA CTGTTACTGG TGTAGAAATG 400
 TTCCGTAAAT TATTAGACTA CGCTGAAGCT GGTGACAACA TCGGTGCTTT 450
 ATTACGTGGT GTTGCTCGTG AAGATGTACA ACGTGGTCAA GTATTAGCTG 500
 5 CTCCAGGTTT AATTACACCT CACACAAAAT TCAAAGCAGA CGTATACGTT 550
 TTATCAAAAG ATGAAGGTGG ACGTCATACT CCATTCTTCA CTAACATATCG 600
 TCCACAATTC TATTTCCGTA CTACTGACGT AACTGGTGTT GTTAACCTTAC 650
 CAGAAGGTAC TGAAATGGTA ATGCCTGGCG ACAAC 685

10

2) INFORMATION FOR SEQ ID NO: 196

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 611 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus hominis*
 (B) STRAIN: CSG 62

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196

GACTTATTAT CTGAATACGA CTTCCCAGGT GACGACGTAC CTGTAATCGC 50
 TGGTTCAGCT TTAAAAGCTT TAGAAGGCGA TGCTCAATAC GAAGAAAAAA 100
 30 TCTTAGAATT AATGCAAGCA GTTGATGATT ACATTCCAAC TCCAGAACGT 150
 GACTCTGATA AACCATTCTAT GATGCCAGTT GAGGACGTAT TCTCAATCAC 200
 TGGTCGTGGT ACTGTTGCTA CAGGCCGTGT TGAACGTGGT CAAATCAAAG 250
 TTGGTGAAGA AGTTGAAATT ATTGGTATCA AAGATACTTC TAAAACAACT 300
 GTTACTGGTG TAGAAATGTT CCGTAAATTA TTAGACTACG CTGAAGCTGG 350
 35 TGACAACATC GGTGCTTTAT TACGTGGTGT TGCTCGTGAA GATGTACAAC 400
 GTGGTCAAGT ATTAGCTGCT CCAGGTTCAT TCACACCTCA CACAAAATTC 450
 AAAGCAGACG TATATGTTTT ATCAAAAGAT GAAGGTGGAC GTCATACTCC 500
 ATTCTTCACT AACTATCGTC CACAATTCTA TTTCCGTACT ACTGACGTAA 550
 CTGGTGTGTT TAACTTACCA GAAGGTACTG AAATGGTAAT GCCTGGCGAC 600
 40 AACGTTGAAA T 611

2) INFORMATION FOR SEQ ID NO: 197

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: *Staphylococcus lugdunensis*
 (B) STRAIN: ATCC 43809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197

60 CGGCGGTATC TTAGTAGTTT CTGCTGCAGA TGGTCCAATG CCACAACTC 50

	GTGAACACAT	TCTTTTATCA	CGTAACGTTG	GTGTGCCAGC	ATTAGTAGTA	100
	TTCTTAAACA	AAGTTGACAT	GGTTGACGAT	GAAGAATTAT	TAGAATTAGT	150
	AGAAATGGAA	GTTTCGTGATT	TATTAACCTGA	ATATGACTTC	CCAGGTGACG	200
	ATGTGCCTGT	AATCGCTGGT	TCAGCATTA	AAGCTTTAGA	AGGCGACGAA	250
5	AAATACGAAG	CTAAAATCTT	AGAATTAATG	GATGCAGTTG	ATAACTACAT	300
	TCCAACCTCA	GAACGTGACT	CTGACAAACC	ATTTCATGATG	CCAGTTGAGG	350
	ACGTATTCTC	AATCACTGGT	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400
	CGTGGTCAAA	TCAAAGTCGG	TGAAGAAAGT	GAAATTATTG	GTATCCACGA	450
	TACTACTAAA	ACAACTGTTA	CTGGTGTTAGA	AATGTTCCGT	AAATTATTAG	500
10	ACTACGCTGA	AGCTGGTGAC	AACATCGGTG	CGTTATTACG	TGGTGTTGCT	550
	CGTGAAGATG	TACAACGTGG	ACAAGTATTA	GCTGCTCCAG	GTTCAATTAC	600
	ACCTCACACT	AAATTTAAAG	CTGACGTATA	TGTTTTATCT	AAAGATGAAG	650
	GTGGACGTCA	TACACCATT	TTCTCAAAC	ACCGCCACA	ATTCTATTTC	700
	CGTACTACAG	ACGTAACCTG	TGTTGTTAAC	TTACCAGAAG	GTACAGAAAT	750
15	GTTTATGCCT	GGCGACAACG	TTGAAATGAC	AGTTGAATTA	ATCGCTCCAA	800
	TCGCTATCGA	AGACGGAAC	CGTTTCTC			828

20 2) INFORMATION FOR SEQ ID NO: 198

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 690 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*
 (B) STRAIN: ATCC 35552

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198

35	AGTAGTATCT	GCTGCTGATG	GCCCAATGCC	ACAAACTCGT	GAACACATTC	50
	TTTTATCACG	TAACGTTGGT	GTTCCAGCAT	TAGTTGTATT	CTTAAACAAA	100
	GTTGACATGG	TTGACGATGA	AGAATTATTA	GAATTAGTAG	AAATGGAAGT	150
	TCGTGACTTA	TTAAGCGAAT	ATGACTTCCC	AGGTGACGAT	GTACCTGTAA	200
40	TCTCTGGTTC	TGCATTAAAA	GCTTTAGAAG	GCGACGCTGA	CTATGAGCAA	250
	AAAATCTTAG	ACTTAATGCA	AGCTGTTGAT	GACTTCATTC	CAACACCAGA	300
	ACGTGATTCT	GACAAACCAT	TCATGATGCC	AGTTGAGGAC	GTATTCTCAA	350
	TCACTGGTCG	TGGTACTGTT	GCTACAGGCC	GTGTTGAACG	TGGTCAAATC	400
	AAAGTCGGTG	AAGAAATCGA	AATCATCGGT	ATGCAAGAAG	AATCAAGCAA	450
45	AACAACCTGTT	ACTGGTGTTAG	AAATGTTCCG	TAAATTATTA	GACTACGCTG	500
	AAGCTGGTGA	CAACATTGGT	GCATTATTAC	GTGGTGTTTC	ACGTGATGAC	550
	GTACAACGTG	GTCAAGTTT	AGCTGCTCCT	GGTACTATTA	CACCACATAC	600
	AAAATTCAAA	GCGGATGTTT	ACGTTTTATC	TAAAGATGAA	GGTGGTCGTC	650
50	ATACACCATT	CTTCACTAAC	TACCGCCAC	AATTCTATTT		690

2) INFORMATION FOR SEQ ID NO: 199

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 723 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus saprophyticus*

(B) STRAIN: CSG 83

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199

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10 GCATTAGTTG TATTCTTAAA CAAAGTTGAC ATGGTTGACG ATGAAGAATT 50
   ATTAGAATTA GTAGAAATGG AAGTTCGTGA TTTATTAAGC GAATATGACT 100
   TCCCAGGTGA CGATGTACCT GTAATCTCTG GTTCTGCATT AAAAGCTTTA 150
   GAAGGCGACG CTGACTATGA GCAAAAAATC TTAGACTTAA TGCAAGCTGT 200
   TGATGACTTC ATTCCAACAC CAGAACGTGA TTCTGACAAA CCATTTCATGA 250
   TGCCAGTTGA GGACGTATTG TCAATCACTG GTCGTGGTAC TGTTGCTACA 300
   GGCCGTGTTG AACGTGGTCA AATCAAAGTC GGTGAAGAAA TCGAAATCAT 350
   CGGTATGCAA GAAGAATCAA GCAAAACAAC TGTTACTGGT GTAGAAATGT 400
   TCCGTAAATT ATTAGACTAC GCTGAAGCTG GTGACAACAT TGGTGCTTAA 450
   TTACGTGGTG TTTACAGTGA TGACGTACAA CAAAGCGGAT GTTTACGTTT 500
   TCCTGGTACT ATTACACCAC ATACAAAATT CAAAGCGGAT GTTTACGTTT 550
   TATCTAAAGA TGAAGGTGGT CGTCATACAC CATTCTTCAC TAACTACCGC 600
   CCACAATTCT ATTTCCGTAC TACTGACGTA ACTGGTGTTG TTAATTACC 650
   AGAAGGTACT GAAATGGTTA TGCCTGGCGA TAACGTTGAA ATGGATGTTG 700
   AATTAATTTC TCCAATCGCT ATT 723

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25

2) INFORMATION FOR SEQ ID NO: 200

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 697 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus saprophyticus*

(B) STRAIN: CSSa 18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200

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45 CGTTGGTGTT CCAGCATTAG TTGTATTCTT AAACAAAGTT GACATGGTTG 50
   ACGATGAAGA ATTATTAGAA TTAGTAGAAA TGGAAGTTCG TGACTTATTA 100
   AGCGAATATG ACTTCCCAGG TGACGATGTA CCTGTAATCT CTGGTTCCTGC 150
   ATTAAAAGCT TTAGAAGGCG ACGCTGACTA TGAGCAAAAA ATCTTAGACT 200
   TAATGCAAGC TGTGATGAC TTCATTCCAA CACCAGAACG TGATTCTGAC 250
   AAACCATTC A TGATGCCAGT TGAGGACGTA TTCTCAATCA CTGGTCGTGG 300
   TACTGTTGCT ACAGGCCGTG TTGAACGTGG TCAAATCAAA GTCGGTGAAG 350
   AAATCGAAAT CATCGGTATG CAAGAAGAAT CAAGCAAAAC AACTGTTACT 400
   GGTGTAGAAA TGTTCGGTAA ATTATTAGAC TACGCTGAAG CTGGTGACAA 450
   CATTGGTGCA TTATTACGTG GTGTTTCACG TGATGACGTA CAACGTGGTC 500
   AAGTTTTAGC TGCTCCTGGT ACTATTACAC CACATACAAA ATTCAAAGCG 550
   GATGTTTACG TTTTATCTAA AGATGAAGGT GGTCGTCATA CACCATTCTT 600
   CACTAACTAC CGCCACAAT TCTATTTCCG TACTACTGAC GTAACGGTG 650
   TTGTAACTT ACCAGAAGGT ACTGAAATGG TTATGCCTGG CGATAAC 697

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2) INFORMATION FOR SEQ ID NO: 201

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus sciuri* subsp. *sciuri*
 (B) STRAIN: ATCC 29060

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201

```

CGGCGGTATC TTAGTAGTAT CTGCTGCTGA CGGTCCAATG CCTCAAACCTC   50
GTGAGCACAT TCTTTTATCA CGTAACGTAG GTGTTCCTGC ATTAGTAGTA   100
TTCTTAAACA AAGTTGACAT GGTGACGAT GAAGAATTAT TAGAATTAGT   150
TGAAATGGAA GTTCGTGACT TATTATCTGA ATATGACTTC CCAGGCGACG   200
ACGTTCTGT AATTGCTGGT TCAGCATTA AAGCATTAGA AGGCGACGAA   250
GCTTACGAAG ACAAATCAT GGAATTAATG GATGCTGTTG ATACATTCAT   300
CCCAACTCCA GAACGTGACT CTGACAAACC ATTCATGATG CCAGTTGAGG   350
ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTGAA   400
CGTGGTCAAA TCACTGTTGG TGAAGAAGTT GAAATCATCG GTTTAACTGA   450
AGAATCTTCT AAAACAACCTG TAACTGGTGT TGAAATGTTC CGTAAATTAT   500
TAGACTTCGC TGAAGCTGGA GATAACATCG GTGCATTATT ACGTGGTGT   550
GCTCGTGAAG ACGTTAACCG TGGTCAAGTA TTAGCTAAAC CAGGTTCAAT   600
CACACCTCAC ACTAAATTCA AAGCTGAAGT TTATGTATTA TCTAAAGACG   650
AAGGTGGACG TCATACTCCA TTCTTCACAA ACTACCGCCC ACAATTCTAT   700
TTCCGTACTA CTGACGTAAC TGGTGTAGTT AACTTACCAG AAGGTACTGA   750
AATGGTTATG CCTGGCGACA ACGTTGAAAT GGACGTTGAA TTAATTTAC   800
CAATCGCTAT TGAAGACGGT ATCGTTTCTC AATCA   835

```

2) INFORMATION FOR SEQ ID NO: 202

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus warneri*
 (B) STRAIN: ATCC 27836

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202

```

CGGCGGTATC TTAGTTGTAT CTGCAGCTGA TGGTCCAATG CCACAAACTC   50
GTGAACACAT TCTTTTATCA CGTAACGTTG GTGTACCAGC TTTAGTTGTA   100
TTCTTAAACA AAGTTGATAT GGTAGACGAC GAAGAATTAT TAGAATTAGT   150
AGAAATGGAA GTTCGTGACT TATTATCTGA ATATGACTTC CCAGGTGACG   200
ACGTACCTGT AATCGCTGGT TCAGCATTA AAGCTTTAGA AGGCGACGAA   250
AAATACGAAG AAAAAATCTT AGAATTAATG CAAGCAGTTG ATGACTACAT   300
TCCAACCTCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG   350
ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTGAA   400
CGTGGTCAAA TCAAAGTTGG TGAAGAAGTT GAAATCATCG GTTTACATGA   450

```

CACTTCTAAA ACAACTGTTA CTGGTGTAGA AATGTTCCGT AAGTTATTAG 500
 ACTACGCTGA AGCTGGTGAC AACATCGGTG CTTTATTACG TGGTGTGCT 550
 CGTGAAGACG TACAACGTGG TCAAGTATTA GCTGCTCCTG GTTCAATTAC 600
 ACCACATACA AAATTCAAAG CGGAAGTTTA CGTTTTATCT AAAGACGAAG 650
 5 GTGGACGTCA CACTCCATTC TTCAGTAACT ACCGCCCACA ATTCTATTTC 700
 CGTACTACTG ACGTAACTGG CGTTGTTCAA TTACCAGAAG GTACTGAAAT 750
 GGTATGCCT GGTGATAACG TTGAAATGAC AGTAGAATTA ATCGCTCCTA 800
 TCGCGATTGA AGACGGTACT CGTTTCTCAA C 831

10

2) INFORMATION FOR SEQ ID NO: 203

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus warneri*
 (B) STRAIN: CSG 50

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203

CGGCGGTATC TTAGTTGTAT CTGCAGCTGA TGGTCCAATG CCACAAACTC 50
 GTGAACACAT TCTTTTATCA CGTAACGTTG GTGTACCAGC TTTAGTTGTA 100
 30 TTCTTAAACA AAGTTGATAT GGTAGACGAC GAAGAATTAT TAGAATTAGT 150
 AGAAATGGAA GTTCGTGACT TATTATCTGA ATATGACTTC CCAGGTGACG 200
 ACGTACCTGT AATCGCTGGT TCAGCATTAA AAGCTTTAGA AGGCGACGAA 250
 AAATACGAAG AAAAAATCTT AGAATTAATG CAAGCAGTTG ATGACTACAT 300
 TCCAACCTCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG 350
 35 ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTGAA 400
 CGTGGTCAAA TCAAAGTTGG TGAAGAAGTT GAAATCATCG GTTACATGA 450
 CACTTCTAAA ACAACTGTTA CTGGTGTAGA AATGTTCCGT AAGTTATTAG 500
 ACTACGCTGA AGCTGGTGAC AACATCGGTG CTTTATTACG TGGTGTGCT 550
 CGTGAAGACG TACAACGTGG TCAAGTATTA GCTGCTCCTG GTTCAATTAC 600
 40 ACCACATACA AAATTCAAAG CGGAAGTTTA CGTTTTATCT AAAGACGAAG 650
 GTGGACGTCA CACTCCATTC TTCAGTAACT ACCGCCCACA ATTCTATTTC 700
 CGTACTACTG ACGTAACTGG CGTTGTTCAA TTACCAGAAG GTACTGAAAT 750
 GGTATGCCT GGTGATAACG TTGAAATGAC AGTAGAATTA ATCGCTCCTA 800
 TCGCGATTGA AGACGGTACT CGTTTCTCA 829

45

2) INFORMATION FOR SEQ ID NO: 204

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 839 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 60 (A) ORGANISM: *Bifidobacterium longum*
 (B) STRAIN: ATCC 15707

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204

5	TGGCGCTATC	CTCGTTGTGG	CCGCCACCGA	CGGCCCGATG	GCCCAGACTC	50
	GCGAGCACGT	GCTGCTCGCC	CGTCAGGTTG	GCGTTCCGAA	GATCCTCGTC	100
	GCCCTGAACA	AGTGCGACAT	GGTCGACGAT	GAAGAGCTCA	TCGAGCTCGT	150
	CGAAGAAGAG	GTCCGCGACC	TCCTCGACGA	GAACGGCTTC	GACCGTGAAT	200
	GCCC GGTCAT	CCACACCTCC	GCTTACGGTG	CTCTGCACGA	CGACGCTCCG	250
	GACCACGAGA	AGTGGGTCCA	GTCCGTTAAG	GACCTCATGG	ACGCTGTCGA	300
10	CGACTACATC	CCGACCCCGG	TTCACGACCT	GGACAAGCCG	TTCCTGATGC	350
	CGATCGAGGA	CGTCTTCACC	ATCTCCGGCC	GTGGTACCGT	TGTCACCGGT	400
	CGTGTGAGC	GTGGCCAGCT	GGCCGTCAAC	ACCCCGGTCT	AGATCGTTGG	450
	TATCCGTCCG	ACCCAGCAGA	CCACCGTCAC	CTCCATCGAG	ACCTTCCACA	500
	AGACCATGGA	CGCCTGCGAG	GCTGGCGACA	ACACCGGTCT	GCTTCTGCGT	550
15	GGTCTCGGCC	GTGACGATGT	CGAGCGTGGC	CAGGTTGTGG	CCAAGCCGGG	600
	CTCCGTCACC	CCGCACACCA	AGTTCGAGGG	CGAAGTCTAC	GTGCTGACCA	650
	AGGACGAAGG	CGGCCGTCAC	TCGCCGTTCT	TCTCCAATA	CCGTCCGCAG	700
	TTCTACTTCC	GCACCACCGA	CGTCACCGGC	GTCATCGAGC	TGCCGGAAGG	750
	CGTCGAGATG	GTTGAGCCGG	GCGACCACGC	TACCTTCACC	GTTGAGCTGA	800
20	TTCAGCCCAT	CGCTATGGAG	GAAGGCCTGA	CCTTCGCTG		839

2) INFORMATION FOR SEQ ID NO: 205

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 754 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Stenotrophomonas maltophilia*

(B) STRAIN: CDC F3338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205

40	CGGCGCGATC	CTGGTGTGCT	CGGCCGCTGA	CGGCCCGATG	CCGCAGACCC	50
	GTGAGCACAT	CCTGCTGTCT	CGCCAGGTCG	GCGTGCCGTA	CATCGTCGTG	100
	TTCCTGAACA	AGGCCGACAT	GGTCGACGAC	GCCGAGCTGC	TCGAGCTGGT	150
	CGAGATGGAA	GTGCGCGAAC	TGCTGAGCAA	GTACGAGTTC	CCGGGCGACG	200
	ACACCCCGAT	CATCGCCGGT	TCGGCCCGCC	TGGCGCTGGA	AGGCGACCAG	250
45	AGCGACATCG	GCGTGCCGGC	CATCCTGAAG	CTGGTCGACG	CGCTGGACAG	300
	CTGGATTCCG	GAGCCGGAGC	GTGCGATCGA	CAAGCCGTTC	CTGATGCCGG	350
	TGGAAGACGT	GTTCTCGATC	TCGGGCCGCG	GCACCGTGGT	GACCGGTCTG	400
	ATCGAGCGCG	GCGTGATCAA	GGTTGGCGAC	GAAATCGAAA	TCGTCGGCAT	450
	CCGTCCGGTG	CAGAAGACCA	CCGTGACCGG	CGTTGAAATG	TTCCGCAAGC	500
50	TGCTGGACCA	GGGTCAGGCA	GGCGACAACG	CTGGCCCTGCT	GCTGCGCGGC	550
	ACCAAGCGTG	ATGACGTCGA	GCGTGGCCAG	GTGCTGGCCA	AGCCGGGCAC	600
	GATCAAGCCG	CACACCAAGT	TCGAAGGCGA	AGTGACGTC	CTGTCGAAGG	650
	ACGAGGGCGG	CCGCCACACC	CCGTTCTTCA	ACGGCTACCG	TCCGCAGTTC	700
	TACTTCCGCA	CCACCGACAT	CACCGGCGCC	GCTGCACTGC	CGGAAGGCGT	750
55	CGAA					754

2) INFORMATION FOR SEQ ID NO: 206

60

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus acidominimus*
 (B) STRAIN: ATCC 51726

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206

15	TGGTGCTATC	CTTGTAGTAG	CTTCAACTGA	CGGACCAATG	CCACAAACTC	50
	GTGAGCACAT	CCTTCTTTCA	CGTCAAGTTG	GTGTTAAAAA	CCTTATCGTT	100
	TTCATGAACA	AAGTTGACCT	TGTTGATGAT	GAAGAATTGC	TTGAATTGGT	150
	TGAAATGGAA	ATCCGTGACC	TTCTTTCAGA	ATACGATTTC	CCAGGTGATG	200
	ATCTTCCAGT	TGTTCAAGGT	TCAGCTCTTA	AAGCGCTTGA	AGGTGATTCA	250
20	GCACAAGAAG	ATGTTATCAT	GGAAATTGATG	TCAATCGTTG	ACACATACAT	300
	TCCAGAACCA	GAACGTGATA	CTGACAAACC	ATTGCTTCTT	CCAGTCGAGG	350
	ATGTATTCTC	AATCACTGGA	CGTGGTACTG	TTGCTTCAGG	ACGTATCGAC	400
	CGTGGTACTG	TTAAAGTTAA	TGACGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	CGAAATCTCT	AAAGCAGTTG	TTACTGGTGT	TGAAATGTTC	CGTAAACAAC	500
25	TTGACGAAGG	TCTTGCTGGA	GATAACGTTG	GTGTTCTTCT	TCGTGGTGTA	550
	CAACGTGATG	AAATCGAACG	TGGTCAAGTT	CTTGCTAAAC	CAGGTTCAAT	600
	CAACCCACAC	ACTAAATTCA	AAGGTGAAGT	TTACGTTCTT	TCTAAAGAAG	650
	AAGGTGGACG	TCACACTCCA	TTCTTCGATA	ACTACCGTCC	TCAGTTCTAC	700
	TTCCGTACAA	CTGACGTAAC	TGGTTCAATC	AAATTGCCAG	AAGGTACTGA	750
30	AATGGTAATG	CCTGGTGATA	ACGTAACAT	CGAAGTTGAG	TTGATCCACC	800
	CAATCGCCGT	TGAACAAGGT	ACTACTTTCT	CTATC		835

35 2) INFORMATION FOR SEQ ID NO: 207

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus agalactiae*
 (B) STRAIN: ATCC 12403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207

50	CTATCCTTGT	AGTTGCTTCA	ACTGATGGAC	CAATGCCACA	AACTCGTGAG	50
	CACATCCTTC	TTTCACGTCA	AGTTGGTGTT	AAACACCTTA	TCGTATTCAT	100
	GAACAAAGTT	GACCTTGTTG	ATGATGAAGA	ATTGCTTGAA	TTGGTTGAAA	150
	TGGAAATTCTG	TGACCTTCTT	TCAGAATACG	ACTTCCCAGG	TGATGACCTT	200
55	CCAGTTATCC	AAGGTTGAGC	TCTTAAAGCA	CTTGAAGGCG	ACGAAAAATA	250
	CGAAGACATC	ATCATGGAAT	TGATGAGCAC	TGTTGATGAG	TACATTCCAG	300
	AACCAGAACG	TGATACTGAC	AAACCTTTAC	TTCTTCCAGT	TGAAGATGTA	350
	TTCTCAATCA	CTGGACGTGG	TACAGTTGCT	TCAGGACGTA	TCGACCGTGG	400
	TACTGTTTCGT	GTCAACGACG	AAGTTGAAAT	CGTTGGTATT	AAAGAAGATA	450
60	TCCAAAAAGC	AGTTGTTACT	GGTGTGAAA	TGTTCCGTAA	ACAACCTTGAC	500

GAAGGTCTTG CAGGGGACAA CGTTGGTGTT CTTCTTCGTG GTGTTCAACG 550
 TGATGAAATC GAACGTGGTC AAGTTCTTGC TAAACCAGGT TCAATCAACC 600
 CACACACTAA ATTTAAAGGT GAAGTTTACA TCCTTTCTAA AGAAGAAGGT 650
 GGACGTCATA CTCCATTCTT CAACAACACTAC CGTCCACAAT TCTACTTCCG 700
 5 TACAACTGAC GTAACAGGTT CAATCGAACT TCCAGCAGGA ACAGAAATGG 750
 TTATGCCTGG TGATAACGTT ACTATCGAAG TTGAATTGAT TCACCCAATC 800
 GCCGTAGAAC AAGGTACTA 819

10

2) INFORMATION FOR SEQ ID NO: 208

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus agalactiae*
 (B) STRAIN: ATCC 12973

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208

CTATCCTTGT AGTTGCTTCA ACTGATGGAC CAATGCCACA AACTCGTGAG 50
 CACATCCTTC TTTCACGTCA AGTTGGTGTT AAACACCTTA TCGTATTCAT 100
 GAACAAAGTT GACCTTGTTG ATGATGAAGA ATTGCTTGAA TTGGTTGAAA 150
 30 TGGAAATTCG TGACCTTCTT TCAGAATACG ACTTCCCAGG TGATGACCTT 200
 CCAGTTATCC AAGGTTTCAGC TCTTAAAGCA CTTGAAGGCG ATGAAAAATA 250
 CGAAGACATC ATCATGGAAT TGATGAGCAC TGTTGATGAG TACATTCCAG 300
 AACCAGAACG TGATACTGAC AAACCTTTAC TTCTTCCAGT CGAAGATGTA 350
 TTCTCAATCA CTGGACGTGG TACAGTTGCT TCAGGACGTA TCGACCGTGG 400
 35 TACTGTTTCG GTCAACGACG AAGTTGAAAT CGTTGGTATT AAAGAAGATA 450
 TCCAAAAAGC AGTTGTTACT GGTGTTGAAA TGTTCCGTAA ACAACTTGAC 500
 GAAGGTCTTG CAGGGGACAA CGTTGGTGTT CTTCTTCGTG GTGTTCAACG 550
 TGATGAAATC GAACGTGGTC AAGTTCTTGC TAAACCAGGT TCAATCAACC 600
 CACACACTAA ATTTAAAGGT GAAGTTTACA TCCTTTCTAA AGAAGAAGGT 650
 40 GGACGTCATA CTCCATTCTT CAACAACACTAC CGTCCACAAT TCTACTTCCG 700
 TACAACTGAC GTAACAGGTT CAATCGAACT TCCAGCAGGA ACAGAAATGG 750
 TTATGCCTGG TGATAACGTT ACTATCGAAG TTGAATTGAT TCACCCAATC 800
 GCCGTAGAAC AAGGTACTA 819

45

2) INFORMATION FOR SEQ ID NO: 209

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus agalactiae*
 (B) STRAIN: ATCC 13813

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209

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5  AGCTATCCTT GTAGTTGCTT CAACTGATGG ACCAATGCCA CAAACTCGTG      50
   AGCACATCCT TCTTTCACGT CAAGTTGGTG TTAAACACCT TATCGTATTC      100
   ATGAACAAAG TTGACCTTGT TGATGATGAA GAATTGCTTG AATTGGTTGA      150
   AATGGAAATT CGTGACCTTC TTTCAGAATA CGACTTCCCA GGTGATGACC      200
   TTCCAGTTAT CCAAGGTTCA GCTCTTAAAG CACTTGAAGG CGATGAAAAA      250
   TACGAAGACA TCATCATGGA ATTGATGAGC ACTGTTGATG AGTACATTCC      300
   AGAACCAGAA CGTGATACTG ACAAACCTTT ACTTCTTCCA GTCGAAGATG      350
  10 TATTCTCAAT CACTGGACGT GGTACAGTTT CTTCAGGACG TATCGACCGT      400
   GGTACTGTTC GTGTCAACGA CGAAGTTGAA ATCGTTGGTA TTAAAGAAGA      450
   TATCCAAAAA GCAGTTGTTA CTGGTGTGTA AATGTTCCGT AAACAACCTG      500
   ACGAAGGTCT TGCAGGGGAC AACGTTGGTG TTCTTCTTCG TGGTGTTCOA      550
   CGTGATGAAA TCGAACGTGG TCAAGTTCTT GCTAAACCAG GTTCAATCAA      600
  15 CCCACACACT AAATTTAAAG GTGAAGTTTA CATCCTTTCT AAAGAAGAAG      650
   GTGGACGTCA TACTCCATTC TTCAACAACCT ACCGTCCACA ATTCTACTTC      700
   CGTACAACTG ACGTAACAGG TTCAATCGAA CTTCCAGCAG GAACAGAAAT      750
   GGTATGCCT GGTGATAACG TTACTATCGA AGTTGAATTG ATTCACCCAA      800
   TCGCCGTAGA ACAAGGTACT AC                                     822
20

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2) INFORMATION FOR SEQ ID NO: 210

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25  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 825 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear

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30  (ii) MOLECULE TYPE: Genomic DNA

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      (vi) ORIGINAL SOURCE:

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      (A) ORGANISM: Streptococcus agalactiae
      (B) STRAIN: CDC 1073
35

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210

```

40  CGGAGCTATC CTTGTAGTTG CTTCAACTGA TGGACCAATG CCACAAACTC      50
   GTGAGCACAT CCTTCTTTCA CGTCAAGTTG GTGTTAAACA CCTTATCGTA      100
   TTCATGAACA AAGTTGACCT TGTTGATGAT GAAGAATTGC TTGAATTGGT      150
   TGAAATGGAA ATTCGTGACC TTCTTTCAGA ATACGACTTC CCAGGTGATG      200
   ACCTTCCAGT TATCCAAGGT TCAGCTCTTA AAGCACTTGA AGGCGACGAA      250
   AAATACGAAG ACATCATCAT GGAATTGATG AGCACTGTTG ATGAGTACAT      300
   TCCAGAACCA GAACGTGATA CTGACAAACC TTTACTTCTT CCAGTTGAAG      350
  45 ATGTATTCTC AATCACTGGA CGTGGTACAG TTGCTTCAGG ACGTATCGAC      400
   CGTGGTACTG TTCGTGTCAA CGACGAAGTT GAAATCGTTG GTATTAAAGA      450
   AGATATCCAA AAAGCAGTTG TTAAGTGGTG TGAAATGTTT CGTAAACAAC      500
   TTGACGAAGG TCTTGCAGGG GACAACGTTG GTGTTCTTCT TCGTGGTGTT      550
   CAACGTGATG AAATCGAACG TGGTCAAGTT CTTGCTAAAC CAGGTTCAAT      600
  50 CAACCCACAC ACTAAATTTA AAGGTGAAGT TTACATCCTT TCTAAAGAAG      650
   AAGGTGGACG TCATACTCCA TTCTTCAACA ACTACCGTCC ACAATTCTAC      700
   TTCCGTACAA CTGACGTAAC AGGTTCAATC GAACTTCCAG CAGGAACAGA      750
   AATGGTTATG CCTGGTGATA ACGTTACTAT CGAAGTTGAA TTGATTCAAC      800
  55 CAATCGCCGT AGAACAAGGT ACTAC                                     825

```

2) INFORMATION FOR SEQ ID NO: 211

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus anginosus*
 (B) STRAIN: ATCC 33397

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211

```

15  GGAGCTATCC TTGTAGTAGC TTCAACTGAC GGACCAATGC CTCAAACTCG      50
    TGAACACATC CTTCTTTTCAC GCCAAGTAGG TGTTAAATAC CTTATCGTCT      100
    TCATGAATAA AGTTGACTTG GTTGACGATG AAGAATTGCT TGAATTGGTT      150
    GAAATGGAAA TCCGTGACCT TCTTTCAGAA TACGATTTC CAGGTGATGA      200
    AATCCCAAGTT ATCCAAGGTT CAGCTCTTAA AGCTCTTGAA GGTGATGAAA      250
20  AATATGAAGA CATCATCATG GAATTGATGG ATACTGTTGA TGAATACATT      300
    CCAGAACCAG AACGTGACAC TGACAAACCA TTGCTTCTTC CAGTTGAAGA      350
    TGTATTCTCA ATTACTGGAC GTGGTACTGT TGCTTCAGGA CGTATCGACC      400
    GTGGTACTGT TAAAGTCAAC GACGAAGTTG AAATCGTTGG TATCCGTGAT      450
    GAAATCCAAA AAGCAGTTGT TACTGGTGTT GAAATGTTCC GTAAACAATT      500
25  GGACGAAGGT CTTGCTGGAG ATAACGTAGG GGTTCCTTCTT CGTGGTATCC      550
    AACGTGACGA AATCGAACGT GGACAAGTTC TTGCTAAACC AGGTTCAATT      600
    CATCCACACA CTAAATTCAA AGGTGAAGTT TACATCCTTA CTAAAGAAGA      650
    AGGTGGACGT CATACTCCAT TCTTCAACAA CTACCGTCCT CAATTCTACT      700
    TCCGTACTAC AGACGTTACA GGTTCAATCG AACTTCCTGC AGGTACTGAA      750
30  ATGGTAATGC CTGGTGATAA CGTAACAATC GACGTTGAAT TGATCCACCC      800
    AATTGCCGTA GAACAAGGAA CTACAT

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2) INFORMATION FOR SEQ ID NO: 212

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus bovis*
 (B) STRAIN: ATCC 33317

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212

```

50  TGGTGCTATC CTTGTAGTAG CTTCTACAGA TGGTCCAATG CCACAAACAC      50
    GTGAACACAT CCTTCTTTCA CGTCAAGTTG GTGTTAAACA CCTTATCGTC      100
    TTCATGAACA AAGTTGACCT TGTTGATGAC GAAGAATTGC TTGAATTGGT      150
    TGAAATGGAA ATCCGTGACC TTCTTTCAGA ATATGATTTT CCAGGTGATG      200
55  AAATCCCTGT AATCCAAGGT TCAGCTCTTA AAGCCCTTGA AGGTGACACT      250
    CACTACGAAG ACATCATCAT GGAATTGATG AACACTGTAG ATGAATACAT      300
    TCCAGAACCA AAACGTGATA CTGACAAACC ATTGCTTCTT CCAGTCGAAG      350
    ACGTATTCTC AATCACTGGT CGTGGTACTG TAGCATCAGG ACGTATCGAC      400
    CGTGGTACTG TTAAAGTCAA CGACGAAGTT GAAATCGTTG GTATCCGTGA      450
60  CGACATCCAA AAAGCTGTTG TTACTGGTGT TGAAATGTTC CGTAAACAAC      500

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TTGATGAAGG TATCGCAGGG GATAACGTTG GTGTTCTTCT TCGTGGTATC 550
 CAACGTGATG AAATCGAACG TGGTCAAGTT CTTGCTAAAC CAGGTTCAAT 600
 CCACCCACAC ACTAAATTCA AAGGTGAAGT TTACATCCTT ACTAAAGAAG 650
 AAGGTGGACG TCACACTCCA TTCTTCAACA ACTACCGTCC TCAATTCTAC 700
 5 TTCCGTACAA CTGACGTTAC AGGTTCAATC GAACCTCCAG CAGGTAATGA 750
 AATGGTAATG CCTGGTGATA ACGTTACTAT CGACGTTGAA TTGATTACAC 800
 CAATCGCCGT TGAACAAGGT ACTACAT 827

10 2) INFORMATION FOR SEQ ID NO: 213

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 821 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus anginosus* (deposited as
Streptococcus constellatus)
 (B) STRAIN: ATCC 27823

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213

GCTATCCTCG TAGTAGCTTC AACTGATGGA CCAATGCCTC AAACCTCGTGA 50
 ACATATCCTT CTTTCACGTC AAGTAGGTGT TAAATACCTT ATCGTCTTCA 100
 30 TGAACAAAGT TGACTTGGTT GACGATGAAG AATTGCTTGA ATTGGTTGAA 150
 ATGGAAATCC GTGACCTTCT TTCAGAATAC GATTTCCAG GTGATGAAAT 200
 CCCAGTTATC CAAGGTTGAG CTCTTAAAGC TCTTGAAGGT GATGAAAAAT 250
 ATGAAGACAT CATCATGGAA TTGATGGATA CTGTTGATGA ATACATTCCA 300
 GAACCAGAAC GTGACACTGA CAAACCACTT CTTCTTCCAG TCGAAGATGT 350
 35 ATTCTCAATC ACTGGACGTG GTACTGTTGC TTCAGGACGT ATCGACCGTG 400
 GTACTGTTAA AGTCAATGAT GAAGTTGAAA TTGTTGGTAT TCGTGACGAA 450
 ATCCAAAAAG CAGTTGTTAC TGGTGTGAA ATGTTCCGTA AACAATTGGA 500
 CGAAGGTCTT GCTGGAGATA ACGTAGGGGT TCTTCTTCGT GGTATCCAAC 550
 GTGACGAAAT CGAACGTGGA CAAGTTCTTG CTAAACCAGG TTCAATTCAT 600
 40 CCACACACTA AATTCAAAGG TGAAGTTTAC ATCCTTACTA AAGAAGAAGG 650
 TGGACGTCAT ACTCCATTCT TCAACAACCTA CCGTCCTCAA TTCTACTTCC 700
 GTACTACAGA CGTTACAGGT TCAATCGAAC TTCCTGCAGG TACTGAAATG 750
 GTAATGCCTG GTGATAACGT AACAATTGAT GTTGAGTTGA TCCACCCAAT 800
 TGCCGTAGAA CAAGGAACTA C 821

45 2) INFORMATION FOR SEQ ID NO: 214

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 821 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus cricetus*
 60 (B) STRAIN: ATCC 19642

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214

```

5  GCTATCCTTG TAGTAGCTTC TACAGACGGA CCAATGCCAC AACTCGTGA 50
   ACACATCTTG CTTTCACGCC AAGTTGGTGT TAAGAGCCTT ATCGTCTTCA 100
   TGAACAAGGT TGAAGTGGTT GACGATGAAG AATTGCTTGA ATTGGTTGAA 150
   ATGGAAATCC GTGATCTTCT TTCAGAATAC GATTTCCCAG GTGATGATAT 200
   CCCTGTTGTT CAAGGTTTCAG CTCTTAAAGC CCTTGAAGGT GATACAGCTG 250
   CCGAAGACAA GATCATGGAA TTGATGGACA TCGTTGATGA CTACATTCCA 300
10 GAACCAAAAC GTGATACTGA TAAGCCATTG CTTCTTCCAG TCGAAGACGT 350
   ATTCTCAATC ACTGGACGTG GTACTGTTGC TTCAGGACGT ATCGACCGTG 400
   GTACTGTAA GGTCAATGAC GAAGTTGAAA TCGTTGGTAT CAAGGACGAA 450
   ATCCAAAAG CCGTTGTAC CCGAGTTGAA ATGTTCCGTA AACAATTGGA 500
   TGAAGGTCTT GCAGGGGATA ACGTTGGTGT GCTTCTTCGT GGTATCCAAC 550
15 GTGATGAAAT CGAACGTGGT CAAGTATTGG CTGCACCTGG TTCAATCCAT 600
   CCACACACTA AATTCAAGGG TGAAGTTTAC ATCCTTTCTA AAGATGAAGG 650
   TGGACGTCAC ACTCCATTCT TCAACAATA CCGTCCACAG TTCTACTTCC 700
   GTACAACCTGA CGTAACTGGT TCAATCGAAT TGCCAGCAGG TACTGAAATG 750
   GTTATGCCTG GTGATAACGT TACTATCGAC GTTGAATTGA TCCACCCAAT 800
20 CGCTGTTGAA AAAGGTACTA C 821

```

2) INFORMATION FOR SEQ ID NO: 215

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 821 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus cristatus*
 (B) STRAIN: ATCC 51100

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215

```

40 TATCCTTGTA GTAGCTTCAA CTGACGGACC AATGCCACAA ACTCGTGAGC 50
   ACATCCTTCT TTCACGTCAG GTTGGTGTAA AACACCTTAT CGTCTTCATG 100
   AACAAGATCG ACTTGGTTGA TGACGAAGAA TTGCTTGAAT TGGTTGAAAT 150
   GGAAATCCGT GACCTCTTGT CAGAATACGA CTTCCCAGGT GACGATCTTC 200
   CAGTTATCCA AGGTTTCAGCT CTTAAAGCTC TTGAAGGTGA TACTAAGTAC 250
45 GAAGACATCA TCATGGAATT GATGAACACT GTTGATGAGT ACATCCCAGA 300
   ACCAGAACGT GATACTGACA AACCTCTTCT TCTTCCAGTC GAAGACGTAT 350
   TCTCAATCAC TGGTCGTGGT ACAGTTGCTT CAGGACGTAT CGACCGTGGT 400
   ACTGTTCTGT TCAACGATGA AATCGAAATC GTTGGTATCA AAGAAGAAAT 450
   CCAAAAAGCA GTTGTTACTG GTGTTGAAAT GTTCCGTAAA CAGCTTGACG 500
50 AAGGTCTTGC AGGGGACAAC GTAGGTGTAC TTCTTCGTGG TATCCAACGT 550
   GATGAAATCG AACGTGGTCA AGTTATCGCT AAACCAGGTT CAATCAACCC 600
   ACACACTAAA TTCAAGGGTG AAGTTTACAT CCTTACTAAA GAAGAAGGTG 650
   GACGTCACAC TCCATTCTTC AACAATACT GTCCACAGTT CTACTTCCGT 700
   ACAACTGACG TTACAGGTTT AATCGAACTT CCAGCAGGTA CTGAAATGGT 750
55 AATGCCTGGT GATAACGTAA CTATCGACGT TGAGTTGATC CACCCAATCG 800
   CCGTTGAACA AGGTACTCCT T 821

```

60 2) INFORMATION FOR SEQ ID NO: 216

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 792 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus downei*
 (B) STRAIN: ATCC 33748

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216

```

15 AGTAGCTTCT ACTGATGGAC CAATGCCACA AACTCGTGAA CACATCTTGC      50
   TTTACAGTCA GGTGTTGTTT AAGAACCCTA TCGTCTTCAT GAACAAGGTT      100
   GACTTGGTTG ACGATGAAGA ATTGCTTGAA TTGGTTGAAA TGGAAATCCG      150
   TGACCTGCTT TCAGAATACG ATTTCCCAGG TGATGATATC CCTGTTGTTC      200
20 AAGGTTTCAGC TCTTAAGGCT CTTGAAGGTG ATACAGCTGC CGAAGACAAG      250
   ATCATGGAAT TGATGGACAT CGTTGATGAC TACATTCCAG AACCAAAACG      300
   TGATACTGAT AAGCCTTTGC TTCTTCCAGT CGAAGATGTA TTCTCAATCA      350
   CTGGACGTGG TACTGTAGCT TCAGGACGTA TCGACCGTGG TACTGTTAAG      400
   GTCAACGACG AAGTTGAAAT CGTTGGTATC AAGGACGAAA TCCAAAAAGC      450
25 AGTTGTTACC GGAGTTGAAA TGTTCCGTAA ACAATTGGAC GAAGGTCTTG      500
   CAGGGGATAA CGTTGGTGTG CTTCTTCGTG GTATCCAACG TGATGAAATC      550
   GAACGTGGTC AAGTGTTGGC TGCGCCTGGT TCGATTCCAC CACACACTAA      600
   GTTTAAAGGT GAAGTTTACA TCCTTTCTAA AGAAGAAGGT GGACGTCATA      650
   CTCCATTCTT TAACAACACT CGTCCACAGT TCTACTTCCG TACAACCTGAC      700
30 GTAACCTGGT CAATCGAATT GCCAGCGGGT ACTGAAATGG TTATGCCTGG      750
   TGATAACGTT ACTATCGACG TTGAATTGAT CCACCCAATT GC              792

```

35 2) INFORMATION FOR SEQ ID NO: 217

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 795 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus dysgalactiae*
 (B) STRAIN: ATCC 43078

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217

```

50 GTAGTTGCTT CAACAGACGG ACCAATGCCA CAAACTCGTG AGCACATCCT      50
   CCTTTCACGT CAGGTTGGTG TTAAACACCT TATCGTGTTT ATGAACAAAA      100
   TTGACCTTGT TGACGATGAA GAATTGCTTG AATTGGTTGA AATGGAAATC      150
   CGTGACCTTC TTTCAGAATA CGATTTCCTA GGTGATGACC TTCCAGTTAT      200
55 CCAAGGTTCA GCTCTTAAAG CTCTTGAAGG CGACACTAAA TTTGAAGACA      250
   TCATCATGGA ATTGATGGAT ACTGTTGATT CATAATTCC AGAACCAGAA      300
   CGTGACACTG ACAAACCATT GCTTCTTCCA GTCGAAGACG TATTCTCAAT      350
   CACAGGTCGT GGTACAGTTG CTTCAGGACG TATCGACCGT GGTACTGTTC      400
   GTGTCAACGA CGAAATCGAA ATCGTTGGTA TCAAAGAAGA AACTAAAAAA      450
60 GCTGTTGTGA CTGGTGTGTA AATGTTCCGT AAACAACCTG ACGAAGGTCT      500

```

TGCAGGAGAC AACGTAGGTA TCCTTCTTCG TGGTGTTCAG CGTGACGAAA 550
 TCGAACGTGG TCAAGTTATT GCTAAACCAG GTTCAATCAA CCCACACACT 600
 AAATTCAAAG GTGAAGTATA TATCCTTTCT AAAGACGAAG GTGGACGTCA 650
 CACTCCATTG TTCAACAACAT ATCGTCCACA ATTCTACTTC CGTACAACGTG 700
 5 ACGTAACAGG TTCAATCGAA CTTCCAGCTG GTACAGAAAT GGTTATGCCT 750
 GGTGATAACG TGACAATCAA CGTTGAGTTG ATCCACCCAA TCGCC 795

10 2) INFORMATION FOR SEQ ID NO: 218

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus equi* subsp. *equi*
 (B) STRAIN: ATCC 9528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218

25 CGGAGCTATC CTTGTAAGTTG CTTCAACTGA CGGACCAATG CCACAAACTC 50
 GTGAGCACAT CCTTCTTTCA CGTCAGGTTG GTGTTAAGCA CCTTATCGTG 100
 TTCATGAACA AGGTTGACCT TGTGACGAT GAAGAATTGC TTGAGCTTGT 150
 TGAAATGGAA ATTCGTGACC TTCTTTCAGA ATATGATTC CCAGGTGATG 200
 30 ACCTTCCAGT TATCCAAGGT TCAGCGCTTA AGGCTCTTGA AGGCGACAGC 250
 AAATACGAAG ATATCATCAT GGAATTGATG GATACTGTTG ATTCATACAT 300
 TCCAGAACCA GAACGTGACA CAGACAAGCC ATTGCTTCTT CCAGTCGAGG 350
 ACGTATTCTC AATCACTGGA CGTGGTACTG TTGCTTCAGG ACGTATCGAC 400
 CGCGGTACTG TTCGTGTTAA CGACGAAATC GAAATCGTTG GTATCAGAGA 450
 35 CGAGATCAAA AAAGCAGTTG TTAGTGGTGT CGAAATGTTC CGTAAACAGC 500
 TTGACGAAGG TCTTGCAAGG GACAACGTTG GTGTTCTTCT TCGTGGTGTA 550
 CAACGTGATG AAATCGAAGC TGGTCAAGTT ATTGCTAAGC CAGGTTCTAT 600
 CAACCCACAC ACTAAATTTA AAGGTGAAGT ATATATCCTT ACTAAAGAAG 650
 AAGGTGGACG TCACACACCA TTCTTCAACA ACTATCGTCC ACAATTCTAC 700
 40 TTCCGTACTA CTGACGTAAC AGGTTCAATC GAGCTTCCAG CAGGTACAGA 750
 AATGGTTATG CCTGGTGATA ACGTACTAT TGACGTTGAG TTGATCCACC 800
 CAATCGCCGT AGAACAAGGT ACTACATT 828

45

2) INFORMATION FOR SEQ ID NO: 219

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 825 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus ferus*
 (B) STRAIN: ATCC 33477

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219

5 CGGTGCAATC CTTGTAGTAG CTTCTACAGA TGGACCAATG CCACAAACTC 50
 GTGAGCACAT CCTTCTTTCA CGTCAGGTAG GTGTTAAACA CCTTATCGTC 100
 TTCATGAACA AAGTTGACTT GGTTGACGAT GAAGAATTGC TTGAATTGGT 150
 10 TGAAATGGAA ATCCGTGACC TGCTTTCAGA ATATGATTTC CCAGGTGATG 200
 ACCTTCCAGT TATCCAAGGT TCAGCTCTTA AAGCGCTTGA AGGTGATACT 250
 GCTCAAGAAG ATGTTATCAT GGAATTGATG AAAACCGTTG ATGAGTACAT 300
 CCCAGAACCA GAACGTGATA CTGACAAACC ATTGCTTCTT CCAGTCGAAG 350
 ATGTATTCTC AATCACAGGT CGTGGTACTG TAGCTTCAGG ACGTATCGAT 400
 15 CGTGGTACTG TAAGAGTCAA CGATGAAGTT GAAATCGTTG GTATCAAAGA 450
 CGAAATCACT AAAGCAGTTG TTACCGGTGT TGAAATGTTT CGTAAACAAT 500
 TGGACGAAGG TCTTGCTGGT GATAACGTTG GTGTGCTTCT CCGTGGTGTG 550
 CAACGTGATG AAATCGAACG TGGTCAAGTA TTGGCTAAAC CAGGTTCAAT 600
 CAACCCACAC ACTAAATTGA AAGGTGAAGT TTACATCCTT ACTAAAGAAG 650
 20 AAGGTGGACG TCATACACCA TTCTTCAACA ACTACCGTCC ACAGTTCTAC 700
 TTCCGTACAA CTGACGTAAC TGGTTCAATC GAATTGCCAG CAGGTACTGA 750
 AATGGTTATG CCTGGTGATA ACGTGACTAT CGACGTTGAA TTGATCCACC 800
 CAATCGCCGT TGAACAAGGT ACTAC 825

20

2) INFORMATION FOR SEQ ID NO: 220

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus gordonii*
 (B) STRAIN: ATCC 10558

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220

40 CGGAGCTATC CTTGTAGTAG CTTCAACTGA TGGTCCTATG CCACAAACTC 50
 GTGAGCACAT CCTTCTCTCA CGCCAAGTTG GTGTTAAACA CTTGATCGTG 100
 TTCATGAACA AAGTTGACTT GGTTGACGAT GAAGAATTGC TTGAGTTGGT 150
 TGAAATGGAA ATCCGTGACC TCTTGTCAGA ATACGACTTC CCAGGTGACG 200
 ATCTTCCAGT TATCCAAGGT TCAGCTCTTA AAGCTCTTGA AGGTGACTCT 250
 AAATATGAAG ATATCATCAT GGAATTGATG AACACTGTTG ATGAGTACAT 300
 CCCAGAACCA GAACGCGACA CTGACAAACC ATTGCTTCTT CCAGTCGAAG 350
 45 ACGTATTCTC AATCACTGGA CGTGGTACAG TTGCTTCAGG ACGTATCGAC 400
 CGTGGTATCG TTAAAGTCAA TGACGAAATC GAAATCGTTG GTATCAAAGA 450
 AGAAATCCAA AAAGCAGTTG TTACTGGTGT TGAAATGTTT CGTAAACAGC 500
 TTGACGAAGG TCTTGCAAGG GACAACGTTG GTGTGCTTCT TCGTGGTATC 550
 CAACGTGATG AAATCGAACG TGGACAAGTT ATTGCTAAAC CAGGTTCAAT 600
 50 CAACCCACAC ACTAAATTCA AAGGTGAAGT TTATATCCTT ACTAAAGAAG 650
 AAGGTGGACG TCACACTCCA TTCTTCAACA ACTACCGTCC ACAGTTCTAC 700
 TTCCGTACAA CTGACGTTAC AGGTTCAATC GAACTTCCAG CAGGTACTGA 750
 AATGGTAATG CCTGGTGATA ACGTAACTAT CGACGTTGAG TTGATCCACC 800
 CAATCGCCGT TGAACAAGGT ACTACT 825

55

2) INFORMATION FOR SEQ ID NO: 221

60 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus anginosus*
 (B) STRAIN: ATCC 27335

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221

15	TGTAGTAGCT	TCAACTGACG	GACCAATGCC	TCAAACCTCGT	GAACATATCC	50
	TTCTTTTACG	TCAAGTAGGT	GTAAATAACC	TTATTGTCTT	CATGAACAAA	100
	GTTGACTTGG	TTGACGATGA	AGAATTGCTT	GAATTGGTTG	AAATGGAAAT	150
	CCGTGATCTT	CTTTCAGAAAT	ACGATTTCCC	AGGTGATGAT	ATTCCAGTAA	200
	TCCAAGGTTT	AGCACTTAAA	GCTCTTGAAG	GTGATGAAAA	ATATGAAGAC	250
	ATCATCATGG	AATTGATGAA	TACTGTTGAT	GAATATATTC	CAGAACCAGA	300
20	ACGTGATACT	GACAAACCAT	TGCTTCTTCC	AGTCGAAGAT	GTATTCTCAA	350
	TCACTGGACG	TGGTACTGTT	GCTTCAGGAC	GTATCGACCG	TGGTACTGTT	400
	AAAGTCAACG	ATGAAGTTGA	AATCGTTGGT	ATCCGCGAGG	AAATCCAAAA	450
	AGCAGTTGTT	ACTGGTGTTG	AAATGTTCCG	TAAACAATTG	GACGAAGGTC	500
	TTGCTGGAGA	TAACGTAGGG	GTTCTTCTTC	GTGGTATCCA	ACGTGACGAA	550
25	ATTGAACGTG	GACAAGTTCT	TGCTAAACCA	GGTTCAATTC	ATCCACACAC	600
	TAAATTCAAA	GGTGAAGTTT	ACATCCTTAC	TAAAGAAGAA	GGTGGACGTC	650
	ATACTCCATT	CTTCAACAAC	TACCGTCCTC	AATTCTACTT	CCGTACTACA	700
	GACGTTACAG	GTTCAATCGA	ACTTCCTGCA	GGTACTGAAA	TGGTAATGCC	750
30	TGGTGATAAC	GTAACAATTG	ATGTTGAGTT	GATCCACCCA	ATTGCCGTA	799

2) INFORMATION FOR SEQ ID NO: 222

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus macacae*
 (B) STRAIN: ATCC 35911

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222

50	TGGTGCTATT	CTTGTAAGTAG	CTTCAACTGA	CGGTCCAATG	CCTCAAACGC	50
	GTGAACATAT	CCTTCTTTCA	CGCCAAGTAG	GTGTTAAAAA	CCTTATTGTT	100
	TTTCATGAATA	AAGTTGACTT	AGTTGATGAT	GAAGAATTGC	TTGAATTGGT	150
	TGAAATGGAA	ATCCGTGATC	TTCTTACAGA	ATATGATTTT	CCAGGCGATG	200
	AACTTCCAGT	TATCCAAGGT	TCAGCACTTA	AAGCTCTTGA	AGGTGATACT	250
	AAGTACGAAG	ATATTATCAT	GGAATTGTTG	GATACTGTAG	ATGATTACAT	300
55	CCCAGAACCA	CAACGTGATA	CTGACAAGCC	ATTGCTTCTT	CCAGTCGAAG	350
	ATGTTTTCTC	TATTACTGGA	CGTGGTACTG	TTGCTTCAGG	ACGTATTGAC	400
	CGTGGTACTG	TTAAGGTTAA	TGATGAAGTT	GAAATCGTTG	GTATTTCGTA	450
	CGATATTCAA	AAAGCAGTTG	TTACTGGTGT	TGAAATGTTT	CGTAAACAGC	500
	TTGACGAAGG	TCTTGCTGGT	GATAACGTCG	GTGTCCTTCT	TCGTGGTATC	550
60	CAACGTGATG	AAATTGAACG	CGGTCAAGTT	CTTGCTAAAC	CAGGATCAAT	600

TCATCCACAT ACTAAATTCA AAGGTGAAGT TTATATTCTT ACTAAAGAAG 650
 AAGGTGGACG TCATACTCCA TTCTTTAACA ACTACCGTCC ACAGTTCTAC 700
 TTCCGTACAA CTGATGTAAC TGGTTCAATT GATTTGCCAG CAGGTACTGA 750
 AATGGTTATG CCTGGTGATA ATGTTACGAT TGATGTTGAA CTGATCCACC 800
 5 CAATCGCTGT TGAACAAGGT ACAAC 825

2) INFORMATION FOR SEQ ID NO: 223

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

20 (A) ORGANISM: *Streptococcus gordonii* (deposited as
Streptococcus mitis)
 (B) STRAIN: ATCC 33399

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223

25 CTATCCTTGT AGTAGCTTCA ACTGACGGAC CAATGCCACA AACTCGTGAG 50
 CACATCCTTC TTTCACGTCA GGTGTTGTT AAACACCTTA TCGTCTTCAT 100
 GAACAAAGTT GACTTGGTTG ACGACGAAGA ATTGCTTGAA TTGGTTGAAA 150
 TGGAAATCCG TGACCTATTG TCAGAATACG ACTTCCCAGG TGACGATCTT 200
 30 CCAGTTATCC AAGGTTTCAGC TCTTAAAGCC CTTGAAGGTG AACTTAAATA 250
 CGAAGACATC GTTATGGAAT TGATGAACAC AGTTGATGAG TACATCCCAG 300
 AACCAGAACG TGACACTGAC AAACCATTGC TTCTTCCAGT CGAAGACGTA 350
 TTCTCAATCA CTGGTCGTGG TACAGTTGCT TCAGGACGTA TCGACCGTGG 400
 TATCGTTAAA GTCAACGACG AAATCGAAAT CGTTGGTATC AAAGAAGAAA 450
 35 CTCAAAAAGC AGTTGTTACT GGTGTTGAAA TGTTCCGTAA ACAACTTGAC 500
 GAAGGTCTTG CCGGAGATAA TGTAGGTGTC CTTCTTCGTG GTGTTCAACG 550
 TGATGAAATC GAACGTGGAC AAGTTATTGC TAAACCAGGT TCAATCAACC 600
 CACACACTAA ATTCAAAGGT GAAGTTTACA TCCTTACTAA AGAAGAAGGT 650
 GGACGTCACA CTCCATTCTT CAACAACTAC CGTCCACAAT TCTACTTCCG 700
 40 TACTACTGAC GTTACAGGTT CAATCGAAT TCCAGCAGGT ACTGAAATGG 750
 TAATGCCTGG TGATAACGTG ACAATCGACG TTGAGTTGAT CCACCCAATC 800
 CCCGTAGAAC AAGGTACTAC AT 822

45 2) INFORMATION FOR SEQ ID NO: 224

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 827 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus mutans*
 (B) STRAIN: ATCC 25175

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224

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CCCTGGTGCT ATCCTTGTA TAGCTTCAAC TGATGGACCA ATGCCACAAA      50
CTCGTGAACA CATTCTTCTT TCACGTCAAG TTGGTGTTAA ATACCTCATT      100
GTCTTCATGA ATAAAGTTGA TTTGGTTGAC GATGAAGAAT TGCTTGAATT      150
5  GGTGAAATG GAAATCCGTG ATCTTCTTTC AGAATATGAT TTCCCAGGTG      200
ATGATATTCC AGTTATTCAA GGTTTCAGCTC TTAAAGCTCT TGAAGGCGAT      250
ACTGCTCAAG AAGATATCAT CATGGAATTA ATGCATACTG TTGATGACTA      300
CATTCCAGAT CCAGAACGTG AACTGACAA GCCGCTCCTT CTTCCAGTCG      350
AAGATGTTTT CTCAATCACT GGTCGTGGTA CTGTTGCTTC AGGACGTATT      400
10 GATCGTGGTA CTGTTAAAGT TAACGATGAA GTTGAAATCG TTGGTATCCG      450
TGATGACATT CAAAAGCTG TTGTTACTGG TGTGAAATG TTCCGTAAAC      500
AATTGGATGA AGGTATTGCA GGGGATAATG TTGGTGTTCCT CTTTCGTGGT      550
ATCCAACGTG ATGAAATCGA ACGTGGTCAA GTTCTTGCTA AACCAGGTTC      600
AATTCACCCA CATACTAAAT TCAAAGGTGA AGTTTATATC CTTACTAAAG      650
15 AGGAAGGTGG ACGTCATACA CCATTCTTCA ATAACATATCG TCCACAATTC      700
TACTTCCGTA CAACTGACGT AACTGGTTCA ATTGAGTTGC CAGCAGGTAC      750
TGAAATGGTT ATGCCTGGTG ATAACGTTAC TATTGACGTT GAATTGATCC      800
ATCCAATCGC TGTGAAACAA GGTA      827

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20

2) INFORMATION FOR SEQ ID NO: 225

(i) SEQUENCE CHARACTERISTICS:

```

25  (A) LENGTH: 824 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear

```

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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      (A) ORGANISM: Streptococcus parasanguinis
      (B) STRAIN: ATCC 15912

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35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225

```

AGCTATCCTT GTAGTAGCTT CAACTGACGG ACCAATGCCA CAAACACGTG      50
AACACATCCT TCTTTCACGT CAGGTTGGTG TTAAACACTT GATCGTCTTC      100
40 ATGAACAAAG TTGACTTGGT TGATGATGAA GAATTGCTTG AATTGGTTGA      150
AATGGAAATC CGTGACCTTC TTTCAGAATA CGATTTCCCA GGTGATGACC      200
TTCCAGTTAT CCAAGGTTCA GCTCTTAAAG CTCTTGAAGG TGACTCTAAA      250
TATGAAGATA TCATCATGGA ATTGATGGAT ACTGTTGATG AGTACATCCC      300
AGAACCAGAA CGCGATACTG ACAAACCATT GCTTCTTCCA GTCGAAGACG      350
45 TATTCTCAAT CACTGGACGT GGTACAGTTG CTTCAGGACG TATCGACCGT      400
GGTGTGTGTC GTGTCAATGA TGAAATCGAA ATCGTTGGTA TCAAAGAAGA      450
AATCCAAAAA GCAGTTGTTA CTGGTGTTGA AATGTTCCGT AAACAACCTG      500
ACGAAGGTCT TGCAGGGGAT AACGTTGGTG TGCTTCTTCG TGGTATCCAA      550
CGTGATGAAA TCGAACGTGG ACAAGTTATC GCTAAACCAG GTTCAATCAA      600
50 CCCACACACT AAATTCAAAG GTGAAGTTTA CATCCTTACT AAAGAAGAAG      650
GTGGACGTCA TACTCCATTC TTCAACAACT ACCGTCCACA GTTCTACTTC      700
CGTACAACCTG ACGTAACTGG ATCTATCGAA CTTCCACCAG GAACTGAAAT      750
GGTAATGCCT GGTGATAACG TGACTATCGA CGTTGAGTTG ATCCACCCAA      800
TCGCCGTTGA ACAAGGTACT ACAT      824

```

55

2) INFORMATION FOR SEQ ID NO: 226

(i) SEQUENCE CHARACTERISTICS:

60

(A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus ratti*
 (B) STRAIN: ATCC 19645

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226

15	TGGTGCTATC	CTTGTAAGTAG	CTTCAACTGA	TGGACCAATG	CCGCAAACCTC	50
	GTGAACACAT	CTTGCTTTCA	CGTCAAGTTG	GTGTTAAATA	CCTTATCGTC	100
	TTCATGAACA	AGGTTGACTT	GGTTGATGAT	GAAGAATTGC	TTGAATTGGT	150
	TGAAATGGAA	ATCCGTGATC	TTCTTTTCAGA	ATACGATTTC	CCAGGTGATG	200
	ACATTCCAGT	TATCCAAGGT	TCAGCCCTTA	AAGCTCTTGA	AGGTGACACT	250
	GAACAAGAAG	ATGTTATCAT	GGAATTGATG	AAAACAGTTG	ATGAGTACAT	300
20	CCCAGATCCA	GAACGCGATA	CTGATAAGCC	ATTGCTTCTT	CCAGTCCGAAG	350
	ACGTGTTCTC	AATCACTGGA	CGTGGTACTG	TTGCATCAGG	ACGTATCGAC	400
	CGTGGTACTG	TTAAAGTCAA	TGACGAAGTT	GAAATCGTTG	GTATCCGTGA	450
	TGACATCCAA	AAAGCTGTTG	TTACTGGTGT	TGAAATGTTT	CGTAAACAGC	500
	TTGACGAAGG	TCTTGCTGGT	GATAACGTTG	GTGTACTTCT	TCGTGGTATC	550
25	CAACGTGATG	AAATCGAACG	CGGTCAAGTT	CTTGCTAAAC	CAGGTTCAAT	600
	TCATCCGCAT	ACTAAATTTA	AAGGTGAAGT	TTACATCCTT	ACTAAAGAAG	650
	AAGGCGGACG	TCACACTCCA	TTCTTCAACA	ACTACCGTCC	ACAGTTCTAC	700
	TTCCGTACAA	CTGACGTAAC	TGGTTCAATC	GAATTGCCAG	CAGGTACTGA	750
	AATGGTTATG	CCTGGTGATA	ACGTGACTAT	CGACGTTGAA	TTGATCCACC	800
30	CAATCGCTGT	TGAACAAGGT	ACTA			824

2) INFORMATION FOR SEQ ID NO: 227

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 795 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus sanguinis*
 (B) STRAIN: ATCC 10556

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227

50	TGTAGTAGCT	TCAACTGACG	GACCAATGCC	ACAAACTCGT	GAGCACATCT	50
	TGCTTTTACG	TCAGGTTGGT	GTAAACACT	TGATCGTCTT	CATGAACAAA	100
	GTTGACTTGG	TTGACGATGA	AGAATTGCTT	GAATTGGTTG	AAATGGAAAT	150
	CCGTGACCTC	TTGTCAGAAT	ACGACTTCCC	AGGTGACGAT	CTTCCAGTTA	200
	TCCAAGGTTT	AGCTCTTAAA	GCTCTTGAAG	GTGACTCTAA	ATATGAAGAC	250
55	ATCATCATGG	AATTGATGGA	CACTGTTGAT	GAGTACATCC	CAGAACCAGA	300
	ACGCGATACT	GACAAGCCAT	TGCTTCTTCC	AGTCGAAGAC	GTATTCTCAA	350
	TCACTGGTCG	TGGTACAGTT	GCTTCAGGAC	GTATCGACCG	TGGTATCGTT	400
	AAAGTCAACG	ACGAAATCGA	AATCGTTGGT	ATCAAAGAAG	AAATCCAAAA	450
	AGCAGTTGTT	ACTGGTGTG	AAATGTTCCG	TAAACAGCTT	GACGAAGGTC	500
60	TTGCAGGGGA	CAACGTAGGT	GTGCTTCTCC	GTGGTATCCA	ACGTGATGAA	550

ATCGAACGTG GACAAGTTAT CGCTAAACCA GGTTCATCA ACCCACACAC 600
TAAATTCAAG GGTGAAGTTT ATATCCTTAC TAAAGAAGAA GGCGGACGTC 650
ACACTCCATT CTTCAACAAC TACCGTCCAC AGTTCTACTT CCGTACAACT 700
GACGTTACAG GTTCAATCGA ACTTCCAGCA GGTACTGAAA TGGTAATGCC 750
5 TGGTGATAAC GTAACAATCG ACGTTGAGTT GATCCACCCA ATCGC 795

2) INFORMATION FOR SEQ ID NO: 228

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 795 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
15 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

20 (A) ORGANISM: *Streptococcus sobrinus*
(B) STRAIN: ATCC 33478

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228

25 TGTAGTAGCT TCTACTGACG GACCAATGCC ACAAACCTCGT GAACACATCT 50
TGCTTTCACG CCAAGTTGGT GTTAAGAACC TCATCGTCTT CATGAACAAG 100
GTTGACTTGG TTGATGATGA AGAATTGCTT GAATGGTTG AAATGGAAAT 150
CCGTGATCTT CTTTCAGAAT ACGATTTCCC AGGTGACGAC ATTCCTGTTG 200
TTCAAGGTTT AGCTCTTAAG GCTCTTGAAG GTGATACAGC TGCCGAAGAC 250
30 AAGATTATGG AATTGATGGA CATCGTTGAT GATTACATTC CAGAACCAAA 300
ACGCGATACT GATAAGCCAT TGCTTCTCCC AGTCGAAGAC GTATTCTCAA 350
TCACTGGTCTG TGGTACTGTT GCTTCAGGAC GTATTGACCG TGGTACTGTT 400
AAGGTTAACG ACGAAGTTGA AATCGTTGGT ATCCGTGACG ATATCCAAAA 450
AGCAGTTGTT ACTGGAGTTG AAATGTTCCG TAAGCAATTG GACGAAGGTC 500
35 TTGCTGGAGA TAACGTTGGT GTGCTTCTTC GTGGTATCCA ACGTGATGAA 550
ATTGAACGTG GTCAAGTATT GGCTGCACCT GGTTCATCC ACCCACACAC 600
TAAGTTCAAG GGTGAAGTTT ACATCCTTTC TAAAGATGAA GGTGGACGTC 650
ACACTCCATT CTTCAACAAC TACCGTCCAC AGTTCTACTT CCGTACAACT 700
GACGTAAC TGTTCAATCGA ATTGCCAGCA GGTACTGAAA TGGTTATGCC 750
40 TGGTGATAAC GTTACTATCG ACGTTGAATT GATCCACCCA ATCGC 795

2) INFORMATION FOR SEQ ID NO: 229

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 797 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

55 (A) ORGANISM: *Streptococcus suis*
(B) STRAIN: ATCC 43765

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229

60 TGTAGTAGCT TCAACTGACG GTCCAATGCC ACAAACCTCGT GAGCACATCC 50

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2) INFORMATION FOR SEQ ID NO: 230

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 793 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

30 (A) ORGANISM: *Streptococcus uberis*

(B) STRAIN: ATCC 19436

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230

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2) INFORMATION FOR SEQ ID NO: 231

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 798 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Streptococcus vestibularis*
(B) STRAIN: ATCC 49124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231

10	TTGTAGTAGC ATCTACTGAC GGACCAATGC CACAAACTCG TGAGCACATC	50
	CTTCTTTCAC GTCAGGTTGG TGTTAAACAC CTTATCGTCT TCATGAACAA	100
	AGTTGACTTG GTTGACGATG AAGAATTGCT TGAATTGGTT GAAATGGAAA	150
	TCCGTGACCT TCTTTCAGAA TACGATTTC CAGGTGATGA TATTCCAGTT	200
	ATCCAAGGTT CAGCTCTTAA AGCTCTTGAA GGTGATTCTA AATACGAAGA	250
15	CATCATCATG GACTTGATGA ACACTGTTGA CGAATACATT CCAGAACCAG	300
	AACGTGACAC TGACAAACCA TTGTTGCTTC CAGTCGAAGA CGTATTCTCA	350
	ATCACTGGTC GTGGTACTGT TGCTTCAGGA CGTATCGACC GTGGTGTGTG	400
	TCGTGTTAAT GACGAAGTTG AAATCGTTGG TCTTAAAGAA GAAATCCAAA	450
	AAGCAGTTGT TACTGGTGTA GAAATGTTCC GTAAACAACT TGACGAAGGT	500
20	ATTGCCGAG ATAACGTCGG TGTCTTCTT CGTGGTATCC AACGTGATGA	550
	AATTGAACGT GGTCAAGTAT TGGCTGCACC TGGTTCAATC AACCCACACA	600
	CTAAATTCAA AGGTGAAGTT TACATCCTTT CTAAAGAAGA AGGTGGACGT	650
	CACACTCCAT TCTTCAACAA CTACCGTCCA CAGTTC TACT TCCGTACAAC	700
	TGACGTAACA GGTTCATCG AACTTCCTGC AGGTACTGAA ATGGTTATGC	750
25	CTGGTGATAA CGTGACTATC GACGTTGAGT TGATCCACCC AATCGCCG	798

2) INFORMATION FOR SEQ ID NO: 232

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Tatumella ptyseos*
(B) STRAIN: ATCC 33301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232

45	GGCGCTATCC TGTTTGTGTC TGCAACTGAC GGCCCTATGC CTCAGACCCG	50
	TGAGCACATC CTGCTGGGCC GCCAGGTAGG CGTTCCTTAC ATCATCGTGT	100
	TCCTGAACAA ATGTGACATG GTTGATGATG AAGAGCTGCT GGAACCTGGTA	150
	GAAATGGAAG TCCGTGACCT GCTGTCACAG TACGACTTCC CGGGTGACGA	200
	CACGCCAATC GTTCGCGGTT CAGCGCTGAA AGCACTGGAA GGTGAAGGCG	250
50	AGTGGGAAGA GAAGATTCTG GAGCTGGCTG GCTTCCTGGA TTCTTACATC	300
	CCTGAGCCAG AGCGTGCTAT CGATCAGCCG TTCCTGCTGC CAATCGAAGA	350
	CGTATTCTCA ATCTCCGGTC GTGGTACAGT TGTTACCGGT CGTGTAGAGC	400
	GCGGGATCAT CAAAGTCGGT GAAGAAGTTG AGATCGTTGG TATCAAAGAT	450
	ACTGCGAAAT CAACCTGTAC CGGTGTTGAA ATGTTCCGTA AACTGCTGGA	500
55	CCAGGGTCAG GCGGGTGAGA ACGTTGGTGT TCTGCTGCGT GGTATCAAGC	550
	GTGAAGAGAT CGAACGTGGT CAGGTTCTGG CTAAACCAGG TTCAATCAAA	600
	CCACACACCC AGTTCGAGTC AGAAGTTTAT ATTCTGTCTA AAGACGAAGG	650
	CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCACAG TTCTACTTCC	700
	GTACAACTGA CGTGACCGGA ACCATCGAAC TGCCGGAAGG CGTAGAGATG	750
60	GTAATGCCTG GTGACAACAT CAAAATGGTT GTTACCCTGA TCCATCCAAT	800

CGCGATGGAC GATGGTCTGC GTTTCGCAA

5 2) INFORMATION FOR SEQ ID NO: 233

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 829 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trabulsiella guamensis*
(B) STRAIN: ATCC 49490

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233

20 GGCGCAATCC TGGTAGTAGC AGCGACTGAC GGCCCGATGC CGCAGACTCG 50
TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT 100
TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTA 150
GAGATGGAAG TTCGTGAACT GCTGTCTCAG TACGATTTC CGGGCGATGA 200
25 CACGCCGATC GTACGTGGTT CTGCTCTGAA AGCGCTGGAA GGCGACGCAG 250
AGTGGGAAGC GAAAATCATC GAACTGGCAG GTTTCCTGGA TTCTTACATT 300
CCGGAACCAG AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CGATCGAAGA 350
CGTATTCTCC ATCTCTGGTC GTGGTACCGT TGTACCGGT CGTGTAGAGC 400
GCGGTATCAT CAAAGTGGGT GAAGAAGTAG AAATCGTTGG TATCAAAGAG 450
30 ACTGCGAAGT CAACCTGTAC TGGCGTAGAA ATGTTCCGCA AACTGCTGGA 500
CGAAGGCCGT GCTGGTGAGA ACGTAGGTGT TCTGCTGCGT GGTATCAAAC 550
GTGAAGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG CACCATCAAC 600
CCGCACACCA AGTTCGAATC TGAAGTGTAC ATTCTGTCCA AAGACGAAGG 650
CGGCCGTCAC ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC 700
35 GTACAACTGA CGTGAAGTGC ACCATCGAAC TGCCGGAAGG CGTAGAGATG 750
GTAATGCCGG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT 800
CGCGATGGAC GACGGTCTGC GTTTCGCAA 829

40 2) INFORMATION FOR SEQ ID NO: 234

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 825 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Veillonella parvula*
(B) STRAIN: ATCC 10790

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234

CGGCGCTATC TTGGTTGTAT CCGCAGCTGA CGGCCCTATG CCTCAAATC 50
GCGAACACAT CTTGTTGGCT CGCCAAGTTG GTGTTCTGCT AATCGTAGTA 100
TTCTTGAACA AAGCTGACAT GGTGACGAT GAAGAATTGA TCGAATTGGT 150
60 AGAAATGGAA GTTCGTGAAC TTCTTTCTTC CTACGAATTC CCTGGCGACG 200

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AAGTACCTAT CGTTGTAGGT TCCGCGTTGA AAGCTTTGGA AGGCGATGCT 250
CAATATGTAG CTAAAATTGA CGAATTGATG GACGCTGTAG ACTCCTACAT 300
CCCAACACCA GTTCGTGACA CTGATAAACC ATTCTTGATG CCTGTGGAAG 350
ATGTTTTTCAC AATCACTGGT CGTGGTACAG TAGCAACTGG CCGTGTTGAA 400
5 CGTGGTCAAG TAAACGTTGG TGATACTGTT GAAGTAGTAG GCTTGAAAGA 450
AAAAGCTGAA CAATACGTAG TAACAGGTCT TGAAATGTTC CGTAAAGTGT 500
TGGATTCTGC AGTAGCAGGT GACAACGTAG GTGCATTGCT TCGTGGTGTT 550
GATCGTAAAG ACATYGAACG TGGTCAAAGTA TTGGCTAAAC CAGGTTCCAT 600
CAACCCACAY ACAAATTCA AAGCAGAAAGT ATACGTATTG ACTAAAGAAG 650
10 AAGGTGGTCC TCATACTCCA TTCTTCTCCA ACTACCGTCC ACAATTCTAC 700
TTCCGTACAA CAGACGTAAC AGGTGTTGTA AACCTTCCTG AAGGTGTAGA 750
AATGTGTATG CCTGGCGATA ACGTAACAAT GGAAATCGAA TTGATTACTC 800
CAATCGCTAT CGAAGAAGGT CTTCG 825

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2) INFORMATION FOR SEQ ID NO: 235

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(i) SEQUENCE CHARACTERISTICS:
20 (A) LENGTH: 825 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Yersinia enterocolitica
        (B) STRAIN: ATCC 9610

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235

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CGCTATCCTG GTTGTGCTG CAACTGATGG CCCAATGCCA CAGACTCGTG 50
AGCACATCCT GTTGGGTCGT CAGGTTGGTG TTCCTTACAT CATCGTATTC 100
35 ATGAACAAAT GTGACATGGT TGACGATGAA GAGCTGCTAG AACTGGTAGA 150
AATGGAAGTG CGCGATCTTC TGCTACCTA CGATTTCCCA GGCGATGATA 200
CGCCAGTTGT TCGTGGTTCC GCGCTGAAAG CATTGGAAGG CGAACCTGAG 250
TGGGAAGCAA AAATTATCGA ACTGGCTGGC TACCTGGATT CTTACATCCC 300
AGAACCAGAG CGTGCTATCG ATAAGCCGTT CCTGCTGCCA ATCGAAGACG 350
40 TATTCTCTAT CTCTGGTCGT GGTACTGTTG TAACGGGTCG TGTAGAGCGC 400
GGTATCGTTA AAGTTGGTGA AGAAGTCGAA ATTGTTGGCC TGAAAGATAC 450
CGTTAAATCT ACTTGACTG GCGTTGAAAT GTTCCGCAA CTGCTGGATG 500
AAGGCCGTGC AGGTGAGAAC GTTGGTGTTG TGCTGCGTGG TATCAAGCGT 550
GAAGATATCG AACGTGGTCA AGTTCTTGCT AAACCAGGTT CGATTAAACC 600
45 ACACACCAAA TTTGAATCAG AAGTTTATAT TCTGAGCAA GATGAAGGTG 650
GTCGCCATAC TCCGTTCTTC AAAGGCTACC GTCCTCAGTT CTAATTCCGT 700
ACAACGTATG TAACCGGTAC TATTGAACTG CCAGAAGGCG TTGAGATGGT 750
GATGCCAGGT GATAACATTC AAATGATTGT TAACCTGATT GCTCCTATCG 800
CAATGGATGA CGGCTTGCGC TTTGC 825
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2) INFORMATION FOR SEQ ID NO: 236

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55 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 828 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
60

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(ii) MOLECULE TYPE: Genomic DN A

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Yersinia frederiksenii*

(B) STRAIN: ATCC 33641

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236

	GGCGCGATCC	TGGTTGTTGC	TGCCACTGAT	GGCCCGATGC	CACAGACTCG	50
10	CGAGCACATT	CTGTTAGGGC	GTCAGGTGGG	TGTTCCCTTAC	ATCCTGGTCT	100
	TCCTGAACAA	ATGTGACATG	GTTGACGACG	AAGAGCTGCT	GGAAGCTGGTA	150
	GAAATGGAAG	TTCGTGAACT	TCTGTCTCAG	TACGATTTCC	CTGGCGACGA	200
	CACTCCAGTT	ATCCGTGGTT	CTGCGCTGAA	AGCGCTGGAA	GGCGAAGCTG	250
	AGTGGGAAGC	AAAAATCATC	GAATTGGCTG	AGGCGCTGGA	TAGCTATATT	300
15	CCACAGCCAG	AGCGTGCGAT	TGATAAACCA	TTCCTGCTGC	CAATCGAAGA	350
	CGTATTCTCA	ATCTCTGGCC	GTGGTACTGT	TGTCACCGGT	CGTGTAGAGC	400
	GCGGTATCGT	TAAAGTCGGC	GAAGAAGTCG	AAATCGTTGG	TATCATTGAT	450
	ACCATCAAGA	CTACCTGTAC	TGGTGTTGAA	ATGTTCCGCA	AATTGCTGGA	500
	CGAAGGCCGT	GCGGGTGAGA	ACGTTGGTGT	TCTGCTACGT	GGTACTAAAC	550
20	GTGATGACGT	ACAACGTGGT	CAGGTATTGG	CAAAACCAGG	TTCTATCAAG	600
	CCACACACCA	AATTTGAATC	AGAAGTTTAT	ATTCTGAGCA	AAGATGAAGG	650
	TGGTCGCCAT	ACTCCGTTCT	TCAAAGGTTA	TCGTCCTCAG	TTCTACTTCC	700
	GTACAACTGA	CGTGACCGGT	ACTATCGAAC	TGCCAGAAGG	CGTTGAGATG	750
	GTGATGCCAG	GTGATAACAT	TCAAATGATT	GTTAACCTGA	TTGCTCCTAT	800
25	CGCAATGGAT	GACGGTCTGC	GCTTTGCG			828

2) INFORMATION FOR SEQ ID NO: 237

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 813 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Yersinia intermedia*

(B) STRAIN: ATCC 29909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237

45	CTTGGTTGTC	GCTGCAACTG	ATGGTCCTAT	GCCACAGACT	CGCGAGCACA	50
	TCCTGCTAGG	TCGTCAGGTG	GGTGTTCCTT	ACATCCTGGT	CTTCCTGAAC	100
	AAGTGTGACA	TGGTTGACGA	TGAGGAGTTG	CTGGAATTGG	TAGAAATGGA	150
	AGTCCGCGAA	CTTCTGTCTC	AATATGATTT	CCCTGGCGAT	GATACTCCTG	200
	TTATCCGTGG	TTCAGCGCTG	AAGGCGTTGG	AAGGCGAGCC	TGAATGGGAA	250
50	GCAAAAATTA	TCGAATTAGC	TGAGGCGCTG	GATAGTTATA	TTCCACAGCC	300
	AGAGCGCGCG	ATTGATAGAC	CATTCTTGCT	GCCAATCGAA	GACGTATTCT	350
	CTATCTCAGG	TCGTGGTACA	GTCGTCACTG	GTCGTGTAGA	GCGTGGGATC	400
	GTTAAAGTTG	GCGAAGAAGT	TGAAATCGTT	GGTATTATCG	ATTCCATTAG	450
	AACAACATGT	ACTGGCGTTG	AAATGTTCCG	CAAATTGCTG	GACGAAGGCC	500
55	GCGCGGGTGA	GAACGTTGGT	GTTCTACTGC	GTGGGACTAA	ACGTGATGAC	550
	GTACAGCGTG	GTCAGGTATT	AGCTAAGCCA	GGTTCTATCA	AGCCACATAC	600
	TAAATTCGAA	TCCGAAGTTT	ATATTCTGAG	CAAAGATGAA	GGCGGGCGTC	650
	ACACGCCGTT	CTTCAAAGGC	TACCGTCCTC	AGTTCTACTT	CCGTACAACG	700
	GATGTAACCG	GTACTATTGA	ATTGCCAGAC	GGCGTTGAGA	TGGTGATGCC	750
60	AGGTGATAAC	ATTCAAATGA	TTGTTAACCT	GATTGCACCT	ATTGCGATGG	800

ATGATGGTCT GCG

813

5 2) INFORMATION FOR SEQ ID NO: 238

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia pestis*
 (B) STRAIN: KIM D27

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238

20 GGAGCGATCT TGGTTGTTGC TGCAACCGAT GGCCCTATGC CGCAGACTCG 50
 TGAGCATATC CTGCTGGGCC GCCAGGTTGG TGTCCCATAC ATTATTGTCT 100
 TCCTGAACAA ATGTGACATG GTTGACGATG AAGAGTTGCT AGAGTTGGTT 150
 25 GAAATGGAGG TTCGTGAGCT TCTGTCTCAA TACGATTTC CAGGCGACGA 200
 CACTCCAGTC ATCCGTGGTT CAGCGTTGAA AGCCCTGGAA GGTGACGCTG 250
 AGTGGGAAGC TAAAATTATC GAGTTGGCAG AAGCTCTGGA TAGCTATATT 300
 CCGCAACCAG AACGCGCTAT TGATAGACCA TTCCTATTGC CAATTGAAGA 350
 CGTATTCTCT ATTTCTGGTC GTGGTACTGT AGTTACTGGT CGTGTAGAAC 400
 GTGGTATTGT TAAGGTCGGC GAAGAAGTTG AAATCGTTGG TATTATCGAT 450
 30 ACGATTAAAA CAACTTGATC TGGCGTTGAA ATGTTCCGCA AGCTGCTGGA 500
 TGAAGGCCGT GCTGGTGAAA ATGTTGGTGT TCTGCTGCGT GGTACTAAGC 550
 GTGACGATGT TCAGCGTGGT CAAGTACTGG CGAAACCAGG TTCTATCAAG 600
 CCACACACGA AGTTTGAGTC AGAAGTTTAT ATTCTGAGCA AAGATGAAGG 650
 CGGCCGTCAT ACACCGTTCT TCAAGGGCTA CCGTCCTCAG TTCTACTTCC 700
 35 GTACAACTGA CGTGACCGGT ACCATTGAGC TGCCAGAAGG CGTTGAAATG 750
 GTCATGCCTG GTGACAACGT AAACATGGTT GTTAACCTAA TTGCTCCTAT 800
 CGCAATGGAT GATGGTCTGC GCTTCGCAA 829

40

2) INFORMATION FOR SEQ ID NO: 239

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
 45 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia pseudotuberculosis*
 (B) STRAIN: ATCC 29833

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239

TGGAGCGATC TTGGTTGTTG CTGCAACCGA TGGCCCTATG CCGCAGACTC 50
 GTGAGCATAT CCTGCTGGGC CGCCAGGTTG GTGTCCCATC CATTATTGTC 100
 TTCTGAACA AATGTGACAT GGTTGACGAT GAAGAGTTGC TAGAGTTGGT 150
 60 TGAAATGGAG GTTCGTGAGC TTCTGTCTCA ATACGATTTC CCAGGCGACG 200

5 ACACTCCAGT CATCCGTGGT TCAGCGTTGA AAGCCCTGGA AGGTGACGCT 250
 GAGTGGGAAG CTAAAATTAT CGAGTTGGCA GAAGCTCTGG ATAGCTATAT 300
 TCCGCAACCA GAACGCGCTA TTGATAGACC ATTCTATTG CCAATTGAAG 350
 ACGTATTCTC TATTTCTGGT CGTGGTACTG TAGTTACTGG TCGTGTAGAA 400
 CGCGGTATTG TTAAGGTCGG CGAAGAAGTT GAAATCGTTG GTATTATCGA 450
 TACGATTAAA ACAACTTGTA CTGGCGTTGA AATGTTCCGC AAGCTGCTGG 500
 ATGAAGGCCG TGCTGGTGAA AATGTTGGTG TTCTGCTGCG TGGTACTAAG 550
 CGTGACGATG TTCAGCGTGG TCAAGTACTG GCGAAACCAG GTTCTATCAA 600
 GCCACACACG AAGTTTGAGT CAGAAGTTTA TATTCTGAGC AAAGATGAAG 650
 10 GCGGCCGTCA TACACCGTTC TTCAAGGGCT ACCGTCCTCA GTTCTACTTC 700
 CGTACAACG ACCTGACCGG TACCATTGAG CTGCCAGAAG GCGTTGAAAT 750
 GGTGATGCCT GGTGACAACG TAAACATGGT TGTTAACCTA ATTGCTCCTA 800
 TCGCAATGGA TGATGGT 817

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2) INFORMATION FOR SEQ ID NO: 240

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 25 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Yersinia rohdei*
 (B) STRAIN: ATCC 43380

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240

35 TGGCGCGATC CTGGTTGTTG CTGCAACTGA TGGCCCAATG CCACAGACTC 50
 GCGAGCACAT CCTGTTGGGT CGTCAAGTGG GTGTTCTTCA CATCTTAGTC 100
 TTCCTGAACA AGTGTGACAT GGTGACGAC GAAGAGTTGC TGGAAGTGGT 150
 TGAAATGGAA GTTCGTGAGC TTCTGTCTCA ATACGATTC CCTGGCGATG 200
 ACACTCCGGT TATTCGTGGT TCCGCGCTGA AAGCGCTGGA AGGCGAGGCC 250
 GAGTGGGAAG CCAAAATTAT TGAACCTGCT GAAGCACTGG ATAGCTACAT 300
 TCCACAGCCA GAGCGCGCGA TTGATAAACC ATTCTTGCTG CCAATCGAAG 350
 40 ACGTATTCTC TATCTCAGGC CGTGGAACAG TTGTTACCGG GCGTGTGAG 400
 CGCGGTATCG TCAGAGTGGG CGAAGAAGTT GAAATCGTGG GTATCATCGA 450
 CACCATTAAC ACCACTTGTA CCGGTGTTGA AATGTTCCGC AAAGTCTGCTGG 500
 ACGAAGGCCG TGCCGGTGAG AACGTTGGTG TTCTGCTGCG CCGTACTAAA 550
 CGCGATGACG TGCAACGTGG TCAAGTGGTG GCTAAACCAG GTTCTATTAA 600
 45 GCCGCATACC AAATTTGAGT CAGAAGTTTA TATTCTGAGC AAAGATGAAG 650
 GTGGTCGTCA TACTCCGTTC TTCAAAGGTT ACCGTCCACA GTTCTACTTC 700
 CGTACAACG ACCTGACCGG TACCATCGAA CTGCCAGACG GTGTTGAGAT 750
 GGTGATGCCA GGTGATAACA TTCAAATGAT TGTTAACCTG ATTGCGCCTA 800
 50 TTGCAATGGA TGACGGTCTA CGATTGCA 829

2) INFORMATION FOR SEQ ID NO: 241

- 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 804 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Yokenella regensburgei*

(B) STRAIN: ATCC 35313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241

	TGGCGCGATC	CTGGTTGTTG	CTGCGACTGA	CGGCCCGATG	CCGCAGACTC	50
10	GTGAGCACAT	CCTGCTGGGT	CGTCAGGTAG	GCGTTCCGTA	CATCATCGTG	100
	TTCCTGAACA	AATGCGACAT	GGTTGATGAC	GAAGAGCTGC	TGGAAGTGGT	150
	AGAAATGGAA	GTTCTGTAAC	TTCTGTCTCA	GTACGATTTC	CCGGGCGACG	200
	ACACTCCGAT	CATCCGTGGT	TCTGCTCTGA	AAGCGCTGGA	AGGCGAAGCA	250
	GAGTGGGAAG	CTAAAATCGT	TGAGCTGGCT	GGCTTCCTGG	ATTCTTACAT	300
15	CCCAGAACCA	GTTCTGTGCTA	TCGACCTGCC	GTTCTGTCTG	CCGATCGAAG	350
	ACGTATTCTC	CATCTCCGGT	CGTGGCACCG	TTGTTACCGG	TCGTGTAGAG	400
	CGCGGTATCG	TTAAAGTTGG	CGAAGAAGTT	GAAATCGTTG	GTATCAAAGA	450
	GACTGCTAAG	TCTACCTGTA	CCGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
	ACGAAGGCCG	TGCTGGTGAG	AACGTTGGTG	TTCTGCTGCG	TGGTATCAAA	550
20	CGTGAAGAAA	TCGAACGTGG	TCAGGTACTG	GCTAAGCCGG	GTTCCATCAA	600
	GCCGCACACC	AAATTCGAAT	CTGAAGTTTA	TATCCTGTCC	AAAGACGAAG	650
	GCGGCCGTCA	TACTCCGTTT	TTCAAAGGCT	ACCGTCCGCA	GTTCTACTTC	700
	CGTACAAC TG	ACGTGACTGG	TACCATCGAA	CTGCCGGAAG	GCGTAGAGAT	750
	GGTAATGCCG	GGCGACAACA	TCAAATGGT	TGTTACCCTG	ATCCACCCGA	800
25	TCGC					804

2) INFORMATION FOR SEQ ID NO: 242

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 849 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Achromobacter xylosoxidans* subsp. *denitrificans*

(B) STRAIN: ATCC 15173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242

45	TCAGTTCCCC	CGCGATCACA	TGCCCAAGAT	CTACGAAGCG	CTTACTCTGG	50
	CCGACGAGGG	TTCCTCGTTC	GCCGAAAAGG	GTCTGACGCT	GGAAGTGCAG	100
	CAACAGCTGG	GCGACGGCGT	GGTGCGTACC	ATCGCGCTGG	GCTCCAGCGA	150
	CGGCCTGCGC	CGCGGTATGA	AGGTCACCGG	TACGGGCGCG	CCGATCTCGG	200
50	TGCCGGTTCG	CACCGGCACG	CTGGGCCGCA	TCATGGACGT	GCTGGGTCTG	250
	CCCATCGACG	AAGCCGGCCC	GATCCAGCAC	GAAGAAAAGC	GTGGCATTCA	300
	CCAGCCGGCT	CCCCGTTTCG	ACGAACTGTC	GCCGTCGGTG	GAAGTCTGCT	350
	AAACCGGCAT	CAAGGTTATT	GACCTGGTCT	GCCCGTTTCG	CAAGGGCGGC	400
	AAGGTCGGCC	TGTTCCGGCG	CGCCGGCGTG	GGCAAGACCG	TCAACATGAT	450
55	GGAAGTGATC	AACAACATCG	CCAAGCAGCA	CAGCGGCTTG	TCGGTGTTCG	500
	CCGGCGTGGG	CGAGCGTACC	CGCGAAGGCA	ACGACTTCTA	CCACGAAATG	550
	GAAGAGTCGA	ACGTTCTGGA	CAAGGTTGCG	ATGGTGTTCG	GTCAGATGAA	600
	CGAACCCTCG	GGCAACCGTC	TGCGCGTGCG	GCTGACCGGC	CTGACCATGG	650
	CCGAGAAAGTT	CCGCGACGAA	GGCCGCGACA	TCCTGTTCTT	CGTGGACAAC	700
60	ATCTACCGCT	ACACCCTGGC	CGGTACGGAA	GTGTCCGCGC	TGCTGGGCGG	750

TATGCCGTCG GCAGTGGGCT ACCAGCCCAC GCTGGCCGAA GAAATGGGCA 800
 AGCTGCAAGA GCGCATCACC TCGACCAAGA CCGGCTCGAT CACCTCGAT 849

5 2) INFORMATION FOR SEQ ID NO: 243

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 787 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Acinetobacter baumannii*
 (B) STRAIN: ATCC 19606

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243

	TGAAACTACT	TTAGAAGTTC	AGCAACAAC	TGGTGATGGT	GTTGTTCGTA	50
	CCATCGCAAT	GGGTTCTACA	GAAGGTCTTA	AACGTGGTCT	TACTGTAACT	100
	AGCACAAACG	CACCGATCTC	TGTTCCAGTT	GGTACAGCCA	CTCTTGGCCG	150
25	TATCATGGAC	GTTTTAGGTC	GTCCTATCGA	TGAAGCAGGT	CCTGTTGCGA	200
	CTGAAGAACG	TTTGCCGATT	CACCGTCAAG	CGCCTTCTTA	TGCTGAACAA	250
	GCAGCTTCTA	CTGACCTTTT	AGAAACTGGT	ATTAAAGTCA	TCGACTTACT	300
	TTGCCCCGTT	GCGAAAGGTG	GTAAAGTTGG	TTTATTCGGT	GGTGCTGGTG	350
	TTGGTAAAC	CGTTAACATG	ATGGAATTGA	TCAACAACAT	CGCGAAAGCA	400
30	CACTCAGGTT	TATCTGTGTT	TGCTGGTGTT	GGTGAGCGTA	CTCGTGAAGG	450
	TAATGACTTC	TATCAGGAAA	TGAAAGATTC	TAACGTTCTT	GACAAAGTAG	500
	CAATGGTCTA	CGGTCAGATG	AACGAGCCAC	CAGGTAACCG	TTTACGCGTA	550
	GCGTTAACTG	GTTTGACTAT	GGCTGAATAC	TTCCGTGATG	AAAAAGACGA	600
	AAACGGTAAA	GGTCGTGACG	TATTATTATT	CGTCGACAAC	ATCTACCGTT	650
35	ATACACTTGC	AGGTACTGAA	GTATCAGCAT	TGTTAGGTCG	TATGCCATCT	700
	GCGGTAGGTT	ACCAACCTAC	ACTTGCAGAA	GAAATGGGTG	TTCTTCAAGA	750
	GCGTATTACA	TCTACTAAAT	CTGGTTCGAT	CACTTCG		787

40 2) INFORMATION FOR SEQ ID NO: 244

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Acinetobacter lwoffii*
 (B) STRAIN: CDCF 3697

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244

	GTTCTTAAGA	TCTATGACGC	TCTCCACGTT	GATGGCACTG	AAACTACATT	50
	AGAAGTTCAG	CAACAACCTG	GTGATGGCGT	AGTTCGTACT	ATTGCAATGG	100
	GTTCTACTGA	AGGCCTTAAG	CGTGGTTTGA	ACGTAACATA	CACTAACGCG	150
60	CCGATTCTCTG	TACCAAGTAG	TACAGCGACT	CTAGGTCGTA	TCATGGACGT	200

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TCTTGGTCGC CCAATCGACG AAGCTGGTCC AGTTGCGACT GAAGCGCGTT 250
TGCCGATTCA CCGTCAAGCA CCTTCTTATG CTGAACAAGC AGCTTCTACT 300
GACCTTTTAG AAAGTGGTAT TAAAGTCATC GACTTACTTT GCCCGTTCGC 350
5 TAAAGGTGGT AAAGTTGGTC TGTTCCGGTGG TGCCGGTGTT GGTAAACTG 400
TAAACATGAT GGAGTTGATC AACAAACATCG CTAAAGCGCA CTCAGGTTTA 450
TCTGTATTTC CTGGTGTGG TGAGCGTACT CGTGAAGGTA ATGACTTCTA 500
TCACGAGATG AAAGACTCAA ACGTTCTAGA CAAAGTAGCA ATGGTCTACG 550
GTCAGATGAA CGAGCCACCG GGTAACCGTT TACGCGTAGC GTTGACTGGT 600
TTGACCATGG CTGAGTACTT CCGTGACGAG AAAGACGAAA ACGGCAAAGG 650
10 CCGTGACGTA CTATTGTTCG TAGATAACAT CTACCGTTAT AACTAGCAG 700
GTACTGAAGT ATCAGCACTT CTAGGTCGTA TGCCGCTGTC AGTAGGTTAC 750
CAACCGACAC TTGCAGAAGA GATGGGTGTT CTTCAAGAAC GTATTACATC 800
GACTAAGTCT GGTTCGATTA CGTCA 825

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15

2) INFORMATION FOR SEQ ID NO: 245

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20 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 837 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Staphylococcus saprophyticus
        (B) STRAIN: CSG-197
30

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245

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CAATGAAGTT CCAGAAATTA ACAATGCCTT AGTCGTAGAC GTTGAAAGAG 50
ATGAAGGTAC AGTATCTCTT ACATTAGAAG TGGCATTACA ACTTGGCGAT 100
35 GATGTCGTAC GTACAATTGC AATGGATTCT ACTGATGGTG TTAAACGTGG 150
TACAGAAGTT CGAGATAGCG GAGATAGCAT CAGTGTTCCA GTTGGTGATG 200
CTACGTTAGG ACGTGTGTTT AATGTTCTTG GTGATACAAT TGACTTAGAC 250
GAGAAGCTTG ATACTTCTGT CAAACGTGAT CCAATTCATA GAGAAGCACC 300
TGCATTTCGAT CAATTATCAA CAAAAGTTGA AATCTTAGAA ACAGGTATTA 350
40 AAGTAATTGA TTTACTTGCA CCATATATTA AAGGTGGTAA AATCGGTTTA 400
TTCGGTGGCG CTGGTGTAGG TAAAACAGTA TTAATTCAAG AATTAATTAA 450
TAATATAGCT CAAGAACATG GTGGTATTTC AGTATTTGCC GGCGTAGGTG 500
AACGTACGCG TGAAGGTAAT GACTTATACT ACGAAATGAG TGATAGTGGT 550
GTTATTAAGA AAACAGCTAT GGTCTTCGGA CAAATGAATG AGCCACCTGG 600
45 TGCGCGTATG CGTGTTCCTT TATCAGGCTT AACAAATGGCT GAACACTTCC 650
GTGATGTACA AGGACAAGAT GTTTTACTAT TTATTGATAA CATATTTCAGA 700
TTTACGCAAG CTGGTTCAGA AGTATCAGCA CTATTAGGTC GTATGCCATC 750
AGCCGTTGGT TATCAACCTA CCCTTGCTAC TGAAATGGGT CAATTACAAG 800
50 AACGTATTAC ATCAACAAC TAAAGGATCTG TAACGTC 837

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2) INFORMATION FOR SEQ ID NO: 246

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55 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 851 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
60

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Alcaligenes faecalis*

(B) STRAIN: ATCC 15554

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246

10	TTCCCCCGCG	ACAGCATCCC	TAAAGTCTAC	GAAGCATTGA	CGCTCGTTGA	50
	CGAAAGTTTCG	GCTTTCGCAG	AAAAAGGCCT	GACTTTTGAA	GTACAGCAAC	100
	AATTGGGTGA	CGGTGTAGTT	CGCACCATCG	CCATGGGTTC	CAGCGACGGC	150
	CTGCGCCGCG	GTATGGAAGT	GGCCGGTTTCG	GGCGCTCCCA	TCTCCGTTCC	200
	CGTGGGTGTC	GGCACCTTGG	GTCGCATTAT	GGACGTTCTG	GGTCGCCCTA	250
	TTGACGAAGT	CGGTCTTATT	CAGTCCGACG	AGCGTCGCGC	CATTACACCAG	300
	CCTGCGCCTA	CTTTCGACGA	ACTGTGCCT	TCCGTAGAGC	TGCTGGAAAC	350
15	CGGTATTAAA	GTGATTGACC	TGGTTTGCCC	GTTCCGCCAAG	GGTGGTAAGG	400
	TTGGTCTGTT	CGGTGGTGCC	GGTGTGGGCA	AGACCGTGAA	CATGCTGGAG	450
	CTGATCAACA	ACATCGCCAA	GGCACACAGC	GGTCTGTCCG	TGTTTGCCCG	500
	TGTGGGTGAG	CGTACCCGTG	AAGGTAACGA	CTTCTACCAC	GAAATGGCCG	550
	ATGCTGGCGT	TATCCAGATG	GACAACTGA	GCGAGTCCAA	AGTGGCCATG	600
20	GTGTTCCGGT	AGATGAACGA	ACCTCCAGGC	AACCGTCTGC	GTGTGGCACT	650
	GTCCGGCCTG	ACCATGGCCG	AGAAGTTCGG	TGACGAAGGC	CGTGACATCC	700
	TGTTCTTTGT	GGACAACATC	TACCGCTACA	CGCTGGCCCG	TACAGAAGTG	750
	TCCGCTCTGC	TGGGTCTGAT	GCCTTCCGCA	GTGGGTACC	AGCCTACGCT	800
25	GGCCGAGGAA	ATGGGTAAGC	TGCAAGAGCG	CATTACCTCC	ACCAAGACCG	850
	G					851

30 2) INFORMATION FOR SEQ ID NO: 247

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 846 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bacillus anthracis*

(B) STRAIN: 4229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247

45	GATGGCGGAA	AGCTACCAGA	AATCTACAAC	GCCCTTACGG	TAAAACAGAG	50
	CAACGAAAAC	GGAACAAGCA	TTAACTTAAC	ATTTGAAGTT	GCACTTCATT	100
	TAGGTGATGA	CACAGTTCGT	ACAGTTGCAA	TGTCTTCCAC	AGATGGACTT	150
	GTTCTGTGGCA	CAGAAGTAGA	AGATACTGGT	AAAGCAATCT	CTGTACCAGT	200
	TGGTGATGCA	ACACTTGGTC	GTGTATTTAA	CGTATTAGGT	GATGCAATTG	250
50	ACTTAGATGG	TGAGGTTCCT	GCGGATGTAC	GTCGTGATCC	AATTCACCGT	300
	CAAGCACCTG	CATTCTGAAGA	ATTATCTACT	AAAGTAGAAA	TTCTTGAAAC	350
	TGGTATTAAA	GTAGTAGACT	TACTTGCTCC	TTACATTAAG	GGTGGTAAGA	400
	TCGGTCTATT	CGGTGGTGCC	GGTGTAGGTA	AAACGGTATT	AATTCAGGAA	450
	TTAATCAATA	ACATCGCACA	AGAACACGGT	GGTATCTCTG	TATTCGCTGG	500
55	TGTAGGTGAG	CGTACTCGTG	AGGGTAATGA	CTTATACCAC	GAAATGAGCG	550
	ATTCTGGCGT	AATTAAGAAA	ACTGCGATGG	TATTCGGACA	AATGAACGAG	600
	CCACCTGGAG	CACGTCAACG	TGTTGCGTTA	ACAGGTTTAA	CAATGGCTGA	650
	GCATTTCCGT	GATGAGCAAG	GACAAGATGT	ACTTCTGTTT	ATCGATAATA	700
60	TCTTCCGTTT	CACGCAAGCA	GGTTCTGAAG	TATCTGCCCT	TCTTGGCCGT	750

ATGCCATCTG CGGTAGGTTA CCAACCAACA CTTGCAACAG AAATGGGTCA 800
 ATTACAAGAG CGTATTACAT CTACAAATAA AGGGTCTATC ACGTCT 846

5

2) INFORMATION FOR SEQ ID NO: 248

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 810 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacillus cereus*
 (B) STRAIN: ATCC 14579

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248

CCAGAAATCT	ACAATGCCCT	TACGGTAAAA	CAAAGCAACG	AAAACGGAAG	50
CATGAACCTA	ACATTTGAAG	TTGCACTTCA	TTTAGGTGAT	GATACAGTTC	100
GTACAGTTGC	GATGTCTTCC	ACAGATGGAC	TTGTTCTGGT	CACAGAAGTA	150
25 GAAGATACTG	GTAAAGCAAT	CTCTGTACCA	GTGTTGATG	CAACACTTGG	200
ACGTGTATTC	AACGTATTAG	GTGATGCAAT	TGACTTAGAT	GGTGAACCTC	250
CTGCGGATGT	ACACCGTGAT	CCAATTCACC	GTCAAGCACC	TGCATTGCGA	300
GAATTATCTA	CTAAAGTAGA	AATTCTTGAA	ACTGGTATTA	AAGTAGTAGA	350
CTTACTTGCT	CCTTACATTA	AGGGTGGTAA	GATCGGCCTA	TTCGGTGGTG	400
30 CCGGCGTAGG	TAAAACAGTA	TTAATTCAGG	AGTTAATCAA	TAACATCGCA	450
CAAGAGCACG	GTGGTATCTC	TGTATTGCTG	GGTGTAGGTG	AGCGTACTCG	500
TGAGGGTAAT	GACTTATACC	ACGAAATGAG	CGATTCTGGC	GTAATCAAGA	550
AAACTGCGAT	GGTATTGCGA	CAAATGAACG	AGCCACCTGG	AGCACGTCAA	600
CGTGTTGCAT	TAACAGGTTT	AACAATGGCT	GAGCATTTCC	GTGATGAGCA	650
35 AGGACAAGAC	GTACTTCTGT	TCATCGATAA	CATCTTCCGT	TTCACGCAAG	700
CGGGTTCTGA	AGTATCTGCC	CTTCTTGGTC	GTATGCCATC	TGCGGTAGGT	750
TACCAACCAA	CACCTGCAAC	AGAAATGGGT	CAATTACAAG	AGCGTATTAC	800
ATCTACAAAT					810

40

2) INFORMATION FOR SEQ ID NO: 249

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 944 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacteroides distasonis*
 (B) STRAIN: ATCC 8503

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249

CTTTGATTAT	GGGACAGAAG	AAACAGTAAC	CCTCCCCCGT	ATCCACGACG	50
CCATGGAGAT	TTCCCGCCCA	AACGGAAAGA	TCTTGATCGT	CGAAGTTCAG	100
60 CAACACATCG	GGGAAAACAC	CGTCCGTACC	GTAGCGATGG	ATACGACCGA	150


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CGGATTGAGA CGAGGCATGG AGGCCGTGTC ATACGGAATG CCCATCACCA 200
TGCCGACCGG CGACCAAGTC AAAGGACGTT TAATGAATGT CACCGGCGAC 250
CCTATCGATG GCATGGCCCA GCTTACTAAA GACGGGGCTC TTCCCATCCA 300
TCGTGAGCCT CCTAAATTCG AGGATCTGAC AACGACCCAA GAGGTCTTGT 350
5 ACACGGGTAT TAAAGTAATC GATTTATTGG AACCTTACGC CAAAGGAGGC 400
AAGATCGGAC TTTTCGGAGG AGCCGGAGTC GGCAAAACGG TATTGATCAT 450
GGAATTGATC AACAAACATCG CAAAGAAAAA CAACGGATTG TCCGTCTTCG 500
CCGGTGTGGG TGAACGTACA CGTGAAGGAA ATGACCTATT GCGTGAAATG 550
ATCCAATCCG GTGTCATCCG ATACGGCGAG GAGTTTAAGA AGAGTATGGA 600
10 GGCAGGCAAC TGGGACTTGT CGAAGATCGA TTACGATGAA TTGGCTAAGT 650
CGCAGGCTAC CTTGGTATTC GGGCAGATGA ACGAACCGCC GGGCGCCCGC 700
TCGTCCGTGG CTTTATCCGG TTTGACGATG GCCGAATCCT TCCGTGACAA 750
AGCCTCTGAG GGAGAAAGAA AAGATATATT ATTCTTCATC GATAATATCT 800
TCCGTTTCAC CCAAGCCGGT TCCGAGGTTT CCGCCTTGCT GGGGCGTATG 850
15 CCTTCCGCCG TAGGTTACCA ACCGACATTG GCCACGAAA TGGGAGCTAT 900
GCAAGAGCGT ATCACTTCAA CCAAGAAGGG CTCCATCACC TCCG 944

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20 2) INFORMATION FOR SEQ ID NO: 250

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 939 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bacteroides ovatus*
 (B) STRAIN: ATCC 8483

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250

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35 TTGAGGGTAC GGATGCAGAA TTGGTGCTGC CAAGCATCCA CGACGCACTG 50
GAGATAAAGA GGCCAAACGG CAAAATACTG GTTGTAGAAG TTCAGCAACA 100
TATCGGCGAA AATACGGTGC GTACCGTAGC GATGGACAGT ACTGACGGAC 150
TTCAGAGAGG CATGAAAGTG TATCCCACCG GAGGCCCGAT CACGATGCCG 200
40 ATTGGCGAAG AGATTAAAGG ACGACTGATG AACGTAGTCG GTGATTTCGAT 250
CGACGGTATG AAAGGACTCG ACCGCAAAGG TGCATATTCC ATTCATCGCG 300
ACCCCCCTAA GTTTGAGGAT TTGACTACTG TGCAAGAGGT GCTCTTCACA 350
GGTATCAAAG TGATCGACCT GCTCGAACCG TATGCCAAAG GTGGTAAAAT 400
CGGTTTGTTC GGCGGTGCCG GTGTAGGAAA GACTGTATTG ATTCAGGAAC 450
45 TTATCAATAA TATCGCCAAG AAACATAATG GATTCTCTGT ATTTGCCGGA 500
GTAGGTGAAC GTACCCGTGA AGGTAACGAC TTGCTGCGCG AAATGATTGA 550
ATCCGGTGTA ATCCGTTACG GCGAAGCATT CAAAGAAGGA ATGGAGAAAG 600
GTCACTGGGA TCTTTCGAAA GTGGATTATA ACGAACTGGA GAAATCGCAA 650
GTGTCTCTGA TTTTCGGTCA GATGAACGAG CCTCCGGGCG CACGTGCCTC 700
50 TGTGGCATTG TCCGACTGA CGGTGGCGGA ATCTTTCCGC GACGCAGGAA 750
AAGAAGGTGA GAAACGCGAT ATTCTGTTCT TTATTGATAA TATCTTCCGT 800
TTCACGCAAG CAGGTTTCAGA AGTGCCGCC CTTTTGGGAC GTATGCCCTC 850
CGCTGTTGGT TACCAGCCCA CGTTGGCTAC GGAAATGGGT GCGATGCAGG 900
AACGTATCAC GTCTACCCGC AAAGGTTCTA TCACCTCCG 939
55

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2) INFORMATION FOR SEQ ID NO: 251

60 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 833 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

10

(A) ORGANISM: *Leclercia adecarboxylata*

(B) STRAIN: ATCC 23216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251

15	CGAATTCCCT CAGGATGCCG TACCGCGCGT GTACGATGCT CTTGAGGTTC	50
	AGAATGGTAA TGAGAGCCTG GTGCTGGAAG TTCAGCAGCA GCTCGGCGGC	100
	GGTATTGTGC GTACCATCGC CATGGGTCTT TCCGACGGTC TCGTCTGTGG	150
	TCTGGAAGTT AAAGACCTCG AGCACCCAAT CGAAGTACCA GTAGGTAAAG	200
	CAACCCTGGG CCGTATCATG AACGTCCTGG GTCAGCCGAT CGACATGAAA	250
	GGCGACATCG GCGAAGAAGA GCGTTGGGCT ATCCACCGTT CAGCACCTTC	300
20	CTATGAAGAG CTGTCCAGCT CTCAGGAAC GCTGGAAACC GGCATCAAAG	350
	TTATCGACCT GATGTGTCCG TTCGCGAAGG GCGGTAAAGT TGGTCTGTTC	400
	GGCGGTGCGG GTGTAGGTAA AACC GTAAAC ATGATGGAGC TGATCCGTAA	450
	CATCGCGATC GAGCACTCCG GTTACTCCGT GTTTCAGGC GTGGGTGAGC	500
	GTAATCGTGA GGGTAACGAC TTCTACCACG AAATGACCGA CTCCAACGTT	550
25	CTGGACAAAG TATCCCTGGT TTACGGCCAG ATGAACGAGC CACCAGGAAA	600
	CCGTCTGCGC GTTGCCTGA CCGGCCTGAG CATGGCTGAG AAGTTCCGTG	650
	ACGAAGGTCG TGACGTACTG CTGTTCGTTG ACAACATCTA CCGTTACACC	700
	CTGGCCGGTA CCGAAGTATC CGCACTGCTG GGTCTGATGC CATCAGCAGT	750
	AGGCTACCAG CCGACCCTGG CCGAAGAGAT GGGTGTCTTG CAGGAACGTA	800
30	TCACCTCTAC CAAAACCGGT TCTATCACCT CCG	833

2) INFORMATION FOR SEQ ID NO: 252

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 819 bases

(B) TYPE: Nucleic acid

40

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

45

(A) ORGANISM: *Stenotrophomonas maltophilia*

(B) STRAIN: CDC F3338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252

50	GTGTACGACG CACTGAAGGT GGAAACACC GAGATCACCC TCGAAGTCCA	50
	GCAGCAGCTG GCGCAGGCG TGGTGCGTAC CATCGCCCTC GGTTCCACCG	100
	ACGGCCTGAA GCGCAACCTG GTTGCCGTCA ACACCGGCCG TGGCATCTCG	150
	GTGCCGGTCG GCGCCGGCAC CCTGGGCCGC ATCATGGACG TGCTGGGCCG	200
	TCCGATCGAC GAAGCCGGCC CGTCTGCTGC CAGCGACAAC TGGGAAATCC	250
55	ACCGCGCTGC GCCGTCGTAT GAAGACCAGT CCCC GGCCAC CGAGCTGCTG	300
	GAAACCGGCA TCAAGGTCAT CGACCTGATG TGCCCGTTTC CCAAGGGCGG	350
	CAAGGTCGGC CTGTTCCGCG GCGCCGGCGT CCGCAAGACC GTCAACATGA	400
	TGGAACATGAT CAACAACATC GCCAAGGCGC ACAGCGGCCT GTCCGTGTTC	450
	GCCGGCGTGG GTGAGCGTAC CCGTGAGGGC AACGACTTCT ACCACGAGAT	500
60	GAAGGACTCC AACGTCCTGG ACAAGGTGGC GATGGTGTAC GGCCAGATGA	550

ACGAGCCGCC GGGCAACCGT CTGCGCGTCG CCCTGACCGG CCTGACCATG 600
 GCCGAGTACT TCCGCGATGA GAAGGACGAA AACGGCAAGG GCAAGGACGT 650
 CCTGCTGTTT GTCGACAACA TCTACCGCTA CACCCTGGCC GGTACCGAAG 700
 TGTCGGCACT GCTGGGCCGC ATGCCGTCCG CGGTGGGTTA CCAGCCGACC 750
 5 CTGGCCGAGG AAATGGGCGT CCTGCAGGAG CGCATCACCT CGACCAAGAA 800
 TGGTTCGATC ACCTCGATC 819

10 2) INFORMATION FOR SEQ ID NO: 253

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 864 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bartonella henselae*
 (B) STRAIN: ATCC 49882

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253

25 AGTTTGAAGG CCCTTTGCCA AATATTCTCA ATGCATTAGA AACAGATAAT 50
 TTGGGCAATC GGCTAGTTTT AGAAGTTGCT CAGCATTTGG GTGAAAATAC 100
 CGTGCGTACC ATTGCCATGG ATACTACCGA TGGTCTTGTC CGTGGTCAAA 150
 AAGTTTTTGA TACAGGAACA CAGATCAGTG TTCCCGTGGG AGAAGCAACA 200
 30 CTTGGTCGTA TTATGAATGT GATTGGAGAG CCGGTGATA ATGTTGGCCC 250
 AATTGCTACA AGCAAAACCC GTTCCATTCA CCAAGAGGCT CCTGAATATG 300
 TGGAGCAATC AACC GCATCA GAAATCCTTG TGACTGGTAT TAAAGTCGTT 350
 GATCTGTTAG CTCCTTATTC TAAAGGGGGG AAGGTTGGTT TGTGTTGGAGG 400
 TGCCGGTGTG GGTAAAACCG TTCTCATTAT GGAGCTTATC AACAAATATTG 450
 35 CAAAGGCGCA TGGTGGCTAT TCAGTGTGTTG CCGGTGTTGG TGAACGTACA 500
 CGTGAGGGGAA ATGATCTTTA TTATGAAATG ATCGAAAGCC GTGTGAATGT 550
 GAATCCAAAA GACAACAATG GTTCAACAGA AGGATCAAAA TGTGCACTCG 600
 TTTATGGGCA AATGAATGAA CCACCAGGGG CGCGTGCACG TGTGGCTCTT 650
 TCAGGATTGA CCATTGCAGA AAGTTTCCGT GATGAGGGAC AAGATGTTTT 700
 40 GTTCTTCGTA GATAATATTT TCCGTTTAC GCAAGCAGGC GCTGAAGTGT 750
 CAGCTCTTTT AGGGCGTATT CCTTCTGCTG TAGGGTATCA GCCAACTTTG 800
 GCAACTGATA TGGGGGCTTT GCAAGAGCGT ATTACCACTA CAAGAACAGG 850
 CTCTATTACC TCTG 864

45

2) INFORMATION FOR SEQ ID NO: 254

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 866 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bifidobacterium adolescentis*
 (B) STRAIN: ATCC 15703

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254

	TTCCCCGGTGG	GCCACCTGCC	CGACATTTAC	AATGCACTTA	CCGTTGAACT	50
	GKCCAACACC	GGYGTCCACG	AASAGGGCGA	GACCACCAAG	AAGATCACCC	100
5	TTGMGGTTGA	ACAGCATCTT	GGCGATTCCA	CCGTGCGTAC	CGTCGCTCTG	150
	AAGCCGACTG	ACGGCCTTGT	GCGTGGCGCC	ACCGTGTATG	ACACCGGCGG	200
	CCCgatctct	GTGCCGGTTG	GCGATGTCAC	CAAGGGCCAC	GTATTGACG	250
	TGTCCGGCAA	CATCCTCAAC	AAGAAGGCCG	ACGAGACCGT	TAAGGTTACC	300
	GAACGTTGGT	CTATCCACCG	TAACCCGCCG	GCATTCGACC	AGCTGGAGTC	350
10	CAAGACCCAG	ATGTTGAAA	CCGGTATCAA	GGTCATCGAT	TTGCTGACCC	400
	CGTATGTGCA	GGGCGGCAAG	ATCGGTCTGT	TCGGCGGCGC	AGGCGTCGGC	450
	AAGACCGTGC	TGATCCAGGA	AATGATTCAG	CGTGTGGCTC	AGAACCACGG	500
	CGGTGTGTCC	TGTTTCGCAG	GCGTCGGCGA	GCGTACCCGT	GAGGGTAACG	550
	ATCTGATCGG	CGAAATGGAC	GAAGCCGGCG	TGCTCGAGAA	GACCGCACTG	600
15	GTCTTCGGCC	AGATGGATGA	GCAGCCGGGT	ACCCGTCTGC	GCGTGCCGCT	650
	GACCGCACTG	ACCATGGCAG	AGTACTTCCG	TGACGTACAG	AATCAGGACG	700
	TGCTGCTGTT	CATCGATAAC	ATCTTCCGTT	TCACCCAGGC	TGGTTCGAG	750
	GTGTCCACCC	TGCTCGGCCG	TATGCCGTCC	GCAGTGGGCT	ACCAGCCGAA	800
	CCTGGCCGAT	GAGATGGGCG	CGCTGCAGGA	GCGAATCACT	TCGACCCGTG	850
20	GACACTCCAT	CACCTC				866

2) INFORMATION FOR SEQ ID NO: 255

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 842 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Brucella abortus*
 (B) STRAIN: S2308

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255

40	AAGGCCAGCT	GCCGCTGATC	CTGAACGCGC	TTGAAGTGGA	CAATCAGGGC	50
	CATCGTCTGG	TTCTCGAAGT	TGCCCAGCAC	CTCGGCGAAG	ACACCGTGCG	100
	CACCATCGCC	ATGGACGCGA	CCGAAGGTCT	CGTTCGCGGT	CAGGAAGCAC	150
	GCGACACTGG	CGAACCgATC	ATGGTGCCGG	TCGGCGTCTGA	AACGCTTGGC	200
	CGCATCATGA	ACGTCATCGG	CGAGCCGGTT	GACGAAGCAG	GCCCCATCAA	250
45	GACCAAGGCA	ACCCGCGCCA	TCCACCAGAA	CGCGCCGGAA	TATATCGAAC	300
	AGTCGACCGA	AGCCGAAATT	CTGGTCACGG	GCATCAAGGT	CGTCGACCTT	350
	CTGGCGCCTT	ACGCCAAGGG	CGGCAAGATC	GGCCTCTTCG	GCGGTGCAGG	400
	CGTCGGCAAG	ACCGTTCTCA	TCATGGAACT	CATCAACAAC	GTCGCCAAGG	450
	CGCACGGCGG	TTATTCCGTG	TTCGCAGGCG	TCGGTGAGCG	TACCCGTGAG	500
50	GGCAACGACC	TTTACCACGA	AATGATCGAG	TCGGGCGTGA	ACAAGCTCGG	550
	CGGCGGCGAA	GGCTCCAAGG	CAGCCCTCGT	TTACGGCCAG	ATGAACGAAC	600
	CCCCGGGTGC	CCGCGCCCCG	GTTGCCCTTT	CCGGTCTGAC	GGTTGCTGAA	650
	AACTTCCGTG	ACCAGGGCCA	GGACGTTCTG	TTCTTCGTGG	ACAACATCTT	700
	CCGCTTCACG	CAGGCAGGTT	CGGAAGTGTC	GGCTCTTCTC	GGCCGTATTC	750
55	CTTCCGCTGT	GGGTTATCAG	CCGACGCTGG	CAACCGACAT	GGGCGCCATG	800
	CAGGAACGCA	TCACCACGAC	GACCAAGGGT	TCGATCACCT	CG	842

60 2) INFORMATION FOR SEQ ID NO: 256

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cedecea davisae*
 (B) STRAIN: ATCC 33431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256

```

15  CGAGTTCCCT CAGGACGGCG TACCGCGCGT TKATGATGCG CTTGAAGTAC      50
    AAAATAACAG CGAGCAGCTG GTGCTGGAAG TTCAGCAGCA GCTCGGCGGC      100
    GGTATCGTGC GTACCATCGC TATGGGTCTT TCCGACGGTC TCGTTCGTGG      150
    TCTGGAAGTT AAAGACCTCG AGCACCCGAT CGAAGTCCCG GTAGGTAAAG      200
    CGACCCTTGG CCGTATCATG AACGTGCTGG GTCAGCCGAT CGACATGAAA      250
20  GGCGATATCG GCGAAGAAGA CCGTTGGGCT ATTACCCGCG CTGCACCTTC      300
    CTATGAAGAG CTGTCCAGCT CTCAGGAACT GCTGGAAACC GGCATCAAAG      350
    TAATCGACCT TATCTGTCCG TTCGCTAAGG GCGGTAAAGT AGGTCTGTTC      400
    GGTGGTGCGG GCGTGGGTAA AACCGTAAAC ATGATGGAGC TTATCCGTAA      450
25  CATCGCGATC GAGCACTCCG GCTACTCCGT GTTTCGCGGC GTGGGTGAGC      500
    GTACTCGTGA GGGTAACGAC TTCTATCACG AAATGACCGA CTCCAACGTT      550
    CTGGACAAAG TTGCCCTGGT TTACGGCCAG ATGAACGAGC CACCGGGTAA      600
    CCGTCTGCGC GTAGCGCTGA CCGGTCTGAC CATCGCGGAG AAATTCCGTG      650
    ACGAAGGTCG TGACGTTCTG CTGTTCGTTG ATAACATCTA CCGTTACACC      700
30  CTGGCCGGTA CTGAAGTATC CGCGCTGCTG GGTTCGTATGC CTTCTGCGGT      750
    AGGTTACCAG CCAACTCTGG CGGAAGAGAT GGGTGTTCCT CAGGAGCGTA      800
    TTACCTCCAC CAAGACCGGT TCCATCACCT CCG                                833
  
```

2) INFORMATION FOR SEQ ID NO: 257

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cedecea lapagei*
 (B) STRAIN: ATCC 33432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257

```

50  TTCCCTCAGG ACGGCGTACC GCGCGTATAT GACGCGCTTG AGGTACAGAA      50
    TAACAGCGAG AAGCTGGTGC TGGAAGTTCA GCAGCAGCTC GGCGGCGGTA      100
    TCGTACGTAC CATCGCAATG GGTTCCTCCG ACGGTCTGCG TCGTGGTCTG      150
55  GAAGTGAAAG ACCTCGAGCA CCCGATCGAA GTCCCGGTAG GTAAAGCGAC      200
    TCTGGGTCGT ATCATGAACG TGCTGGGTCA GCCAATTGAT ATGAAAGGCG      250
    ACATCGGCGA AGAAGATCGT TGGGCGATTG ACCGCGCAGC ACCTTCCTAT      300
    GAAGAGCTGT CCAGCTCTCA GGAACCTGCTG GAAACCGGCA TCAAAGTTAT      350
    CGACCTGATT TGTCCGTTTC CTAAGGGCGG TAAAGTTGGT CTGTTCGGTG      400
60  GTGCGGGCGT AGGTAAAACC GTAAACATGA TGGAGCTGAT CCGTAACATC      450
  
```

```

GCGATCGAGC ACTCCGGTTA CTCCGTGTTT GCAGGCGTGG GTGAGCGTAC      500
TCGTGAGGGT AACGACTTCT ACCACGAGAT GACCGACTCC AACGTTCTGG      550
ACAAAGTTGC ACTGGTTTAC GGCCAGATGA ACGAGCCGCC AGGTAACCGT      600
CTGCGCGTAG CGCTGACCGG TCTGACCATC GCGGAGAAAT TCCGTGACGA      650
5  AGGCCGTGAC GTTCTGCTGT TCGTCGATAA CATCTATCGT TATACCCTGG      700
   CCGGTACAGA AGTTTCTGCA CTGCTGGGTC GTATGCCATC TCGGTAGGT      750
   TATCAGCCTA CTCTGGCAGA AGAGATGGGT GTTCTTCAGG AGCGTATTAC      800
   CTCCACCAAG ACCGGTTCCA TCACTTCCG      829

```

10

2) INFORMATION FOR SEQ ID NO: 258

(i) SEQUENCE CHARACTERISTICS:

```

15  (A) LENGTH: 830 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Cedecea neteri
    (B) STRAIN: ATCC 33855

```

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258

```

TCCCTCAGGA CGGCGTACCG CGCGTTTATG ACGCGCTTGA GGTACAGAAC      50
AACAATGAGA AGCTGGTGCT GGAAGTTCAG CAGCAGCTCG GCGGCGGTAT      100
30  CGTGCGTACC ATCGCAATGG GTTCTTCCGA CCGTCTGCGT CGTGGTCTGG      150
   TAGTAACAGA CCTCGAGCAC CCGATCGAAG TCCCAGTAGG TAAAGCGACC      200
   CTTGGCCGTA TCATGAACGT GCTGGGTCAG CCGATCGACA TGAAAGGCGA      250
   CATCGGCGAA GAAGACCGTT GGGCGATTCA CCGCGCAGCA CCTTCCTACG      300
   AAGAGCTGTC CAGCTCTCAG GAATTGCTGG AAACCGGCAT CAAAGTTATC      350
35  GACCTGATTT GTCCGTTCGC TAAGGGCGGT AAAGTAGGTC TGTTCGGTGG      400
   TGCGGGCGTA GGTAAAACCG TAAACATGAT GGAGCTGATC CGTAACATTG      450
   CGATCGAGCA CTCCGGTTAT TCCGTGTTTG CGGGCGTGGG TGAGCGTACT      500
   CGTGAGGGTA ACGACTTCTA CCACGAAATG ACCGACTCCA ACGTTCTGGA      550
   TAAAGTAGCA CTGGTTTACG GCCAGATGAA CGAGCCACCA GGTAACCGTC      600
40  TGCGCGTAGC GCTGACCGGT CTGACCATCG CGGAAAAATT CCGTGACGAA      650
   GGCCGCGACG TTTTGCTGTT CGTTGATAAC ATCTACCGTT ATACCCTGGC      700
   CGGTACCGAA GTATCTGCAC TGCTGGGTCG TATGCCTTCT GCGGTAGGTT      750
   ATCAGCCAAC TCTGGCAGAA GAGATGGGTG TTCTTCAGGA GCGTATTACC      800
45  TCCACCAAGA CCGGTTCTAT CACCTCCGTA      830

```

2) INFORMATION FOR SEQ ID NO: 259

(i) SEQUENCE CHARACTERISTICS:

```

50  (A) LENGTH: 931 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Chryseobacterium meningosepticum
    (B) STRAIN: CDC B7681

```

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259

```

5   TTTCAGGAAG TAGAGGAACT ACCAAACATT TATGACGCAC TTGAAGTTGT      50
    CAGAGAAGGC CAGAAAGGTC TGATCTTAGA AGTTGAACAA CACATCGGTG      100
    AGGATACAGT GAGATGTATC GCTATGGATG CAACAGACGG ACTTCAAAGA      150
    GGACAATCTG TAATAGGACA TGAAGACAA ATTACTATGC CTATTGGTGA      200
    AGAAGTAAAT GGTAGATTGT TCAACGTGGT AGGAGATGCT ATCGACGGAC      250
    TTCAGGAATT ATCTAAAGAC AATGGTTTGC CAATCCACAG AGAAGCACCT      300
10  AAATTCGATC AGTTATCAAC TTCTGCTGAA GTACTATATA CAGGTATCAA      350
    AGTAATCGAC CTTATCGAGC CTTATGCAA AGGTGGTAAA ATTGGTTTGT      400
    TCGGTGGTGC TGGTGTAGGT AAAACAGTAT TGATCCAGGA ATTGATTAAT      450
    AACATTGCTA AAGGACACGG TGGTCTTTCT GTATTGCGAG GAGTAGGTGA      500
    GAGAACAAGA GAAGGAAATG ACCTTCTTCG TGAGATGTTA GAGTCTGGTA      550
15  TTATTAAATA TGGTGACGAA TTCATGCATT CTATGGAGAA CGGTGGATGG      600
    GATCTTTCTA AAGTTGACAG TGAGTTGATG AAAGAGTCTA AAGCTGCTTT      650
    CGTTTTTCGA CAGATGAACG AGCCACCAGG TGCAAGAGCA CGTGTAGCCC      700
    TTTCTGGTCT TACTTTAGCT GAATACTACC GTGATGGTGG CGAAAGCGGA      750
    CAAGGTAGAG ACGTTCTTTT CTTCTAGTAC AACATCTTCC GTTTTACACA      800
20  GGCTGGTTCT GAGGTGTCTG CACTTCTAGG TCGTATGCCT TCAGCGGTAG      850
    GTTACCAACC AACTCTAGCT TCTGAGATGG GTGCAATGCA GGAGAGAATT      900
    ACTTCAACTA AAAACGGATC TATTACATCT G                      931

```

25

2) INFORMATION FOR SEQ ID NO:260

(i) SEQUENCE CHARACTERISTICS:

```

30  (A) LENGTH: 726 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Citrobacter amalonaticus
    (B) STRAIN: ATCC 25405

```

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260

```

    GTATCGTACG TACCATCGCA ATGGGTTCTT CCGACGGTCT GCGTCGTGGT      50
    CTGGAAGTCA AAGACCTCGA GCACCCGATC GAAGTCCCGG TAGGTAAAGC      100
    AACCTTGGGT CGTATCATGA ACGTCTGGG TCACCCGATC GACATGAAAG      150
45  GCGATATCGG TGAAGAAGAG CGTTGGGCTA TCCACCGCGC AGCACCGTCC      200
    TATGAAGAGC TGTCCAGCTC TCAGGAAGTCT CTGGAACCG GTATCAAAGT      250
    TATCGACCTG ATGTGTCCGT TCGCGAASGG CCGTAAAGTG GGTCTGTTCG      300
    GTGGTGCGGG TGTAGGTAAA ACCGTAAACA TGATGGAGCT TATCCGTAAC      350
    ATCGCGATCG AGCACTCCGG TTAATCCGTG TTTGCGGGCG TAGGTGAACG      400
50  TACTCGTGAG GGTAACGACT TCTACCACGA AATGACCGAC TCCAACGTTT      450
    TGGATAAAGT ATCCCTGGTA TATGGCCAGA TGAACGAGCC GCCGGGAAAC      500
    CGTCTGCGCG TTGCACTGAC CGGTCTGACC ATGGCAGAGA AATTCCGTGA      550
    CGAAGGTCGT GACGTACTGC TGTTCGTCGA TAACATCTAT CGTTACACCC      600
    TGGCCGGTAC GGAAGTTTCC GCACTGCTGG GTCGTATGCC ATCAGCGGTA      650
55  GGTTACCAGC CGACCCTGGC GGAAGAGATG GGTGTTCTGC AGGAACGTAT      700
    CACTTCTACC AAAACCGGTT CTATCA                      726

```

60 2) INFORMATION FOR SEQ ID NO: 261

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter braakii*
 (B) STRAIN: ATCC 43162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261

```

15  GCCGTACCGC GCGTGTACGA TGCTCTTGAG GTTATGAATG GTAAAGAGAG      50
    CCTGGTGCTG GAAGTTCAGC AGCAGCTCGG CGGCGGTATC GTACGTACCA      100
    TCGCCATGGG TTCTTCCGAC GGTCTGCGTC GTGGTCTGGA AGTTAAAGAT      150
    CTCGAGCACC CGATCGAAGT CCCGGTAGGT AAAGCAACTC TGGGTCGTAT      200
20  CATGAACGTC CTGGGTCACC CGATCGACAT GAAAGGCGAT ATCGGTGAAG      250
    AAGAGCGTTG GGCTATCCAC CGCGCGGCAC CTTCTTATGA AGAGCTGTCC      300
    AGCTCTCAGG AACTGCTGGA AACCGGCATC AAAGTTATCG ACCTGATGTG      350
    TCCGTTTCGCT AAGGGCGGTA AAGTTGGTCT GTTCGGTGGT GCGGGTGTAG      400
    GTAAAACCGT AAACATGATG GAGCTGATCC GTAACATCGC GATCGAACAC      450
25  TCCGGTTACT CCGTGTTTGC GGGCGTGGGT GAACGTACTC GTGAGGGTAA      500
    CGACTTCTAC CACGAAATGA CCGACTCCAA CGTTCTGGAT AAAGTATCCC      550
    TGGTATATGG CCAGATGAAC GAGCCGCCGG GAAACCGTCT GCGCGTTGCT      600
    CTGACCGGTC TGACCATGGC AGAGAAGTTC CGTGACGAAG GTCGTGACGT      650
    TCTGCTGTTC GTTGATAACA TCTATCGTTA CACCCTGGCC GGTACAGAAG      700
30  TATCCGCTCT GCTGGGTCGT ATGCCATCAG CGGTAGGCTA CCAGCCGACC      750
    CTGGCGGAAG AGATGGGTGT TCTTCAGGAA CGTATCACCT CTACCAAAC      800
    CGGTTCTATC AC                                     812
  
```

2) INFORMATION FOR SEQ ID NO: 262

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 811 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter koseri*
 (B) STRAIN: ATCC 27156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262

```

55  GCGCGTGTAC GACGCCCTTG AGGTGCAGAA TGGTAATGAA CATCTGGTGC      50
    TGGAAAGTTCA GCAGCAGCTC GGTGGCGGTA TCGTACGTAC CATCGCCATG      100
    GGTTCCTCCG ACGGCCTGCG TCGTGGTCTG GATGTGAAAG ACCTTGAGCA      150
    CCCGATCGAA GTCCCGGTAG GTAAAGCAAC GCTGGGTCGT ATCATGAACG      200
    TACTGGGCGA ACCAGTAGAC ATGAAAGGCG AGATCGGTGA AGAAGAGCGT      250
    TGGGCTATCC ACCGTGCGGC ACCGTCCTAC GAAGAGTTGT CAAACTCTCA      300
    GGAAGTGTG GAAACCGGTA TCAAAGTTAT CGACCTGATG TGCCCGTTTC      350
    CGAAGGGCGG TAAAGTGGGT CTGTTCCGGT GTGCGGGTGT AGGTAAACC      400
60  GTAAACATGA TGGAGCTGAT CCGTAACATC GCGATCGAAC ACTCCGGTTA      450
  
```



```

CTCCGTGTTT GCGGGCGTAG GTGAACGTAC TCGTGAGGGT AACGACTTCT 500
ACCACGAAAT GACCGACTCC AACGTTATCG ACAAAGTATC CCTGGTTTAC 550
GGCCAGATGA ACGAGCCGCC GGGAAACCGT CTGCGCGTTG CGCTGACCGG 600
CCTGACCATG GCGGAGAAAT TCCGTGACGA AGGTCGTGAC GTTCTGCTGT 650
5 TCGTCGACAA CATCTACCGT TACACCCTGG CCGGTACGGA AGTATCCGCA 700
CTGCTGGGTC GTATGCCTTC AGCGGTAGGT TACCAGCCGA CCCTGGCGGA 750
AGAGATGGGT GTTTTGCAGG AACGTATCAC CTCCACCAAA ACCGGTTCTA 800
TCACCTCCGT A 811

```

10

2) INFORMATION FOR SEQ ID NO: 263

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 816 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter farmeri*
 (B) STRAIN: ATCC 51112

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263

```

GATGCCGTAC CGCGCGTGTA CGATGCTCTT GAGGTTATGA ATGGTAAAGA 50
GAGTCTGGTG CTGGAAGTTC AGCAGCAGCT CGGCGGCGGT ATCGTACGTA 100
30 CCATCGCGAT GGGTTCTTCC GACGGTCTGC GTCGTGGTCT GGAAGTAAAA 150
GACCTCGAAC ACCCGATCGA AGTCCCGGTA GGTAAAGCAA CTCTGGGTCG 200
TATCATGAAC GTCCTGGGTC ACCCGATCGA CATGAAAGGC GATATCGGTG 250
AAGAAGAGCG TTGGGCTATC CACCGCGCAG CGCCATCCTA TGAAGAGCTG 300
TCCAGCTCTC AGGAACTGCT GGAAACCGGT ATCAAAGTTA TCGACCTGAT 350
35 GTGTCCGTTT GCGAAGGGCG GTAAAGTCGG TCTGTTCCGGT GGTGCGGGTG 400
TAGGTAAAC CGTAAACATG ATGGAAGTCA TCCGTAACAT CGCGATCGAG 450
CACTCCGGTT ACTCCGTGTT TGCGGGCGTA GGTGAACGTA CTCGTGAGGG 500
TAACGACTTC TACCACGAAA TGACCGATTC CAACGTTCTG GATAAAGTAT 550
CCCTGGTATA TGGCCAGATG AACGAGCCGC CGGGAACCG TCTGCGCGTT 600
40 CCGCTGACCG GTCTGACCAT GGCAGAGAAA TTCCGTGACG AAGGTCGTGA 650
CGTACTGCTG TTCGTCGATA ACATCTATCG TTACACCCTG GCCGGTACGG 700
AAGTATCCGC ACTGCTGGGC CGTATGCCAT CAGCGGTAGG CTACCAGCCA 750
ACCCTGGCGG AAGAGATGGG TGTTCTGCAG GAACGTATCA CTTCTACCAA 800
AACCGTTTCT ATTACC 816
45

```

2) INFORMATION FOR SEQ ID NO: 264

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter freundii*
 (B) STRAIN: ATCC 8090

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264

```

5  AGGATGCCGT ACCGCGCGTG TACGATGCTC TTGAGGTTAT GAATGGTAAA      50
   GAGAGCCTGG TGCTGGAAGT TCAGCAGCAG CTCGGCGGCG GTATCGTACG      100
   TACCATCGCC ATGGGTTCTT CTGACGGTCT GCGTCGTGGT CTGGAAGTTA      150
   AAGACCTCGA GCACCCGATC GAAGTCCCGG TAGGTAAAGC AACGCTGGGT      200
   CGTATCATGA ACGTTCTGGG TCACCCGATC GACATGAAAG GCGATATCGG      250
   TGAAGAAGAG CGTTGGGCTA TCCACCGTGC AGCACCTTCC TACGAAGAGC      300
10  TGTCAAGCTC TCAGGAACTG CTGGAAACCG GTATCAAAGT TATCGACCTG      350
   ATGTGTCCGT TCGCTAAGGG CGGTAAAGTT GGTCTGTTCC GTGGTGCGGG      400
   TGTAGGTAAA ACCGTAAACA TGATGGAGCT GATCCGTAAC ATCGCGATCG      450
   AACACTCCGG TTACTCCGTG TTTGCGGGCG TAGGTGAACG TACTCGTGAG      500
   GGTAACGACT TCTACCACGA AATGACCGAC TCCAACGTTT TGGACAAAGT      550
15  ATCCCTGGTA TATGGCCAGA TGAACGAGCC GCCTGGAAAC CGTCTGCGTG      600
   TTGCGCTGAC CGGTCTGACC ATGGCTGAGA AGTTCCGTGA CGAAGGTCGT      650
   GACGTTCTGC TGTTTCGTTG TAACATCTAT CTTACACCC TGGCCGGTAC      700
   AGAAGTATCT GCACTGCTGG GTCGTATGCC ATCAGCGGTA GGCTACCAGC      750
   CGACCCTGGC GGAAGAGATG GGTGTTCTGC AGGAACGTAT CACCTCCACC      800
20  AAAACCGGTT CTATCACCT                                     819

```

2) INFORMATION FOR SEQ ID NO: 265

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter koseri*
- (B) STRAIN: ATCC 27028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265

```

40  GATGCCGTAC CGCGCGTGTA CGACGCCCTT GAGGTGCAGA ATGGTAATGA      50
   ACATCTGGTG CTGGAAGTTC AGCAGCAGCT CGGTGGCGGT ATCGTACGTA      100
   CCATCGCCAT GGGTTCTTCC GACGGCCTGC GTCGTGGTCT GGATGTGAAA      150
   GACCTTGAGC ACCCGATCGA AGTCCCGGTA GGTAAAGCAA CGCTGGGTCTG      200
   TATCATGAAC GTACTGGGCG AACCAGTAGA CATGAAAGGC GAGATCGGTG      250
45  AAGAAGAGCG TTGGGCTATC CACCGTGCGG CACCGTCCTA CGAAGAGTTG      300
   TCAAACCTCT AGGAACTGTT GGAAACCGGT ATCAAAGTTA TCGACCTGAT      350
   GTGTCCGTTT GCGAAGGGCG GTAAAGTGGG TCTGTTCTGGT GGTGCGGGTG      400
   TAGGTAAAAC CGTAAACATG ATGGAGCTGA TCCGTAACAT CGCGATCGAA      450
   CACTCCGGTT ACTCCGTGTT TGCGGGCGTA GGTGAACGTA CTCGTGAGGG      500
50  TAACGACTTC TACCACGAAA TGACCGACTC CAACGTTATC GACAAAGTAT      550
   CTTTGGTTTA CGCCAGATG AACGAGCCGC CGGGAACCG TCTGCGCGTT      600
   GCGCTGACCG GCCTGACCAT GCGCGAGAAA TTCCGTGACG AAGGTCGTGA      650
   CGTTCTGCTG TTCGTCGACA ACATCTACCG TTACACCTTG GCCGGTACGG      700
   AAGTATCCGC ACTGCTGGGT CGTATGCCTT CAGCGGTAGG TTACCAGCCG      750
55  ACCCTGGCGG AAGAGATGGG TGTTTTGCAG GAACGTATCA CCTCCACCAA      800
   AACCGGTTCT ATCACCTCCG TA                                     822

```

2) INFORMATION FOR SEQ ID NO: 266

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter sedlakii*
 (B) STRAIN: ATCC 51115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266

```

15 GATGCCGTAC CGCGCGTGTA CGACGCCCTT GAGGTACAGA ATGGTAATGA      50
   GCGTCTGGTG CTGGAAGTTC AGCAGCAGCT CGGTGGCGGT ATTGTACGTA      100
   CCATCGCCAT GGGTCTTCC GACGGTCTGC GTCGTGGTCT GGAAGTAAAA      150
   GACCTTGAGC ACCCGATCGA AGTCCCGGTA GGTAAGCAA CGCTGGGTCG      200
20 TATCATGAAC GTACTGGGCG AACCAGTAGA CATGAAAGGC GACATCGGTG      250
   AAGAAGAGCG TTGGGCTATC CACCGTGCCG CGCCGTCCTA TGAAGAGTTG      300
   TCTAACTCTC AGGAAGTCTG GAAACCGGC ATCAAAGTTA TCGACCTGAT      350
   GTGTCCGTTC GCGAAGGGCG GTAAAGTCGG TCTGTTCCGT GGTGCGGGCG      400
   TAGGTAAAC CGTAAACATG ATGGAGCTGA TCCGTAACAT CGCGATCGAG      450
25 CACTCCGGTT ACTCTGTGTT TCGGGGCGTG GGTGAACGTA CTCGTGAGGG      500
   TAACGACTTC TACCACGAAA TGACCGACTC CAACGTTATC GACAAAGTAT      550
   CCCTGGTGTA CGGCCAGATG AACGAGCCGC CTGGAAACCG TCTGCGCGTC      600
   GCACTGACCG GTCTGACCAT GGCTGAGAAG TTCCGTGACG AAGGTCGTGA      650
   CGTTCTGCTG TTCGTCGATA ACATCTATCG TTACACCCTG GCCGGTACGG      700
30 AAGTATCCGC ACTGCTGGGT CGTATGCCTT CAGCGGTAGG TTATCAGCCG      750
   ACTCTGGCGG AAGAGATGGG TGTCTGCAG GAACGTATCA CCTCAACCAA      800
   AACCGTTCT ATCACCTCCG                                     820

```

2) INFORMATION FOR SEQ ID NO: 267

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter werkmanii*
 (B) STRAIN: ATCC 51114

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267

```

GCCGTACCGC GCGTGACGA TGCTCTTGAG GTTATGAATG GTAAAGAGAG      50
CCTGGTGCTG GAAGTTCAGC AGCAGCTCGG CGGCGGTATC GTACGTACCA      100
TCGCCATGGG TTCTTCCGAC GGTCTGCGTC GTGGTCTGGA AGTTAAAGAC      150
55 CTTGAGCACC CGATCGAAGT CCCGGTAGGT AAAGCAACCC TGGGTCGTAT      200
   CATGAACGTC CTGGGTCATC CGATCGACAT GAAAGGCGAT ATCGGTGAAG      250
   AAGAGCGTTG GGCTATCCAC CGCGCAGCAC CTACCTATGA AGAACTGTCC      300
   AGTTCTCAGG AACTGCTGGA AACCGGCATC AAAGTTATCG ACCTGATGTG      350
   TCCGTTCCGG AAGGGCGGTA AAGTTGGTCT GTTCGGTGGT GCGGGTGTAG      400
60 GTAAAACCGT AAACATGATG GAGCTGATCC GTAACATCGC GATCGAACAC      450

```

	TCCGGTTACT	CAGTGTTTGC	GGGCGTTGGT	GAACGTACTC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTCTGGAC	AAAGTATCCC	550
	TGGTATATGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCG	600
5	CTGACCGGTC	TGACCATGGC	TGAGAAGTTC	CGTGACGAAG	GTCGTGACGT	650
	TCTGCTGTTT	GTTGATAACA	TCTATCGTTA	CACCCCTGGCC	GGTACTGAAG	700
	TATCTGCACT	GCTGGGTCGT	ATGCCATCAG	CGGTAGGCTA	CCAGCCAACC	750
	CTGGCGGAAG	AGATGGGTGT	TCTGCAGGAA	CGTATCACCT	CTACCAAAAC	800
	CGGTTT					806

10

2) INFORMATION FOR SEQ ID NO: 268

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 810 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Citrobacter youngae*
 (B) STRAIN: ATCC 29935

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268

	GCCGTACCGC	GCGTGTACGA	TGCTCTTGAG	GTTATGAATG	GTAAAGAGAG	50
	CCTGGTGCTG	GAAGTTCAGC	AGCAGCTCGG	CGGCGGTATC	GTACGTACCA	100
30	TCGCCATGGG	TTCTTCCGAC	GGTCTGCGTC	GTGGTCTGGA	AGTTAAAGAC	150
	CTCGAGCACC	CGATCGAAGT	CCCGGTAGGT	AAAGCAACGC	TGGGTCGTAT	200
	CATGAACGTT	CTGGGTCACC	CGATCGACAT	GAAAGGCGAT	ATCGGAGAAG	250
	AAGAGCGTTG	GGCTATTCAC	CGCGCAGCAC	CTTCCTATGA	AGAGCTGTCC	300
	AGCTCTCAGG	AACTGCTGGA	AACCGGCATC	AAAGTTATCG	ACCTGATGTG	350
35	TCCGTTTCGCT	AAGGGCGGTA	AAGTTGGTCT	GTTTCGGTGGT	GCGGGTGTAG	400
	GTAACACCGT	AAACATGATG	GAGCTTATTC	GTAACATCGC	GATCGAGCAC	450
	TCCGGTTACT	CTGTGTTTGC	GGGTGTAGGT	GAACGTACTC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CCGATTCCAA	CGTTCTGGAT	AAAGTATCCC	550
	TGGTTTATGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCG	600
40	CTGACCGGTC	TGACCATGGC	TGAGAAATTC	CGTGACGAAG	GTCGTGACGT	650
	ACTGCTGTTT	GTCGATAACA	TCTATCGTTA	TACCCTGGCC	GGTACGGAAG	700
	TATCCGCACT	GCTGGGTCGT	ATGCCATCAG	CGGTAGGTTA	CCAGCCGACC	750
	CTGGCGGAAG	AGATGGGTGT	TCTGCAGGAA	CGTATCACTT	CTACCAAAAC	800
45	CGGTTCTATC					810

2) INFORMATION FOR SEQ ID NO: 269

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 827 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium innocuum*
 (B) STRAIN: ATCC 14501

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269

```

5  TTGAGAACGG AGATTTGCCG CAGCTATTGA CCGCTATTGA AATTCCTCTG      50
   AAAGACAGTG AATCTCTGAT TGTCGAAGTT GCTCAGCATA TCGGTGATGA      100
   ACGTGTCCGC TGTATCGCTA TGGGCGGTAC AGATGGTCTG GTTCGTGGAA      150
   TGGAAAGCCAT TGATACAGGA TCCGCAATCC GTGTACCGGT GGGAAAAGAA      200
   ATTCTGGGAA GAATGTTCAA TGTCTTCGGA CGTGAAATTG ATGGTCTGGG      250
   ACCTGTAGGA ACGGATAACA CACTGCCGAT CCACAGACAG GCACCGGGCT      300
10  TTGAGGAGCA GCAGACATCC GCAGAAATGC TGGAAACAGG AATTAAGGTC      350
   ATTGACCTGT TATGTCCATA TTCCAAGGGT GGTAAGATTG GTTTGTTTGG      400
   TGGTGCGGGA GTAGGTAAAA CCGTACTGAT TCAGGAGCTG ATTCATAATA      450
   TCGCCAAGGA ACATGGTGGA ATGTCCGTCG TTACCGGTGT AGGGGAGAGA      500
   ACCCGTGAAG GAAACGACAT GTATCATGAA ATGAAGGACA GCGGTGTCCT      550
15  TGATAAGACC GTACTGGTTT ACGGACAGAT GAATGAATCA CCGGGTGCCA      600
   GAATGCGTGT CGGTCTGACC GGGCTGACGA TGGCGGAATA TTTCCGTGAT      650
   CACGACCATC AGGATGTATT GCTGTTTATT GATAATATTT TCCGTTTTAC      700
   CCAGGCGGGA AGTGAAGTAA GTGCCCTGCT GGGACGTATG CCAAGTGCAG      750
   TAGGCTATCA GCCGACACTT GCGACAGAAA TGGGACAGCT GCAGGAGCGC      800
20  ATTACATCCA CGAAGGATGG TTCCATT                                827

```

2) INFORMATION FOR SEQ ID NO: 270

25

(i) SEQUENCE CHARACTERISTICS:

```

   (A) LENGTH: 829 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
30  (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

```

35  (A) ORGANISM: Clostridium perfringens
   (B) STRAIN: ATCC 13124

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270

```

40  GCAAATGATG AACTTCCTAA TATATTTAAT GCAATACACA TAAAAATGGA      50
   CGATGGAAAA ATCTTAGTTT GTGAGGTAGA GCAACACGTA GGAGACGATA      100
   TAGTTAGAAC TATAGCTATG GAAGCTACTG AAGGACTAAG AAGAGGTGTA      150
   GAAGCTGTTG ATACAGGAGC ACCTATATCA GTACCAGTTG GTGAATGCGT      200
   ATTAGGAAGA ATATTTAACG TATTAGGTAA ACCACTAGAT AGTGGAGCTG      250
45  AAGTTAATAA CGAAGAAAAA TATCCAATTC ATAGACCAGC TCCATCATT      300
   GAAGAACAAT CAGTTGTTCC TCAAATGTTT GAGACAGGAA TAAAGGTTAT      350
   CGACCTTTTA GCACCTTACC AAAGAGGGGG AAAAAATCGGT CTATTTGGAG      400
   GTGCAGGTGT TGGTAAACA GTTCTTATCC AAGAGCTTAT AAACAACATA      450
   GCTAAAGAGC ACGGTGGACT TTCTGTATTC ACAGGAGTTG GAGAAAGATC      500
50  AAGAGAAGGT AATGACCTTT ACTATGAAAT GATGGAATCA GGAGTTATAA      550
   AAAATACAGC ATTAGTATTT GGACAAATGA ACGAACCACC TGGAGCAAGA      600
   ATGAGAGTTG CTTTAACAGG ACTTACTATG GCTGAGTACT TCAGAGACCA      650
   AGGTCAAGAC GTGTTATTAT TCATAGATAA CATATTCAGA TTCTCACAAG      700
   CTGGATCAGA GGTTCAGCT TTATTAGGAA GAATACCATC AGCTGTTGGT      750
55  TACCAACCAA CTCTTGCTAC AGAGATGGGA GCTCTTCAAG AGAGAATCAC      800
   ATCAACTACC CATGGATCAA TTACATCAG                                829

```

60 2) INFORMATION FOR SEQ ID NO: 271

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271

TTGTCCACGT TGGATRTCTT CA

22

2) INFORMATION FOR SEQ ID NO: 272

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium diphtheriae*
 (B) STRAIN: ATCC 27010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272

CCCGCGTGGC	GAGCTGCCGG	CACTGTACAA	CGCGTTGACT	GTCGAGGTCA	50
CCCTCGAGGC	AGTCGCTAAG	ACCATTACCC	TTGAGGTTGC	CCAGCACTTG	100
GGCGACAACC	TCGTTCGCGC	CGTGTCATG	GCCCCTACCG	ACGGCCTCGT	150
CCGTGGTGCT	GTTGTGACCG	ACTCGGGCAA	GCCAATCTCC	GTGCCAGTTG	200
GCGACGTTGT	TAAAGGCCAC	GTTTTCAACG	CACTGGGCGA	TTGCTTGGAT	250
GAGCCAGGTC	TCGGCCGCGA	TGGTGAGCAG	TGGGGAATTC	ACCGCGATCC	300
ACCACCATTC	GATCAGCTCG	AAGGTAAGAC	CGAAATCCTC	GAGACCGGTA	350
TTAAGGTCAT	CGACTTGCTC	ACCCCTTACG	TTAAGGGCGG	CAAGATTGGT	400
CTGTTCCGGT	GTGCAGGTGT	GGGTAAGACC	GTGCTCATCC	AGGAGATGAT	450
CACTCGTATT	GCTCGCGAGT	TCTCCGGTAC	CTCCGTCTTC	GCTGGCGTTG	500
GTGAGCGTAC	CCGTGAGGGC	ACCGACCTCT	TCCTCGAAAT	GGAAGAAATG	550
GGCGTTCCTC	AGGACACCGC	TCTCGTGTTT	GGCCAGATGG	ACGAGCCACC	600
AGGAGTCCGT	ATGCGCGTTG	CTCTGTCCGG	TCTGACCATG	GCGGAGTACT	650
TCCGCGATGT	TCAGCACCAG	GACGTGCTTC	TGTTTCATCGA	TAACATTTTC	700
CGTTTCACCC	AGGCCGGTTC	CGAGGTTTCG	ACCCTTCTTG	GTCGTATGCC	750
TTCCGCCGTG	GGTTACCAGC	CAACCTTGGC	TGACGAGATG	GGTGTTCCTC	800
AGGAGCGTAT	TACCTCTA				818

2) INFORMATION FOR SEQ ID NO: 273

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium pseudodiphtheriticum*
 (B) STRAIN: ATCC 10700

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273

CGATGCCTGC TCTGTACAAC GCGCTGACTG TCGAGGTCAC CCTCGAGGCA 50
 GTCGCCAAGA CCATCACGCT TGAGGTTGCA CAGCACCTCG GCGATAACCT 100
 10 GATCCGGACC ATTGCGTTGG CACCTACGGA CGGTCTCGTC CGTGGCGCTG 150
 AGGTTATCGA CACTGGTAAG CCAATTACTG TTCCCGTCGG CGATGCCGTC 200
 AAAGGACACG TCTTCAATGC GCTCGGTGAG TGTTTGACG AACCAGGATT 250
 GGGCCGCGAC GGC GAACAGT GGGGAATCCA CCGCGATCCG CCACCATTCTG 300
 ATGCGCTGGA GGGCAAACG GAGATTCTGG AGACTGGAAT CAAGGTTATC 350
 15 GACCTCCTTA CCCCTTACGT TAAGGGTGGC AAAATTGGTC TGTTCTGGTGG 400
 CGCCGCGCTC GGCAAGACCG TTCTTATCCA GGAAATGATC ACTCGTATCG 450
 CTCGTAACCTT CTCCGGTACT TCCGTGTTCTG CCGGCGTCGG TGAGCGTACC 500
 CGTGAGGGTA CTGACCTGTT CCTGGAATG GAAGAGATGG GCGTGTTGCA 550
 AGACACCGCC CTTGTCTTCG GTCAAATGGA CGAACCACCA GGGGTTCGTA 600
 20 TGCGCGTGGC CTTGTCTGGT CTAACCATGG CTGAATATTT CCGCGACGTT 650
 CAAAACCAGG ACGTTTTGTT GTTCATTGAC AACATCTTCC GTTTTACTCA 700
 GGCAGGTTCC GAGGTTTCCA CGCTGTTGGG CCGTATGCCT TCCGCCGTGG 750
 GTTATCAGCC AACATTGGCT GATGAGATGG GTGTTTTGCA GGAACGGATT 800
 25 ACCTCTACAC GTGGTAAGTC AATTACTTCC CTG 833

2) INFORMATION FOR SEQ ID NO: 274

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium ulcerans*
 40 (B) STRAIN: NCTC 8665

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274

CCGTGCTCAT CCAGGAGATG ATCACCCGTG TGGCCCGCAA CTTCCGGCGGC 50
 45 ACCTCTGTGT TCGCCGGCGT CGGCGAGCGC ACCCGTGAGG GCAACGACCT 100
 CTGGGTCGAG ATGGACGAGG CCGACGTGCT CAAGGACACC GCCCTGGTGT 150
 TCGGCCAGAT GGACGAGCCG CCGGGAACCC GTCTGCGCGT GGCCCTGTCC 200
 GCGCTGACCA TGGCGGAGTA CTTCGCGGAT GTGCAGAACC AGGACGTGCT 250
 GCTGTTTCATC GACAACATCT TCCGCTTCTC CCAGGCCGGC TCCGAGGTCT 300
 50 CCACCCTGCT GGGCCGCATG CCCTCCGCGG TGGGCTACCA GCCGAACCTG 350
 GCGGACGAGA TGGGTGTGCT GCAGGAGCGC ATCACCTCGA CTCGCGGCCA 400
 CTCCATCACC TCGATGC 417

55 2) INFORMATION FOR SEQ ID NO: 275

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 60 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Corynebacterium urealyticum*
(B) STRAIN: ATCC 43042

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275

GGGCAGCAGC	CAGCACTATT	CAACGCGCTG	CACGTCGAGG	TTGACCTCGA	50
GGCAGTTGCG	AAGACCATTA	CCCTGGAGGT	CGCACAGCAC	CTGGGTGACA	100
ACCTGGTGCG	CACCGTCTCC	ATGGCCCCGA	CCGACGGCCT	GGTCCGCGGT	150
GCAGAGGTCA	AGGACACCGG	TAAGCCGATC	TCTGTGCCAG	TCGGCGATGT	200
TGTC AAGGGG	CACGTCTTCA	ACGCCCTGGG	CGACTGCCTG	GATGAGCCAG	250
GTCTCGGCCG	CGACGGCGAG	CAGTGGGGGA	TCCACCGCGA	GCCACCGGCA	300
TTCGACGAGC	TCGAGGGTAA	GACCGAGATC	CTGGAGACCG	GCGTTAAGGT	350
CATCGACCTG	CTGACCCCTT	ACGTCAAGGG	CGGCAAGATT	GGCCTCTTCG	400
GTGGTGCAGG	TGTGGGTAAG	ACCGTCTCTG	TTCAGGAGAT	GATTACCCGT	450
ATCGCCCGCG	AGTTCTCCGG	TACCTCCGTG	TTCCCGGCGG	TCGGCGAGCG	500
TACCCGTGAG	GGTACGGACC	TCTTCCTCGA	GATGGAGGAG	ATGGGCGTGC	550
TCCAGGACAC	CGCGCTGGTG	TTCGGTCAGA	TGGATGAGCC	GCCGGGAGTC	600
CGTATGCGCG	TGGCTCTGTC	CGGTCTGACC	ATGGCGGAGT	ACTTCCGCGA	650
TGTT CAGGGC	CAGGACGTGC	TGCTGTTCAT	CGACAACATC	TTCCGTTTCA	700
CCCAGGCAGG	TTCTGAGGTC	TCCACGCTGC	TCGGCCGCAT	GCCGTCCGCA	750
GTGGGTTACC	AGCCGACCCT	GGCTGACGAG	ATGGGTGTTT	TGCAGGAGCG	800
CATTACCTCC	ACGAAGGGTA	AGTCCATTAC	CTCCC		835

2) INFORMATION FOR SEQ ID NO: 276

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 818 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Coxiella burnetii*
(B) STRAIN: Nine Mile phase II

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276

CCCGTCACGC	TGTCCCGAAA	GTGTACGATG	CTTTGCAGGT	GGATGAAAAT	50
AATTTAACGC	TCGAAGTCCA	ACAGCAACTC	GGGGACGGTG	TCGTGCGCAC	100
AATTGCCATG	GGCAGCACTG	AGGGCTTAAA	ACGCGATATC	GCCGTAAAAA	150
ATACGAAAAA	ACCGATTGAA	GTTCCCGTAG	GAAAAGAAAC	TTTAGGTCGT	200
ATCATGAACG	TGCTGGGTGA	GCCGATCGAT	GAGTTAGGTC	CCATTAATTC	250
AAAAGAAAAA	CTCCCTATTC	ATCGTCTCTG	GCCGAGCTTT	ATTGAGCAAT	300
CTGGCGCTAC	CGAATTATTA	GAAACCGGTA	TTAAAGTGGT	CGATTTGCTT	350
TGCCCCCTTTG	CTAAGGGAGG	CAAAGTGGGT	CTTTTTGGAG	GCGCGGGCGT	400
TGGAAAAACG	GTTAATATGA	TGGAATTAAT	CCGTAATATC	GCCATTGAAC	450
ACAGCGGTTA	TTCTGTTTTT	GCGGGTGTGG	GAGAAAGAAC	GCGAGAAGGC	500
AATGATTTTT	ATCATGAAAT	GAAAGAATCC	AATGTCTTGG	ATAAAGTGGC	550
GTTGGTGTAC	GGACAAATGA	ACGAGCCGCC	AGGGAACCGC	TTGCGGGTGG	600
GTTTGACGGG	GCTTACGCTG	GCGGAAGCCT	TCCGTGACGA	AGGACGCGAC	650

GTTCTGTTAT TTATCGATAA TATCTTTCGT TACACTTTGG CAGGGGTTGA 700
 AGTCTCTGCC CTCCTCGGTC GGATGCCATC GGCTGTGGGT TATCAGCCGA 750
 CGTTGGCCGA AGAGATGGGG GCCCTGCAAG AACGCATTAC TTCCACTAAA 800
 AAAGGGTCCA TTACGTCG 818

5

2) INFORMATION FOR SEQ ID NO: 277

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Edwardsiella hoshinae*
 (B) STRAIN: ATCC 33379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277

TTCCCGCAGG ACGCCGTGCC GAAGGTGTAT AACGCACTGG AAGTAAAAGG 50
 25 CCGTGCCACG AAACCTGGTAC TGGAAGTGCA GCAGCAGCTG GGTGGCGGCG 100
 TAGTTCGCTG CATCGCGATG GGCTCTTCCG ACGGTCTGCG CCGTGGGCTA 150
 GAGGTTGAAG ACCAAGACCA TCCGATCGAG GTTCCTGTTG GCAAGGCGAC 200
 TCTGGGCCGT ATCATGAACG TACTGGGTGA TCCGGTCGAC ATGAAGGGCG 250
 AGATCGGTGA AGAAGAGCGT TGGGCTATCC ATCGTGCTGC ACCGAGCTAT 300
 30 GAAGATCTGT CTAACCTCTCA GGAACCTGCTG GAGACCGGCA TTAAGGTTAT 350
 CGACCTGATT TGCCCGTTCG CTAAAGGCGG TAAAGTGGGC CTGTTCGGTG 400
 GGGCCGGTGT GGGTAAGACC GTTAACATGA TGGAGCTTAT CCGTAACATC 450
 GCTATCGAGC ACTCCGGTTA CTCAGTCTTC GCCGGTGTGG GTGAGCGTAC 500
 CCGTGAGGGT AACGACTTCT ACCACGAGAT GACCGATTCC AACGTATTGG 550
 35 ATAAAGTTTC TCTGGTGAT GGTCAGATGA ACGAGCCACC GGGAAACCGT 600
 CTGCGCGTGG CGCTGACCGG TCTGACCATG GCGGAGAAAT TCCGTGATGA 650
 AGGTGCTGAT GTACTGTTGT TCATCGATAA CATCTACCGT TATACCTTGG 700
 CCGGTACTGA AGTCTCCGCT CTGCTGGGCC GTATGCCGTC GGCGGTAGGT 750
 TATCAGCCGA CTCTGGCGGA GGAAATGGGG GTGCTGCAAG AGCGTATTAC 800
 40 CTCCACTAAG ACCGGGTCCA TCACCTCTG 829

2) INFORMATION FOR SEQ ID NO: 278

45

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 809 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: *Edwardsiella tarda*
 (B) STRAIN: ATCC 15947

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278

60 GCCGTGCCGA AGGTGTATAA CGCACTGGAA GTAAAAGGCG GTGCCACGAA 50

	ACTGGTACTG	GAAGTGCAGC	AGCAGCTGGG	TGGCGGCGTC	GTTCGCTGCA	100
	TCGCGATGGG	CTCCTCCGAC	GGTCTGCGCC	GTGGGCTGGT	GGTTGAAGAC	150
	CAAGACCATC	CGATCGAGGT	TCCGGTCGGT	AAGGCGACCC	TGGGCCGTAT	200
	CATGAACGTA	CTGGGTGATC	CGGTCGACAT	GAAGGGCGAG	ATCGGCGAAG	250
5	AAGAGCGTTG	GGCTATCCAC	CGCGCGGCGC	CGAGCTATGA	AGATCTGTCC	300
	AACTCTCAGG	AGCTGCTGGA	GACCGGCATC	AAGGTTATCG	ACCTGATTTG	350
	CCCGTTCGCC	AAAGGCGGTA	AAGTTGGCCT	GTTCGGTGGT	GCCGGTGTGG	400
	GTAAGACCGT	TAACATGATG	GAGCTTATCC	GTAACATCGC	TATCGAGCAC	450
	TCCGGTTACT	CCGTATTTGC	CGGTGTAGGC	GAGCGTACCC	GTGAGGGTAA	500
10	CGACTTCTAC	CACGAGATGA	CCGACTCCAA	CGTATTGGAT	AAAGTTTCTC	550
	TGGTATACGG	CCAGATGAAT	GAGCCGCCGG	GAAACCGTCT	GCGTGTGGCG	600
	TTGACCGGTC	TGACCATGGC	GGAGAAATTC	CGTGATGAAG	GTCGCGATGT	650
	GTTGTTGTTT	ATCGATAACA	TTTATCGTTA	TACCTTGGCT	GGTACCGAAG	700
	TTTCTGCTCT	GCTGGGTCGT	ATGCCGTCGG	CGGTAGGTTA	TCAGCCGACC	750
15	CTGGCGGAAG	AGATGGGTGT	GTTGCAAGAG	CGTATCACCT	CAACGAAGAC	800
	GGGCTCTAT					809

20 2) INFORMATION FOR SEQ ID NO: 279

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 840 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Eikenella corrodens*
 (B) STRAIN: ATCC 23834

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279

35	TTTCCGCGTA	CCGCCATTCC	GCGTGTTTAC	GATGCACTCA	AACTGGTTGA	50
	TACTGATTTG	ACGCTGGAAG	TACAGCAGCA	GCTTGGTGAC	GGCGTTGTCC	100
	GTACCATTGC	GATGGGTAGT	ACAGACGGTT	TGAAACGTGG	CTTGGCTGTG	150
	CAAAATACTG	GTGCACCGAT	TACTGTGCCG	GTGGGGAAAG	CCACCCTAGG	200
40	CCGCATCATG	GACGTTCTGG	GCAACCCCGT	GGACGAACAA	GGTCCGATCG	250
	GTTCTGACCA	AACCCGTGCT	ATTCATCAAT	TTGCACCTAA	GTTCGACGAA	300
	CTCTCCAGCA	CTACCGAATT	GTTGGAACA	GGCATTAAG	TGATCGATTT	350
	GCTTTGTCCG	TTTGCTAAAG	GTGGTAAAGT	GGGTCTGTTT	GGCGGTGCCG	400
	GTGTGGGCAA	AACCGTGAAC	ATGATGGAGC	TGATTAACAA	CATTGCCAAA	450
45	GCGCACAGTG	GTCTTTCCGT	ATTCGCCGGT	GTGGGTGAGC	GTACTCGTGA	500
	AGGTAACGAC	TTCTACCACG	AAATGAAAGA	CTCCAACGTG	TTGGATAAAG	550
	TGGCAATGGT	GTATGGCCAG	ATGAACGAGC	CGCCTGGTAA	CCGCTTGCGT	600
	GTTGCTCTAA	CTGGTTTGTC	GATGGCTGAA	TACTTCCGTG	ACGAAAAAGA	650
	CGAAAACGGC	AAAGGCCGTG	ACGTATTATT	CTTTGTGGAT	AATATCTACC	700
50	GCTATACTCT	GGCGGGTACC	GAAGTGTCGG	CTCTGCTTGG	CCGTATGCCT	750
	TCTGCTGTGG	GTTATCAGCC	AACTTTGGCT	GAAGAAATGG	GTCGTTTGCA	800
	GGAGCGTATT	ACCTCCACCC	AACTGGTTC	CATTACCTCT		840

55

2) INFORMATION FOR SEQ ID NO: 280

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 803 bases
 60 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterobacter agglomerans*
(B) STRAIN: ATCC 27989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280

	GCCGTACCAC	GAGTGTACGA	TGCACTTGAG	GTAAAGAATG	GTGAAGAGCG	50
	TCTGGTGCTG	GAAGTTCAGC	AACAGCTCGG	CGGTGGCGTT	GTACGTACCA	100
	TCGCAATGGG	TTCTTCTGAT	GGTCTGCGTC	GTGGTCTGGA	AGTAACGGAC	150
15	CTGGCTCACC	CGATCGAAGT	CCCGGTAGGT	AAAGCAACAC	TGGGTCGTAT	200
	CATGAACGTA	CTGGGCGAAC	CAGTAGACAT	GAAAGGCGAC	ATCGGTGAAG	250
	AAGAGCGTTG	GGCGATCCAC	CGTGCAGCAC	CGTCCTACGA	AGAGTTGTCA	300
	AACTCTCAGG	AACTGCTGGA	AACCGGTATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTTCGT	AAGGGCCGTA	AAGTGGGTCT	GTTCCGGTGGT	GCGGGTGTAG	400
20	GTAAAACCGT	AAACATGATG	GAGCTTATTC	GTAACATCGC	GATCGAGCAC	450
	TCCGGTTACT	CTGTGTTTGC	GGGCGTAGGT	GAACGTACTC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTATCGAC	AAAGTATCCC	550
	TGGTGTATGG	TCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCG	600
	CTGACCGGTC	TGACCATGGC	TGAGAAAGTTC	CGTGACGAAG	GTCGTGACGT	650
25	ACTGTTGTTC	GTTGACAACA	TCTACCGTTA	CACCCTGGCC	GGTACGGAAG	700
	TATCCGCACT	GCTGGGCCGT	ATGCCTTCTG	CGGTAGGTTA	TCAGCCGACG	750
	CTGGCGGAAG	AGATGGGCGT	TCTGCAGGAA	CGTATCACCT	CCACCAAAC	800
	CGG					803

2) INFORMATION FOR SEQ ID NO: 281

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 833 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterobacter amnigenus*
(B) STRAIN: ATCC 33072

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281

	CGAATTC CCT	CAGGATGCCG	TACCGCGCGT	GTACGATGCT	CTTGAGGTAC	50
	AGAATGGTAA	CGAGAGTCTG	GTGCTGGAAG	TTCAGCAGCA	GCTCGGTGGT	100
50	GGTATCGTAC	GTACTATCGC	CATGGGTTCT	TCCGACGGTC	TGCGTCGTGG	150
	TCTGGCTGTT	AAAGATCTCG	AACACCCGAT	CGAAGTCCCG	GTAGGTAAAG	200
	CAACACTGGG	TCGTATCATG	AACGTTTTGG	GTCAACCAAT	CGACATGAAA	250
	GGCGACATCG	GTGAAGAAGA	CCGTTGGGCA	ATCCACCGTG	CAGCACCTTC	300
	CTATGAAGAG	CTGTCTAGCT	CTCAGGAACT	GCTGGAAACC	GGCATCAAAG	350
55	TTATCGACCCT	GATGTGTCCG	TTCGCTAAGG	GCGGTAAAGT	TGGTCTGTTC	400
	GGCGGTGCGG	GCGTGGGTAA	AACTGTAAAC	ATGATGGAGC	TGATCCGTAA	450
	CATCGCGATC	GAGCACTCCG	GTTACTCCGT	GTTTGCAGGC	GTGGGTGAGC	500
	GTACTCGTGA	GGGTAACGAC	TTCTACCACG	AAATGACCGA	TTCCAACGTT	550
	CTGGATAAAG	TATCCCTGGT	TTATGGCCAG	ATGAACGAGC	CACCAGGAAA	600
60	CCGTCTGCGC	GTTGCGCTGA	CCGGTCTGAC	TATGGCTGAG	AAGTTCCGTG	650

ACGAAGGTCG	TGACGTACTG	CTGTTCGTAG	ATAACATCTA	CCGTTACACC	700
CTGGCCGGTA	CTGAAGTATC	TGCGCTGCTG	GGCCGTATGC	CTTCAGCGGT	750
AGGTTACCAG	CCGACCCTGG	CGGAAGAGAT	GGGCGTTCTG	CAGGAACGTA	800
TCACTTCTAC	CAAAACCGGT	TCTATCACCT	CCG		833

2) INFORMATION FOR SEQ ID NO: 282

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter asburiae*
 (B) STRAIN: ATCC 35953

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282

GCCGTACCAC	GCGTGTACGA	CGCGCTTGAG	GTACAGAATG	GTAACGAGAG	50
CCTGGTGCTG	GAAGTTCAGC	AGCAGCTCGG	CGGCGGTATC	GTGCGTACCA	100
TCGCGATGGG	TTCTTCCGAC	GGTCTGCGTC	GTGGTCTGGA	AGTCAAAGAC	150
CTTGAGCACC	CGATCGAAGT	CCCGGTAGGT	AAAGCAACAC	TGGGTCGTAT	200
CATGAACGTA	TTGGGTCAAC	CAATCGACAT	GAAAGGCGAC	ATCGGTGAAG	250
AAGAGCGTTG	GGCTATCCAC	CGCGCGGCAC	CTTCCTACGA	AGAGCTGTCC	300
AGCTCTCAGG	AAGTGTCTGA	AACCGGTATC	AAAGTTATCG	ACCTGATGTG	350
TCCGTTTCGG	AAGGGCGGTA	AAGTCCGGTCT	GTTCGGTGGT	GCGGGTGTTG	400
GTAACACCGT	AAACATGATG	GAGCTGATCC	GTAACATCGC	GATCGAGCAC	450
TCCGTTTACT	CCGTGTTTGC	GGGCGTAGGT	GAACGTACTC	GTGAGGGTAA	500
CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTCTGGAC	AAAGTATCCC	550
TGGTTTACGG	CCAGATGAAC	GAGCCACCAG	GAAACCGTCT	GCGCGTTGCG	600
CTGACCGGTC	TGACGATGGC	TGAGAAAGTTC	CGTGATGAAG	GCCGTGACGT	650
TCTGCTGTTT	GTTGATAACA	TCTATCGTTA	CACCCTGGCC	GGTACGGAAG	700
TATCTGCACT	GCTGGGTCGT	ATGCCTTCAG	CGGTAGGTTA	CCAGCCTACG	750
CTGGCGGAAG	AGATGGGTGT	TCTTCAGGAA	CGTATCACCT	CTACCAAAAC	800
CGGTTCTATC					810

2) INFORMATION FOR SEQ ID NO: 283

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 811 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter cancerogenus*
 (B) STRAIN: ATCC 35317

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283

GCCGTACCGC	GCGTGTACGA	TGCTCTTGAG	GTACAGAATG	GTAACGAGAG	50
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CCTGGTGCTG GAAGTTCAGC AGCAGCTCGG CGGCGGTATC GTACGTACTA 100
TCGCCATGGG TTCTTCCGAC GGTCTGCGTC GTGGTCTGGA AGTAAAAGAC 150
CTTGAGCACC CGATCGAAGT CCCGGTAGGT AAAGCAACAC TGGGTCGTAT 200
CATGAACGTA TTGGGTCAAC CAATCGACAT GAAAGGCGAC ATCGGTGAAG 250
5 AAGAGCGTTG GGCTATCCAC CGCGCAGCAC CTTCCTACGA AGAGCTGTCC 300
AGCTCTCAGG AACTGCTGGA AACC GG CATC AAAGTTATCG ACCTGATGTG 350
TCCGTTTCGG AAGGGCGGTA AAGTCGGTCT GTTCGGTGGT GCGGGTGTAG 400
GTAAAACCGT AAACATGATG GAGCTGATCC GTAACATCGC GATCGAGCAC 450
TCCGGTTATT CCGTGTTTGC GGGCGTGGGT GAACGTACTC GTGAGGGTAA 500
10 CGACTTCTAC CACGAAATGA CCGACTCCAA CGTTCTGGAT AAAGTATCCC 550
TGGTGTACGG CCAGATGAAC GAGCCACCAG GAAACCGTCT GCGCGTTGCG 600
CTGACCGGCC TGACCATGGC TGAGAAGTTC CGTGACGAAG GTCGTGACGT 650
ACTGCTGTTT GTTGATAACA TCTACCGTTA CACCCTGGCC GGTACCGAAG 700
TATCTGCACT GCTGGGTCGT ATGCCTTCAG CGGTAGGTTA TCAGCCTACG 750
15 CTGGCGGAAG AGATGGGTGT TCTTCAGGAA CGTATCACCT CAACCAAAC 800
CGTTTCTATC A 811

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20 2) INFORMATION FOR SEQ ID NO: 284

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 817 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter cloacae*
(B) STRAIN: ATCC 13047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284

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35 GCCGTACCAC GCGTGACGA CGCGCTTGAG GTACAGAATG GTAACGAGAG 50
CCTGGTGCTG GAAGTTCAGC AGCAGCTCGG CGGCGGTATC GTGCGTACCA 100
TCGCGATGGG GTCTTCCGAC GGTCTGCGTC GTGGTCTGGA AGTTAAAGAC 150
CTTGAGCACC CGATCGAAGT CCCGGTAGGT AAAGCAACAC TGGGTCGTAT 200
40 CATGAACGTA TTGGGTCAAC CAATCGACAT GAAAGGCGAC ATCGGTGAAG 250
AAGAGCGTTG GGCTATCCAC CGCGCAGCAC CTTCCTACGA AGAGCTGTCC 300
AGCTCTCAGG AACTGCTGGA AACC GG CATC AAAGTTATCG ACCTGATGTG 350
TCCGTTTTCG AAGGGCGGTA AAGTTGGTCT GTTCGGTGGT GCGGGTGTAG 400
GTAAAACCGT AAACATGATG GAGCTGATCC GTAACATCGC GATCGAGCAC 450
45 TCCGGTTACT CCGTATTTGC GGGCGTAGGT GAACGTACTC GTGAGGGTAA 500
CGACTTCTAC CACGAAATGA CCGACTCCAA CGTTCTGGAC AAAGTATCCC 550
TGGTTTACGG CCAGATGAAC GAGCCACCAG GAAACCGTCT GCGCGTTGCG 600
CTGACTGGTC TGACCATGGC TGAGAAGTTC CGTGACGAAG GCGGTGACGT 650
TCTGCTGTTT GTTGATAACA TCTACCGTTA CACCCTGGCC GGTACCGAAG 700
50 TATCTGCACT GCTGGGTCGT ATGCCTTCAG CGGTAGGTTA TCAGCCTACG 750
CTGGCGGAAG AGATGGGTGT TCTTCAGGAA CGTATCACCT CTACCAAAC 800
CGTTTCTATC ACTTCCG 817

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55 2) INFORMATION FOR SEQ ID NO: 285

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 766 bases
(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterobacter gergoviae*

(B) STRAIN: ATCC 33028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285

AATGAGAGCC	TGGTGCTGGA	AGTTCAGCAG	CAGCTCGGCG	GCGGTATCGT	50
GCGTACCATC	GCAATGGGTT	CTTCTGACGG	TCTGCGTCGC	GGTCTGGAAG	100
TTAAAGATCT	CGAACATCCG	ATCGAAGTCC	CGGTAGGTAA	AGCGACCCTC	150
GGCCGTATTA	TGAACGTGCT	GGGTCAGCCG	GTTGATATGA	AAGGCGATAT	200
CGGCGAAGAA	GAGCGTTGGG	CGATCCACCG	CGCTGCGCCG	TCCTATGAAG	250
AGCTCTCCAG	CTCTCAGGAA	CTGCTGGAAG	CCGGTATCAA	GGTAATGGAC	300
CTGATTTGCC	CGTTTCGCGAA	GGGCGGTAAA	GTCGGTCTGT	TCGGCGGTGC	350
GGGCGTTGGT	AAAACCGTAA	ACATGATGGA	GCTGATCCGT	AACATCGCGA	400
TCGAGCACTC	CGGCTACTCC	GTGTTTTCGG	GCGTGGGTGA	ACGTACTCGT	450
GAGGGTAACG	ACTTCTACCA	CGAAATGACC	GACTCCAACG	TTATCGACAA	500
AGTATCCCTG	GTGTACGGCC	AGATGAACGA	GCCGCCGGGA	AACCGTCTGC	550
GCGTGGCGCT	GACCGGTCTG	ACCATGGCTG	AGAAATTCCG	TGACGAAGGT	600
CGTGACGTTT	TGCTGTTTCG	CGATAACATC	TACCGCTATA	CCCTCGCCGG	650
TACTGAAGTA	TCCGCACTGC	TGGGCCGTAT	GCCTTCTGCA	GTAGGTTACC	700
AGCCGACGCT	GGCGGAAGAG	ATGGGTGTTT	TGCAGGAACG	TATCACCTCC	750
ACCAAACCG	GTTCTA				766

2) INFORMATION FOR SEQ ID NO: 286

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 805 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterobacter hormaechei*

(B) STRAIN: ATCC 49162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286

GCCGTACCAC	GCGTGTACGA	CGCGCTTGAG	GTACAGAATG	GTAACGAGAG	50
CCTGGTGCTG	GAAGTTCAGC	AGCAGCTCGG	CGGCGGTATC	GTGCGTACCA	100
TCGCCATGGG	TTCTTCCGAC	GGTCTGCGTC	GTGGTCTGGA	AGTGAAAGAC	150
CTTGAGCACC	CGATCGAAGT	CCCGGTAGGT	AAAGCAACGC	TGGGTCGTAT	200
CATGAACGTA	TTGGGTCAGC	CAATCGACAT	GAAAGGCGAC	ATCGGTGAAG	250
AAGAGCGTTG	GGCTATCCAC	CGCGCGGCAC	CTTCCTACGA	AGAGCTGTCC	300
AGCTCTCAGG	AACTGCTGGA	AACCGGCATC	AAAGTTATCG	ACCTGATGTG	350
TCCGTTTGCG	AAGGGCGGTA	AAGTTGGTCT	GTTCCGGTGGT	GCGGGTGTAG	400
GTAACAAACCGT	AAACATGATG	GAGCTGATCC	GTAACATCGC	GATCGAGCAC	450
TCCGGTTACT	CCGTGTTTGC	GGGCGTGGGT	GAACGTACTC	GTGAGGGTAA	500
CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTCTGGAC	AAAGTATCCC	550
TGGTTTACGG	CCAGATGAAC	GAGCCACCAG	GAAACCGTCT	GCGCGTTGCG	600
CTGACTGGCC	TGACGATGGC	TGAGAAGTTC	CGTGACGAAG	GCCGTGACGT	650
TCTGCTGTTT	GTCGATAACA	TCTACCGTTA	CACCCTGGCC	GGTACGGAAG	700

TATCTGCACT GCTGGGTCGT ATGCCTTCAG CGGTAGGTTA TCAGCCAACG 750
 CTTGCGGAAG AGATGGGTGT TCTTCAGGAA CGTATCACCT CGACCAAAAC 800
 CGGTT 805

5

2) INFORMATION FOR SEQ ID NO: 287

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 791 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter sakasakii*
 (B) STRAIN: ATCC 29544

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287

TACGACGCCC TTGAGGTAAC GAATGGTAAT GAGCGTCTGG TGCTGGAAGT 50
 CCAGCAGCAG CTCGGCGGCG GTATCGTACG TACCATCGCG ATGGGCTCTT 100
 25 CCGACGGTCT GCGTCGCGGT CTGCCTGTTG CAGACCTTGA GCACCCGATC 150
 GAAGTGCCGG TAGGTAAAGC GACGCTGGGT CGTATCATGA ACGTCCTGGG 200
 TCAGCCTATC GACATGAAAG GCGACATCGG CGAAGAAGAG CGTTGGGCGA 250
 TTCATCGCGC GGC GCCGTCC TATGAAGAGC TGTCCAGCTC TCAGGAACTG 300
 CTGGAACCG GCATCAAAGT TATCGACCTG ATGTGTCCGT TCGCGAAGGG 350
 30 CGGTAAAGTC GGTCTGTTCC GTGGTGCAGG TGTAGGTAAA ACCGTAAACA 400
 TGATGGAGCT TATTCGTAAC ATCGCGATTG AGCACTCCGG TTA CTCCGTG 450
 TTTGCGGGCG TGGGCGAAGC TACCCGTGAA GGTAACGACT TCTACCACGA 500
 AATGACCGAC TCCAACGTAC TGGATAAAGT ATCCCTGGTG TACGGCCAGA 550
 TGAACGAGCC GCCGGGAAAC CGTCTGCGCG TTGCGCTGAC CGGCCTGACC 600
 35 ATGGCTGAGA AATTCCTGTA CGAAGGTCGT GACGTTCTGC TGTTCTGTCGA 650
 CAACATCTAC CGTTACACCC TGGCCGGTAC TGAAGTATCC GCACTGCTGG 700
 GCCGTATGCC TTCAGCGGTA GGTATCAGC CGACCCCTGGC GGAAGAGATG 750
 GGTGTTCTGC AGGAGCGTAT CACCTCCACC AAAACCGGTT C 791

40

2) INFORMATION FOR SEQ ID NO: 288

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 839 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus avium*
 (B) STRAIN: ATCC 14025

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288

TTTCTTTAGA TCAATCCTTA CCAGACATCA ACAATGCGTT GATTGTTTAC 50
 AAAAAAGATA AAACAAAAGT TGTTCTTGAA GTTGCTTTGG AACTTGGTGA 100
 60 TGGTGTATC CGCACAAATCG CTATGGAGGC TACTGATGGA TTGCAACGTG 150

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GAATGGAAGT TGTCGATACT GGCAAATCAA TCTCCGTTCC TGTAGGTAAA 200
GATACTCTAG GTCGTGTGTT TAACGTATTA GGTGAAACGA TTGATAAAGA 250
AGCACCTTTT CCAGAAGATG CAGAAAGAAG CGGCATTTCAT AAAAAGGCGC 300
CTGCTTTTGA AGACCTTAGT ACAAGTAACG AGATTTTGGG AACAGGGATC 350
5 AAGGTTATCG ACTTATTAGC CCCTTATTTA AAAGGTGGGA AAGTCGGACT 400
ATTCGGTGGT GCCGGTGTGG GTAAAACCGT TTTGATCCAA GAATTAATTC 450
ATAATATCGC CCAAGAACAC GGTGGTATTT CAGTGTTTAC CGGTGTTGGG 500
GAACGTACTC GTGAAGGGAA CGACCTTTAT TATGAAATGA AAGACTCTGG 550
CGTTATTGAG AAAACAGCCA TGGTGTTCGG ACAAATGAAC GAGCCGCCTG 600
10 GTGCACGTAT GCGTGTGGCC TTGACTGGTT TGACATTAGC TGAATATTTT 650
CGTGATGAAG AAGGACAAGA TGTGTTGCTA TTTATTGACA ACATCTTCCG 700
CTTTACTCAA GCCGGATCAG AAGTTTCTGC CTTATTAGGA CGTATGCCAT 750
CAGCCGTGGG GTATCAACCA ACTTTGGCAA CTGAAATGGG GCAATTACAA 800
GAACGAATCA CTTCAACCAA AAAAGGTTCC ATCACTTCA 839
15

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2) INFORMATION FOR SEQ ID NO: 289

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 847 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus casseliflavus*
- (B) STRAIN: ATCC 25788

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289

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TTCTCTCTAG ACCAATCATT ACCAGATATC AACAAATGCGT TGATTGTTTA 50
35 CAAAAAAGAT GAGCAGAAAA CAAAAGTTGT GTTAGAAGCT GCCTTAGAAC 100
TTGGCGACGG CGTTATCCGT ACGATTGCCA TGGAATCAAC AGATGGCTTA 150
CAACGAGGAA TGGAAGTAAT CGATACAGGC GCCTCCATTT CTGTTCCAGT 200
TGGGACAGAA ACCTTAGGAC GGGTGTTTAA TGTCTTAGGG GACACCATCG 250
ATTTAGAAGC GCCGTTCCCT GAAGAAGCAC CCCGCAGTGG GATTCACAAA 300
40 AAAGCACCTG ACTTTGATGA ATTGTCAACA AGTACGGAGA TCCTTGAAAC 350
TGGGATCAAA GTTATCGATT TGTTAGCCCC TTATTTAAAA GGGGGGAAAG 400
TTGGACTTTT CGGTGGTGCC GGTGTTGGTA AAACCGTCTT GATCCAAGAA 450
TTGATCCACA ACATCGCCCA AGAGCATGGT GGGATCTCTG TCTTCACAGG 500
TGTGTTGTA GCGACACGTG AAGGAAATGA CCTTTATAAT GAAATGAAAG 550
45 AATCTGGCGT TATCGAAAAA ACAGCCATGG TGTGTTGACA AATGAACGAA 600
CCACCAGGTG CTCGGATGCG GGTAGCCTTG ACTGGTTTGA CATTAGCCGA 650
GTACTTCCGT GATGTGGAAG GACAAGACGT GCTCTTGTTT ATCGATAATA 700
TCTTCCGCTT CACTCAAGCA GGTCTGAAG TATCTGCCTT ACTAGGTCGG 750
ATGCCGTCTG CCGTTGGGTA TCAGCCAACA TTAGCAACTG AGATGGGGCA 800
50 ATTACAAGAA CGGATCACAT CGACGAAGAA AGGTTCCGTT ACGTCTA 847

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2) INFORMATION FOR SEQ ID NO: 290

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 845 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Enterococcus durans*
(B) STRAIN: ATCC 19432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290

10	TTTCTTTAGA	CCAATCCTTA	CCAGATATCA	ACAACGCTTT	AGTTGTTTAT	50
	AAAAATGATG	AGAAGAAATC	GAAAGTTGTT	CTTGAAACAG	CGCTAGAATT	100
	AGGTGACGGT	GTCATCCGTA	CAATCGCGAT	GGAATCAACA	GATGGTTTAC	150
	AACGCGGAAT	GGAAGTCATT	GATACAGAAA	AAGCAATTTT	TGTACCAGTG	200
	GGTAAAGAAA	CGTTAGGTCG	TGTATTCAAT	GTATTAGGAG	ATACGATCGA	250
15	TTTATCTGCA	CCTTTCCCGA	AAGATGCAAA	ACGTAGCGAA	ATCCATAAAA	300
	AAGCACCAAA	CTTTGATGAG	TTAAGTACAA	GTACTGAGAT	CCTTGAAACT	350
	GGGATCAAAG	TTATTGACTT	GCTTGCTCCT	TACTTAAAAG	GTGGGAAAAGT	400
	TGGATTATTC	GGTGGTGCCG	GTGTAGGTAA	AACTGTATTG	ATCCAAGAAT	450
	TGATCCATAA	TATCGCTCAA	GAACACGGTG	GTATTTCTGT	ATTTACTGGT	500
20	GTTGGTGAAC	GTACACGTGA	AGGTAATGAC	CTTTATTATG	AAATGAAAGA	550
	TTCAGGAGTT	ATTGAAAAAA	CAGCCATGGT	GTTTGGTCAA	ATGAACGAAC	600
	CACCAGGTGC	ACGTATGCGT	GTTGCCTTGA	CTGGTTTGAC	GATTGCTGAA	650
	TACTTCCGTG	ATGTTGAAGG	GCAAGACGTG	CTATTGTTTA	TTGATAATAT	700
	TTTCCGTTTC	ACTCAAGCCG	GTTCAGAAGT	TTCTGCCCTA	TTAGGTCGTA	750
25	TGCCTTCTGC	CGTTGGGTAC	CAACCAACGC	TAGCAACAGA	AATGGGTCAA	800
	TTACAAGAAC	GGATCACTTC	AACGAAAAAA	GGTTCAATCA	CTTCA	845

30 2) INFORMATION FOR SEQ ID NO: 291

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 840 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
(B) STRAIN: ATCC 29212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291

45	TTAGATCAAT	CCTTACCCGA	TATTAACAAC	GCTTTAGTCG	TTTATAAAAA	50
	TGGCGAAGCA	AAACAAAAAG	TAGTACTTGA	AGTCGCTTTA	GAAC TAGGTG	100
	ATGGAGTGAT	TCGTTCTATC	GCCATGGAAT	CGACAGATGG	TTTACAACGT	150
	GGAATGGAAG	TTATCGATAC	AGGAAAATCA	ATTTCAGTTC	CTGTTGGTAA	200
50	AGATACATTA	GGTCGTGTGT	TTAACGTTTT	AGGAGACACA	ATTGACTTAG	250
	AAGCGCCATT	CCCTGCAGAT	GCTGAACGTA	GTGGGATTCA	TAAAAAAGCG	300
	CCAGCATTTG	ATGAATTAAG	TACCAGTAAT	GAAATTTTAG	AAACAGGGAT	350
	TAAAGTTATT	GACTTATTAG	CACCTTATCT	AAAAGGTGGT	AAAGTCGGAC	400
	TTTTCGGTGG	TGCCGGTGTT	GGTAAAACCG	TCTTAATTCA	AGAATTAATT	450
55	CATAATATTG	CCCAAGAACA	TGGAGGGGAT	TCCGTCTTTA	CTGGTGTTGG	500
	TGAACGGACA	CGTGAAGGGA	ACGATCTGTA	CTATGAAATG	AAAGATTGAG	550
	GCGTTATTGA	AAAAACAGCC	ATGGTTTTTG	GTCAAATGAA	CGAACCGCCA	600
	GGTGACGGGA	TGCGTGTGGC	CTTAAGTGGG	TTAACGATTG	CTGAATATTT	650
	CCGTGATGTG	GAAGGACAAG	ACGTGCTATT	ATTTATTGAT	AACATTTTCC	700
60	GTTTCACCCA	AGCCGGTTCA	GAAGTTTCTG	CCCTTTTAGG	TCGGATGCCG	750

TCAGCCGTTG GTTACCAACC AACCTTAGCG ACTGAAATGG GACAATTACA 800
 AGAACGGATT ACTTCAACGA AAAAAGGATC AATTACCTCT 840

5

2) INFORMATION FOR SEQ ID NO: 292

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: ATCC 19434

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292

TTTCTTTAGA CCAATCCTTA CCAGATATCA ACAACGCATT AGTTGTTTAT 50
 AAAAATGACG AAAATAAATC AAAAGTTGTT CTTGAAGCAG CGTTAGAATT 100
 AGGGGACGGA GTGATCCGGA CCATTGCGAT GGAATCAACA GATGGTTTAC 150
 25 AAAGAGGAAT GGAAGTCATT GATACAGGCA AAGCAATCTC TGTTCTGTGA 200
 GGTAAAGAAA CATTAGGTCG CGTATTCAAC GTACTAGGAG ATACGATCGA 250
 TTTAGAAACA CCTTTCCCAG AAGATGCGGA AAGAAGCGAA ATTCATAAAA 300
 AAGCACCAGC CTTTGACGAA TTAAGTACAA GTACAGAAAT TTTGGAAACA 350
 GGGATCAAAG TTATCGATTT GCTTGCCCCA TATTTAAAAG GTGGGAAAGT 400
 30 CGGACTATTC GGTGGTGCCG GTGTTGGTAA AACCGTACTG ATCCAAGAAC 450
 TGATCCATAA TATCGCCCAA GAACATGGTG GTATTTCTGT ATTTACCGGT 500
 GTAGGTGAAC GTACTCGTGA AGGTAATGAC TTGTATTATG AAATGAAAGA 550
 TTCAGGAGTT ATCGAAAAA CAGCCATGGT GTTCGGACAA ATGAACGAAC 600
 CACCAGGTGC ACGTATGCGT GTTGCTTTGA CTGGTTTGAC GATTGCGGAA 650
 35 TATTTCCGTG ATGTAGAAGG TCAAGATGTA CTGTTGTTTA TCGACAACAT 700
 TTTCCGTTTC ACTCAAGCTG GATCTGAAGT ATCAGCCTTG TTAGGACGGA 750
 TGCCTTCTGC GGTTGGTTAT CAACCAACAT TGGCAACAGA AATGGGTCAA 800
 TTGCAAGAAC GTATCACATC TACGAAAAA G 831

40

2) INFORMATION FOR SEQ ID NO: 293

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
 (B) STRAIN: ATCC 49573

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293

CCTTACCAGA TATCAACAAT GCGTTGATCG TTTACAAAAA AGACGAGAAA 50
 AAAACAAAAG TAGTATTGGA AGCCGCTTTA GAACTAGGGG ATGGTGTGAT 100
 60 CCGCACCATC GCAATGGAAT CTACAGACGG TTTGCAACGA GGAATGGAAG 150

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TCATCGATAC CGGTGCCTCA ATCTCTGTCC CTGTAGGAAC AGATACTCTA 200
GGCCGAGTAT TTAATGTACT AGGCGATACT ATCGACTTGG AAGCACCATT 250
CCCAGAAGAT GCCAAACGTA GTGGCATCCA CAAAAAAGCC CCAGATTTTCG 300
ATGAATTGTC AACAAGTACA GAAATCCTTG AAAGTGGGAT CAAAGTTATC 350
5 GATTTATTAG CTCCTTACTT AAAAGGTGGT AAAGTCGGCT TGTTCGGTGG 400
TGCCGGTGTT GGTAAAACCG TATTGATTCA AGAATTGATT CACAATATCG 450
CTCAAGAGCA TGGGGGAATT TCAGTATTTA CCGGTGTTGG CGAACGGACG 500
CGTGAAGGTA ATGACTTGTA TTATGAAATG AAAGAATCAG GCGTTATCGA 550
AAAGACAGCC ATGGTTTTTCG GTCAAATGAA TGAACCACCA GGTGCCCGGA 600
10 TGCGGGTTGC TTTGACTGGT TTGACCATTG CTGAGTATTT CCGTGACGTT 650
GAAGGACAAG ATGTGCTCTT GTTTATCGAT AATATTTTCC GTTTCACACA 700
AGCGGGTTCT GAAGTATCTG CCTTGTTAGG CCGGATGCCA TCAGCCGTTG 750
GTTATCAACC AACTCTAGCA ACTGAAATGG GTCAATTACA AGAACGAATC 800
ACTTCTACGA AAAAAGGATC TGTAAC 826
15

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2) INFORMATION FOR SEQ ID NO: 294

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20 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 846 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
25 (ii) MOLECULE TYPE: Genomic DNA
    (vi) ORIGINAL SOURCE:
    (A) ORGANISM: Enterococcus saccharolyticus
30 (B) STRAIN: ATCC 43076

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294

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35 TTTCTTTGGA CCAATCCTTA CCAGACATCA ACAATGCGTT GGTGGTCTAT 50
AAAAAGAATG ATGAAAAAAC AAAAGTGGTA CTTGAAACAG CTTTAGAACT 100
TGGTGATGGT GTCGTACGTA CGATTGCTAT GTCGTCAACA GACGGTTTTCG 150
AACGTGGGAT GGAAGTCATC GATACAGGAG CATCAATTTT TGTTCCTGTT 200
GGGAAAGAGA CATTAGACG TGTATTAAAC GTTTTAGGGG AGACTATCGA 250
CTTAGATGGT CCATTTCCAG AAGAAGTAGC ACGAGATGGT ATTCATAAAA 300
40 AGGCACCTGA TTTTGATGAA TTAAGTACAA GTACGGAGAT TCTTGAAACA 350
GGGATTAAAG TAATCGATTT ATTAGCGCCT TACTTAAAAG GTGGGAAAGT 400
TGGTTTATTC GGTGGTGCCG GTGTAGGTAA AACGGTATTA ATTCAAGAAT 450
TGATTAAACA TATTGCGCAA GAACATGGTG GTATTTTCAGT ATTTGCGGGT 500
GTTGGTGAGC GTACTCGTGA AGGAAATGAC CTTTATTATG AAATGAAAGA 550
45 GTCGGGCGTT ATTGAGAAAA CAGCGATGGT TTTTGGACAA ATGAACGAAC 600
CACCAGGTGC ACGTATGCGA GTTGCTTTAA CTGGTTTAAC CATTGCAGAA 650
TACTTCCGTG ATGTTGAAGG ACAAGATGTA TTACTATTTA TTGATAACAT 700
TTTCCGTTTT ACTCAAGCTG GTTCAGAAGT TTCAGCTTTA TTAGGACGTA 750
TGCCTTCAGC GGTAGGGTAT CAACCGACAT TAGCAACAGA AATGGGACAA 800
50 TTACAAGAAC GTATTACGTC AACGAAAAAA GGCTCAATTA CATCAA 846

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2) INFORMATION FOR SEQ ID NO: 295

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55 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 803 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
60 (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Escherichia fergusonii*
(B) STRAIN: ATCC 35469

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295

10	GCCGTACCGC	GCGTGTACGA	TGCTCTTGAG	GTGCAAAATG	GTAATGAGCG	50
	TCTGGTGCTG	GAAGTTCAGC	AGCAGCTCGG	CGGTGGTATC	GTGCGTACCA	100
	TCGCAATGGG	GTCCTCCGAC	GGTCTGCGTC	GCGGTCTGGA	TGTAAAAGAC	150
	CTCGAACACC	CGATCGAAGT	CCC GG TAGGT	AAAGCGACTC	TGGGCCGTAT	200
	CATGAACGTA	CTGGGTGAAC	CGGTCGACAT	GAAAGCGGAG	ATCGGTGAAG	250
15	AAGAGCGTTG	GGCGATTAC	CGCGCAGCAC	CTTCCTACGA	AGAGCTGTCA	300
	AACTCTCAGG	AACTGCTGGA	AACCGGTATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTCGCT	AAGGGCGGTA	AAGTCGGTCT	GTTCCGGTGGT	GCGGGTGTAG	400
	GTAAAACTGT	AAACATGATG	GAGCTTATTC	GTAACATCGC	GATCGAGCAC	450
	TCCGGTTACT	CTGTGTTTGC	GGGCGTAGGT	GAACGTACTC	GTGAGGGTAA	500
20	CGACTTCTAC	CACGAAATGA	CTGACTCCAA	CGTTATCGAC	AAAGTATCCC	550
	TGGTATATGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCA	600
	CTGACCGGCC	TGACCATGGC	TGAGAAATTC	CGTGACGAAG	GTCGTGACGT	650
	TCTGCTGTTT	GTTGACAACA	TCTATCGTTA	CACCCTGGCC	GGTACGGAAG	700
	TATCCGCACT	GCTGGGCCGT	ATGCCTTCAG	CGGTAGGTTA	TCAGCCGACT	750
25	CTGGCGGAAG	AGATGGGCGT	TCTTCAGGAA	CGTATCACCT	CCACCAAAAC	800
	TGG					803

30 2) INFORMATION FOR SEQ ID NO: 296

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 822 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia hermannii*
(B) STRAIN: ATCC 33650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296

45	GATGCCGTAC	CGCGCGTGTA	CGATGCTCTT	GAGGTGCAAA	ATGGTGATGA	50
	GCGTCTGGTG	CTGGAAGTGC	AGCAGCAGCT	CGGCGGCGGT	ATCGTGCGTA	100
	CCATCGCAAT	GGGTTCTTCC	GACGGTCTGC	GTCGTGGTCT	GACTGTTCGT	150
	GACCTCGAGC	ACCCGATCGA	AGTCCCGGTA	GGTAAAGCGA	CCCTGGGCCG	200
50	TATCATGAAC	GTGCTGGGTC	AGCCGATCGA	CATGAAAGGC	GATATCGGTG	250
	AAGAAGAGCG	TTGGGCGATT	CACCGCGCGG	CGCCGTCCTA	TGAAGAGCTG	300
	TCCAGCTCTC	AGGAACTGCT	GGAAACCGGC	ATCAAAGTTA	TCGACCTGAT	350
	GTGTCCGTTT	GCGAAGGGCG	GTAAAGTCGG	TCTGTTCCGGT	GGTGCGGGCG	400
	TAGGTAAAAC	CGTAAACATG	ATGGAGCTGA	TCCGTAACAT	CGCGATCGAG	450
55	CACTCCGGTT	ACTCTGTGTT	TGCGGGCGTG	GGTGAACGTA	CTCGTGAGGG	500
	TAACGACTTC	TACCATGAAA	TGACCGACTC	CAACGTTCTG	GACAAAGTAT	550
	CCCTGGTTTA	CGGCCAGATG	AACGAACCGC	CGGGAAACCG	TCTGCGCGTT	600
	GCACTGACCG	GCCTGACCAT	GGCTGAGAAA	TTCCGTGACG	AAGGTCGTGA	650
	CGTTCTGTTG	TTCGTGACAA	ACATCTACCG	TTACACCTTG	GCCGGTACTG	700
60	AAGTATCCGC	ACTGCTGGGC	CGTATGCCTT	CTGCGGTAGG	TTACCAGCCG	750

ACCCTGGCGG AAGAGATGGG CGTTCTGCAG GAGCGTATCA CCTCCACCAA
AACCGGTTCT ATCACCTCCG TA

800
822

5

2) INFORMATION FOR SEQ ID NO: 297

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 808 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia vulneris*
(B) STRAIN: ATCC 33821

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297

	CCGAACGTGT	ACGACGCCCT	CGAAGTGACA	AATGGTAATG	AGCGTCTGGT	50
	GCTGGAAGTT	CAGCAGCAGC	TCGGCGGCGG	TATCGTACGT	ACCATCGCTA	100
	TGGGTTCTTC	CGACGGTCTG	CGTCGTGGTC	TGGAAGTTCA	GGACCTCGAG	150
25	CACCCGATCG	AAGTGCCGGT	AGGTAAAGCG	ACCCTGGGTC	GTATCATGAA	200
	CGTACTGGGT	CAGCCGATCG	ATATGAAAGG	CGACATCGGT	GAAGAAGAGC	250
	GTTGGGCTAT	TCACCGTGCA	GCACCGTCCT	ATGAAGAGCT	CTCCAGCTCT	300
	CAGGAACTGC	TGGAAACCGG	CATCAAGGTT	ATCGACCTGA	TGTGTCCGTT	350
	CGCCAAGGGC	GGTAAAGTCG	GCCTGTTCCG	CGGCGCGGGC	GTGGGTAAAA	400
30	CCGTAAACAT	GATGGAGCTG	ATCCGTAACA	TCGCGATCGA	GCACTCCGGT	450
	TACTCCGTGT	TTGCAGGCGT	GGGTGAGCGT	ACTCGTGAGG	GTAACGACTT	500
	CTACCACGAG	ATGACCGACT	CCAACGTTCT	GGACAAAGTA	TCCCTGGTGT	550
	ACGGCCAGAT	GAACGAGCCG	CCGGGAAACC	GTCTGCGCGT	GGCACTGACC	600
	GGCCTGACCA	TGGCTGAGAA	GTTCCGTGAC	GAAGGTCGTG	ACGTTCTGCT	650
35	GTTTCGTTGAC	AACATCTATC	GTTACACCCT	GGCCGGTACG	GAAGTATCTG	700
	CACTGCTGGG	CCGTATGCCT	TCAGCGGTAG	GTTACCAGCC	GACGCTGGCG	750
	GAAGAGATGG	GCGTTCTGCA	GGAGCGTATC	ACCTCCACCA	AAACCGGTTC	800
	TATCACCT					808

40

2) INFORMATION FOR SEQ ID NO: 298

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 843 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Eubacterium lentum*
(B) STRAIN: ATCC 43055

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298

	TTCCCCCTG	ATCAGCTGCC	GGCGATTAC	AACGCGCTGA	CGGTTGATGC	50
	CAAGACCCTG	GCGGGCGACT	TGCACCTCGT	GCTCGAGGTC	GAGACGCACC	100
60	TGCCGGGCAA	CCTTGTCGCG	TCGGTGGCCA	TGAGCTCGAC	GGACGGTCTC	150

	GTCCGCGGCC	TCGAGGTCGT	CGACACGGGC	AACCCGATCA	TGATGCCCCGT	200
	GGGTCCCGAG	ACCCTGGGTC	GCATCTGGAA	CGTCATGGGC	GAGCCCGTCG	250
	ACGAGAAGCC	GATGCCCCGAG	GTGAAGGGCT	ACATGCCCCAT	CCACCGTCCG	300
	GCTCCGGA	ACGACGAGCT	GTCCACCACC	ACCGAGATCT	TCGAGACCGG	350
5	CATCAAGGCC	ATCGACCTCG	TCGAGCCCTT	CGTCAAGGGC	GGCAAGACGG	400
	GTCTGTTCGG	CGGCGCCGGC	GTGGGCAAGA	CGGTTATCAT	CCAGGAGCTC	450
	ATCAACAACC	TGGCCAGGA	GCACGGCGGC	ACGTCGGTGT	TCACGGGCGT	500
	GGGCGAGCGT	ACCCGCGAGG	GTACCGACCT	CTACCTGGAG	ATGAGCGACT	550
	CGGGCGTCAT	CAACAAGACC	TGCCTCGTGT	ACGGTCAGAT	GAACGAGCCT	600
10	CCGGGAGCGC	GTCTGCGCGT	GGGTCTCGCG	GGCCTCACCG	AGGCGGAGTA	650
	CTTCCGCGAT	CAGGGCCAGG	ACGTGCTTCT	GTTTCGTGGAC	AACATCTTCC	700
	GCTTCACGCA	GGCCGGCTCC	GAGGTGTCCG	CTCTGCTGGG	CCGCATGCCC	750
	TCTGCCGTGG	GTTACCAGCC	GACGCTGGCA	ACCGAGATGG	GCGACCTGCA	800
15	GGAGCGCATC	ACGTCGACGT	CCACCGGCTC	CATCACGTCC	GTG	843

2) INFORMATION FOR SEQ ID NO: 299

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Ewingella americana*
 (B) STRAIN: ATCC 33852

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299

	TCCCTCAGGA	TGCAGTACCG	AACGTGTACA	ATGCTCTTGA	GGTAGAAAAC	50
35	GGTGCCTCCA	AACTGGTTCT	GGAAGTTTCA	CAACAGTTAG	GCGGCGGCGT	100
	TGTTTCGTTGT	ATCGCAATGG	GTACCTCAGA	CGGCCTTCGT	CGCGGTCTGA	150
	AAGTGAACAA	CCTGGAACAC	CCAATTGAAG	TTCCGGTTGG	TAAAGCGACT	200
	CTGGGTCGTA	TCATGAACGT	ATTGGGTGAA	CCAATCGACA	TGAAAGGTGA	250
	AATCGGCGAA	GAAGAACGTC	GTGCAATTCA	CCGTCCAGCG	CCTTCTTATG	300
40	AAGAGCTGGC	TAACTCCCAA	GAATTGCTGG	AAACCGGTAT	CAAAGTTATG	350
	GACCTGATGT	GTCCGTTTCG	TAAGGGCGGT	AAAGTCGGTC	TGTTTCGGTGG	400
	TGCGGGTGTG	GGTAAACTG	TAAACATGAT	GGAGCTGATC	CGTAACATCG	450
	CGATCGAGCA	CTCCGGTTAC	TCAGTGTGTT	CAGGCGTGGG	TGAGCGTACT	500
	CGTGAGGGTA	ACGACTTCTA	CCACGAAATG	ACTGACTCCA	ACGTTATCGA	550
45	CAAAGTTTCC	CTGGTCTATG	GTCAGATGAA	TGAGCCACCA	GGTAACCGTC	600
	TGCGCGTTGC	ACTGACCGGC	CTGACCATGG	CGGAGAAATT	CCGTGATGAA	650
	GGTCGTGACG	TACTGCTGTT	CGTTGACAAC	ATTTACCGTT	ACACCCTGGC	700
	AGGTACCGAA	GTGTCCGCAC	TTCTGGGCCG	TATGCCATCG	GCGGTAGGTT	750
	ATCAGCCAAC	GCTGGCGGAA	GAGATGGGTG	CTCTGCAAGA	GCGTATCACC	800
50	TCTACCAAAA	GTGGTTCTAT	CACCTCCGT			829

2) INFORMATION FOR SEQ ID NO: 300

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 805 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Francisella tularensis*
(B) STRAIN: LVS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300

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10 AACACGCCTA AAGTATATGA TGCTTTAAAT GTAGTAGAAG CTGGTTTAGT      50
   ATTAGAAGTT CAGCAACAAA TTGGTGATGG CGTAGTTCGT ACAATTGCTA      100
   TGGGATCTAG TGATGGTCTT AGACGTGGTA TGGAAAGTTAA GAACACAAAT      150
   GCGCCTATTT CTGTTCCAGT TGGACATGGC ACACTTGGAC GTATCATGAA      200
   TGTTTTAGGT GAACCAATTG ATGAAGCTGG TCCAATTGAA TATACTGAGA      250
15 AAAGATCTAT CCATCAAGCT CCTCCTGCAT ATGATGAGTT AGCATTAAAGT      300
   ACAGAAATAT TAGAAACAGG TATCAAAGTA GTTGACCTTA TTTGTCCATT      350
   TGCTAAGGGC GGTAAAGTTG GTTTATTTGG CGGTGCAGGT GTTGGTAAAA      400
   CTGTAACGAT GATGGAACCT ATCAACAATA TTGCAAAAGA ACATAGTGGC      450
   TACTCTGTAT TTTCCGGTGT TGGTGAAAGA ACTCGTGAAG GTAATGACTT      500
20 CTACTATGAG ATGAAATATT CTAATGTATT GGATAAAGTA TCATTAGTAT      550
   ATGGTCAGAT GAATGAGCCG CCTGGAAACA GATTAAGAGT AGCTCTTAGT      600
   GGCTTAACAA TAGCAGAAGG ATTCCGTGAT GAAAAGCGTG ATGTTTTGAT      650
   GTTTATCGAT AACATCTATC GTTATACATT AGCAGGTACA GAGGTATCGG      700
   CGCTACTTGG TCGTATGCCA TCTGCTGTGG GTTATCAGCC AACGCTTGCA      750
25 GCTGAGATGG GTGCTTTACA GGAGCGTATT ACATCTACTA AGACAGGATC      800
   TATTA                                     805

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30 2) INFORMATION FOR SEQ ID NO: 301

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 825 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 40 (A) ORGANISM: *Fusobacterium gonidiaformans*
(B) STRAIN: ATCC 25563

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301

```

45 GACGAATTGC CAAAAATATA CAATGCATTA AAGGTGCAAG TTGGAGAAAA      50
   AGAACTTGTA TTGGAAGTGC AACAAACATTT GGGAAATAAT GTTGTGAGAA      100
   CAGTAGCGAT GGACTCAACA GATGGATTGC TTCGAGGAAT GGAAGTAATG      150
   GATACCGGAG CACCGATTAC TGTTCCAGTA GGGAAGGCGG TTTTAGGAAG      200
50 AATATTGAAT GTTTTGGGAG AGCCTGTGGA TCAAAAAGGG CCTGTGGAAA      250
   CAGAAGAATA TTTACCTATC CATAGAGAAG CACCAAAATT TGAAGAACAA      300
   GAAACAGTAA CAGAAATTTT TGAAACAGGA ATTAAAGTCA TAGATTTGTT      350
   AGCCCCTTAT ATCAAAGGAG GAAAGACAGG TCTATTCGGT GGAGCCGGAG      400
   TAGGGAAAAC AGTTTAAATT ATGGAATTAA TTAATAACAT TGCAAAGGGC      450
55 CACGGAGGAA TTTCTGTGTT TGCAGGAGTT GGAGAAAGAA CAAGAGAAGG      500
   AAGAGATTTA TACAACGAAA TGACAGAGTC CGGAGTTTGT AATAAGACCT      550
   CGTTGGTGTA TGGTCAAATG AATGAGCCGC CCGGAGCAAG ACTTCGTGTG      600
   GCGTTGACAG GATTAACGGT TGCTGAAAAC TTTAGAGATA AAGAAGGGCA      650
   AGATGTATTG TTGTTTATCG ACAATATCTT CCGTTTCACA CAAGCAGGAT      700
60 CAGAAGTATC GGCTCTATTG GGAAGAATTC CATCGGCAGT AGGATATCAA      750

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CCGAACTTAG CGACAGAAAT GGGAACCTTTA CAAGAAAGAA TTACTTCTAC 800
 AAAATCAGGA TCTATCACTT CCGTA 825

5

2) INFORMATION FOR SEQ ID NO: 302

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fusobacterium necrophorum* subsp. *necrophorum*
 (B) STRAIN: ATCC 25286

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302

ACAATGCATT AAAGGTACAG GTGGGAGAAA GGGAACCTTGT GTTGGAAGTG 50
 CAGCAACATT TAGGAAATAA TGTTGTCAGA ACAGTAGCAA TGGATTCAAC 100
 AGACGGATTA CTTCCGGGAA TGGAAGTGAG AGATACAGGA GTTCCCATT 150
 25 CTGTTCCGGT AGGAAAGGCG GTTTTGGGAA GAATATTAAA TGTCTTAGGG 200
 GAGCCTGTGG ACGAAAAAGG TCCGATAGAG ACAGAAGAAT ATTTACCAAT 250
 ACATAGAGAA GCACCGAAAT TTGAAGAACA GGAAACGGTG ACAGAAATTT 300
 TTGAAACAGG AATTAAAGTC ATTGATTTGT TAGCTCCTTA TATTAAAGGA 350
 GGAAAAACAG GCCTATTCGG AGGAGCCGGA GTAGGAAAAA CCGTTTTGAT 400
 30 TATGGAACCTG ATCAATAATA TTGCAAAAGG TCATGGAGGA ATTTCTGTTT 450
 TTGCAGGAGT TGGAGAAAGA ACGAGAGAGG GAAGAGATCT ATACAACGAA 500
 ATGACAGAGT CCGGAGTTT GAATAAACT TCTTTGGTAT ATGGGCAAAT 550
 GAATGAGCCG CCCGGAGCAA GACTTCGAGT GGCTTTAACC GGACTTACTG 600
 TTGCCGAAAA TTTCAGAGAT AAAGAGGGAC AGGATGTCTT ATTGTTTATT 650
 35 GACAATATTT TCCGTTTCAC ACAAGCAGGT TCGGAAGTAT CGGCACTTTT 700
 GGGGAGAATT CCTTCTGCAG TGGGATATCA ACCGAACTTG GCGACAGAAA 750
 TGGGAAGCTT ACAAGAAAGA ATTACTTCTA CAAAATCCGG TTCTATCACT 800
 TCCGTG 806

40

2) INFORMATION FOR SEQ ID NO: 303

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 821 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fusobacterium nucleatum* subsp. *polymorphum*
 (B) STRAIN: ATCC 10953

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303

GATGAATTGC CTGCAATATA TAATGCTTTA AAAGTAAAAA TAGAAGATAA 50
 GGAACCTTGT CTAGAAGTTG AACAACATCT TGGTAACAAT GTTGTAAGAA 100
 60 CTGTTGCTAT GGATTCAACT GATGGATTAA AAAGAGGAAT GGAAGTTATA 150


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GATACAGGTA AACCAATTAC AGTACCAGTT GGTAAAGCTG TTCTTGGTAG 200
AATATTAAAT GTTTTAGGAG AACCTGTTGA TAATCAAGGT CCTATAAATG 250
CTGAAACATT TTTACCTATT CATAGAGAAG CACCAGAATT TGATGACTTA 300
GAAACTGAAA CTGAAATATT TGAAACAGGA ATAAAAGTTA TAGACTTATT 350
5 AGCACCATAT ATTAAAGGTG GAAAAATAGG ATTATTTGGT GGAGCTGGAG 400
TAGGAAAAAC AGTTTTAATA ATGGAACCTTA TCAACAACAT TGCAAAAGGA 450
CATGGAGGAA TTTCAGTTTT TGCAGGAGTT GGAGAAAGAA CAAGAGAAGG 500
TAGAGACTTA TATGGTGAAA TGACTGAATC AGGAGTTATC ACAAAAACAG 550
CTCTTGTTTA TGGACAAATG AATGAGCCAC CTGGAGCAAG ACTTAGAGTT 600
10 GCATTAACAG GGCTTACTGT TGCAGAAAAC TTTAGAGATA AAGATGGGCA 650
AGATGTTCTT CTATTTATAG ATAATATATT TAGATTTACA CAAGCAGGTT 700
CAGAAGTTTC AGCTTTACTT GGAAGAATAC CATCAGCTGT TGGATATCAA 750
CCAAACCTAG CAACTGAAAT GGGTGCTTTA CAAGAAAGAA TAACATCTAC 800
AAAATCTGGT TCAATTACAT C 821
15

```

2) INFORMATION FOR SEQ ID NO: 304

```

20 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 864 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
25 (ii) MOLECULE TYPE: Genomic DNA
    (vi) ORIGINAL SOURCE:
    (A) ORGANISM: Gardnerella vaginalis
30 (B) STRAIN: ATCC 49145

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304

```

TTCCCAGTTG GCTATCTTCC AGATATTTAT AATGCTCTCA AGGTTGATAT 50
35 CAACACCGTT GGAAACACGG AGGGAGATAC CGTCCACGAG ATTACATTGG 100
AAGTTGAGCA GCACCTTGGT GATTCAACTG TGCGAGCAGT GGCACCTTAAG 150
CCTACGGAGC GCTTGGTCCG TGGTGCTTTA GTGCGAGATA CTGGTGGCCC 200
AATTTCTGTG CCTGTTGGAG ATGTTACAAA AGGTCACGTT TTTGACGTAA 250
CTGGTAACAT TTTAAACGCT AAACCAGGCG AAAACATTGA GGTGACCGAG 300
40 CGCTGGCCAA TCCACCGCAA CCCACCTGCT TTCGATCAGC TTGAGTCTAA 350
GACTCAAATG TTTGAAACAG GCATTAAGGT TATCGATTTG CTTACGCCTT 400
ACGTTTCAGGG CGGAAAGATT GGTCTGTTCT GTGGTGCAGG CGTTGGTAAA 450
ACTGTGTTGA TTCAGGAGAT GATTCAGCGC GTTGCACAGA ACCACGGCGG 500
TGTGTCTGTG TTTGCTGGCG TTGGCGAACG TACTCGTGAG GGTAACGATT 550
45 TGATTGGCGA AATGGCTGAG GCTGGCGTTT TGGAGAAAAC AGCGCTTGTC 600
TTTGGTCAGA TGGATGAGCC TCCTGGGACT CGTCTTCGTG TGCCTCTTAC 650
TGCTTTGACT ATGGCTGAGT ATTTCCGTGA TGTTTCAAGT CAGGATGTGT 700
TGCTGTTTAT CGACAACATC TTCCGCTTTA CTCAGGCAGG TTCTGAGGTT 750
TCCACGTTGC TTGGTCGTAT GCCTTCTGCA GTTGGTTATC AGCCAAACTT 800
50 GGCGGATGAA ATGGGTGCGT TGCAGGAGCG CATTACTTCT ACGCGCGGTC 850
ATTCTATTAC GTCG 864

```

55 2) INFORMATION FOR SEQ ID NO: 305

```

    (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 848 bases
    (B) TYPE: Nucleic acid
60 (C) STRANDEDNESS: Double

```

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Gemella haemolysans*

(B) STRAIN: ATCC 10379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305

```

10  TCGAATCAGG GCATATGCCA AATCTATTAA ACGCTTTAGA AGTTTACATA      50
    GAAAAAGGCG ATGGGAAAAA AGAAAAATTA GTTCTTGAAG TTTCTCTTGA      100
    AATTGGTGAT AACGTAGTAA GAACAATCGC TATGTCATCT ACTGATGGAT      150
    TAAATAGGGG AGCAGAAGTA GTAGATACAG GAGCACCAAT TACAGTTCCT      200
15  GTAGGTAAC TACACATTAGG TCGTGTGTTT AACGTATTAG GTGAAGCAGT      250
    TGACCACGGT GAAGAAGCAG GAGCAGAAGT TCGTAAAGAT TCAATTCACA      300
    AAGAAGCTCC AACATTTCGAT GAATTATCAA CTCACGTTGA GGTTCCTTGAA      350
    ACAGGTATTA AAGTTATCGA CTTACTTGCA CCATATATTA AAGGTGGTAA      400
    AATCGGTCTT TTCGGTGGTG CGGGAGTTGG TAAAACGGTT CTTATCCAAG      450
20  AACTTATCAA CAACGTTGCG CAACAACACG GTGGATTATC AGTATTCACA      500
    GGTGTAGGTG AGCGTACTCG TGAAGGAAAT GACTTATACT ATGAAATGAA      550
    AGATTCTGGT GTTATTAACA AAACAGCCAT GGTATTTCGA CAAATGAACG      600
    AACCACCAGG TGCTCGTATG CGTGTAGCAT TAACAGGATT AACAATGGCG      650
    GAATACTTCC GTGATGAAGA AGGACAAGAC GTGCTTCTAT TCATCGATAA      700
25  CATTTTCCGT TTCACACAAG CAGGTTCTGA GGTTCCTGCG TTATTAGGAC      750
    GTATGCCATC AGCCGTTGGT TACCAACCAA CACTTGCTAC AGAGATGGGA      800
    CGTTTACAAG AACGTATAAC ATCAACTAAA AAAGGTTCTG TTACATCT      848

```

30

2) INFORMATION FOR SEQ ID NO: 306

(i) SEQUENCE CHARACTERISTICS:

```

35  (A) LENGTH: 848 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Gemella morbillorum*

(B) STRAIN: ATCC 27824

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306

```

    TCGAATCAGG GCATATGCCT AATCTACTAA ACGCTTTAGA AGTTTATATA      50
    GAAAAAGGCG ATGGAAAAAA AGAAAAATTA GTTCTTGAAG TTTCTCTTGA      100
    AATCGGGGAT AATGTCGTAA GAACTATTGC GATGTCATCT ACTGATGGAT      150
50  TAAACAGAGG GGCAGAAGTA GTTGATACTG GAGCGCCAAT TACAGTGCCA      200
    GTAGGTAAC TACATTAGG ACGTGTGTTT AACGTATTAG GTGAAGCAGT      250
    TGACCACGGA GAAGAAGCTG GAGCAGAAGT TCAAAAAGAA TCTATTCATA      300
    AAGAAGCTCC AACTTTCGAA GAATTATCAA CACATGTTGA GGTATTAGAA      350
    ACAGGTATTA AAGTTATCGA CCTTCTTGCA CCATATATTA AAGGTGGTAA      400
55  GATTGGACTA TTCGGTGGTG CTGGAGTTGG GAAAACAGTT CTTATCCAAG      450
    AACTTATTAA CAACGTAGCA CAACAACACG GAGGACTTTC AGTATTTACT      500
    GGGGTAGGTG AACGTACTCG TGAGGGTAAC GACTTGTAAT ATGAAATGAA      550
    AGACTCTGGA GTTATTAATA AAACGTCAT GGTATTTGGT CAAATGAATG      600
    AGCCACCAGG TGCACGTATG CGTGTGCCT TAACAGGATT AACAATGGCA      650
60  GAGTACTTCC GTGATGAAGA AGGACAAGAC GTACTATTAT TTATCGATAA      700

```

```

TATCTTCCGT TTCACACAAG CAGGGTCTGA GGTATCTGCA TTATTAGGGC 750
GTATGCCTTC AGCCGTTGGA TATCAACCAA CTCTTGCAAC AGAAATGGGA 800
CGTCTTCAAG AACGTATTAC ATCAACTAAA AAAGGATCTG TTACATCT 848

```

5

2) INFORMATION FOR SEQ ID NO: 307

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 813 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus ducreyi*
 (B) STRAIN: DSM 8925

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307

```

GATGCAGTAC CAAAAGTATA TGATGCTTTA AAAGTTGAAT CAGGTTTAAAC 50
CTTAGAAGTT CAACAACAAT TAGGTGGTGG TTTAGTACGT TGTATCGCAT 100
25 TAGGTACCTC AGATGGTTTA AAGCGTAGCT TAAAGGTTGT AAATACAGGT 150
AACCCTATTC AAGTTCCTGT AGGCACTAAA ACATTAGGCC GTATTATGAA 200
TGTATTAGGC GAACCAATTG ATGAAAAAGG ACCTATTAGC GAAGAAGCTC 250
GTTGGGATAT TCATCGTGCG GCTCCAAATT ATGAAGAACA GTCAAATAGT 300
ACTGAATTAC TTGAAACCGG TATCAAAGTT ATTGACTTAA TTTGTCCATT 350
30 TGCAAAAGGT GGTAAAGTCG GCTTATTTGG TGGAGCTGGT GTAGGTAAAA 400
CCGTTAATAT GATGGAATTG ATCCGTAATA TTGCTATTGA GCACTCAGGT 450
TATTCGGTTT TTGCTGGTGT AGGTGAGCGT ACTCGTGAAG GTAATGATTT 500
TTATCATGAA ATGACGGATT CTAATGTATT AGATAAAGTA TCACTAGTAT 550
ATGGTCAAAT GAATGAACCA CCAGGTAACC GCCTACGTGT TCGGTTAACA 600
35 GGTTTAACTA TGGCTGAAAA ATTCCGTGAT GAAGGTCGTG ATGTATTATT 650
TTTCGTAGAT AATATTTATC GTTATACTTT AGCCGGTACA GAAGTTTCTG 700
CTTTATTAGG CCGTATGCCA TCAGCGGTAG GTTATCAACC AACCCTTGCA 750
GAAGAAATGG GTGTATTACA AGAACGTATT ACCTCAACTA AAACCTGGTTC 800
AATCACGGCA GTA 813
40

```

2) INFORMATION FOR SEQ ID NO: 308

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 826 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus haemolyticus*
 55 (B) STRAIN: ATCC 33390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308

```

TGAATTTCCA CAAGATGCAG TGCCAAAAGT TTACGATGCA TTAAAAGTTG 50
60 AATCAGGTTT AACACTTGAG GTGCAACAAC AATTAGGTGG CGGTGTGGTA 100

```

```

CGTTGTATCG CATTAGGTGC TTCTGACGGT TTAAAACGTG GTTTAAAAGT 150
AGAAAAACACG AATGATCCGA TTCAAGTACC GGTAGGCACA AAAACCCTTG 200
GTCGTATCAT GAATGTATTG GGTGAACCAA TTGACGAACA AGGTCCAATC 250
GGTGAAGAAG AGCGTTGGGC TATCCATCGT TCTGCACCAA GCTATGAAGA 300
5 ACAATCAAAC AGTACGGAAT TATTAGAGAC TGGTATCAAA GTTATCGACT 350
TAATTTGTCC ATTCGCAAAA GGTGGTAAAG TTGGTCTATT CGGTGGTGCG 400
GGTGTAGGTA AAACCGTTAA CATGATGGAA TTAATCCGTA ACATCGCGAT 450
CGAGCACTCA GGTACTCCG TATTTGCGGG TGTAGGTGAA CGTACTCGTG 500
AAGGTAACGA CTTCTATCAT GAAATGAAAG ATTCTAACGT ATTAGATAAA 550
10 GTATCTTTGG TTTATGGTCA GATGAATGAG CCACCAGGTA ACCGTTTACG 600
TGTTCGTTA ACTGGTTTAA CCATGGCAGA AAAATTCCGC GATGAAGGTC 650
GTGATGTATT ATTCTTCGTG GATAATATCT ATCGTTATAC CCTTGCTGGT 700
ACGGAAGTAT CTGCGTTATT AGGTCGTATG CCATCTGCGG TAGGTTACCA 750
ACCAACTCTT GCTGAAGAAA TGGGTGTGTT ACAAGAACGT ATCACTTCAA 800
15 CCAAACAGG TTCTATTACA TCTGTA 826

```

2) INFORMATION FOR SEQ ID NO: 309

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 809 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus parahaemolyticus*
 (B) STRAIN: ATCC 10014

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309

```

35 GATGCAGTAC CAAAAGTATA TGATGCGTTA AAAGTTGAAT CAGGTTTAAAC 50
GCTTGAAGTT CAACAACAAT TAGGCGGTGG CTTAGTGCGC TGTATCGCAT 100
TAGGTACGTC TGATGGTTTA AAACGTGGCT TAAAAGTAGA AAATACAGGC 150
AACCCAATTG AAGTGCCAGT GGGCACTAAA ACCCTTGGTC GTATTATGAA 200
CGTATTGGGT GAGCCGATTG ACGAAAAAGG TCCTATCGGT GAAGAAGCAC 250
40 GCTGGGCAAT CCACCGTGCA GCACCAAGCT ACGAAGAGCA ATCAAATAGC 300
ACGGAATTAC TCGAAACAGG TATCAAAGTT ATCGACTTAA TCTGCCCATT 350
CGCAAAAGGG GGTAAAGTTG GTTTATTTGG TGGTGCAGGT GTAGGTAAAA 400
CCGTAAATAT GATGGAGTTA ATCCGTAACA TCGCGATCGA ACACTCTGGT 450
TACTCTGTAT TTGCAGGGGT AGGTGAGCGT ACTCGTGAAG GTAATGACTT 500
45 CTACCACGAA ATGACAGACT CTAACGTATT AGATAAAGTA TCGTTAGTGT 550
ATGGTCAAAT GAACGAACCA CCAGGTAACC GTTTACGCGT AGCTTTAACA 600
GGCTTAACCA TGGCGGAAAA ATTCCGCGAT GAAGGTCGTG ACGTATTATT 650
CTTCGTCGAT AACATCTACC GTTATACCCT AGCAGGTACG GAAGTGTCAG 700
CACTTCTCGG TCGTATGCCA TCTGCGGTAG GTTATCAGCC AACCTTAGCA 750
50 GAAGAAATGG GTGTATTACA AGAGCGTATC ACTTCAACCA AAAGTGGTTC 800
TATCACCTC 809

```

55 2) INFORMATION FOR SEQ ID NO: 310

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 60 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Haemophilus parainfluenzae*

(B) STRAIN: ATCC 7901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310

```

10 CGAATTTCCA CAAGATGCAG TACCAAAAAGT TTATGATGCA TTAAAAGTTG      50
   AATCGGGTTT AACCTTGAA GTTCAACAAC AATTAGGTGG TGGTGTGGTA      100
   CGTTGTATCG CACTGGGAGC TTCTGACGGT TTAAAACGCA GTTTAAGCGT      150
   TGAATAATACC AATAAACCAA TTTCAGTACC GGTGTTGGTGA AAAACTCTCG      200
15  GTCGTATTAT GAACGTATTG GCGGAACCGA TTGATGAAAG AGGTCCTATC      250
   GGTGCGGAAG AAGAATGGGC AATTCACCGT TCTACTCCAA GTTATGAAGA      300
   ACAGTCCAAC AGTACCGAAT TATTAGAAAC CGGTATCAAA GTTATCGACT      350
   TAATTTGTCC ATTCGCGAAG GGTGGTAAAG TTGGTTTATT CGGTGGTGCG      400
   GGTGTAGGTA AGACCGTAAA TATGATGGAA TTAATCCGTA ATATTGCGAT      450
20  TGAGCACTCA GGTTACTCCG TATTTGCCGG TGTAGGTGAG CGTACCCGTG      500
   AAGGTAACGA CTTCTACCAT GAAATGACAG AATCTAACGT ATTAGACAAA      550
   GTATCCCTAG TTTACGGACA AATGAATGAG CCGCCGGGTA ACCGTTTACG      600
   TGTTGCTTTA ACCGGTTTAA CCATGGCAGA AAAATTCCGT GACGAAGGTC      650
   GTGATGTATT ATTCTTCGTG GATAACATCT ATCGTTATAC CCTTGCAGGG      700
25  ACTGAAGTAT CGGCACTTTT AGGCCGTATG CCATCAGCGG TAGGTTATCA      750
   GCCGACACTT GCAGAAGAAA TGGGTGTGTT ACAAGAACGT ATTACATCAA      800
   CCAAAACAGG TTCTATTACT TCTG                                     824

```

30

2) INFORMATION FOR SEQ ID NO: 311

(i) SEQUENCE CHARACTERISTICS:

```

35  (A) LENGTH: 811 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Hafnia alvei*

(B) STRAIN: ATCC 13337

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311

```

   GCCGTGCCTA AAGTGTATAA CGCACTTGAG GTGAAAGGCG GTGCCACTAA      50
   ACTGGTACTG GAAGTTCAGC AGCAGCTAGG CGGCGGCGTT GTACGCTGTA      100
   TCGCTATGGG TACTTCTGAC GGTCTGCGTC GCGGACTGGA CGTTGTTGAC      150
50  CTGGAGCACC CGATTGAAGT CCCAGTAGGT AAAGCGACCT TAGGCCGCAT      200
   TATGAACGTA CTGGGTGAGC CAATTGATAT GAAGGGTGAT ATCGGCGAAG      250
   AAGATCGCTG GGCTATTAC CAGTGAAGCTC CAAGCTACGA AGAACTGTCT      300
   AACTCGCAAG AACTGCTGGA AACTGGTATC AAGGTAATGG ACCTGATTTG      350
   TCCGTTTCGCT AAGGGCGGTA AAGTTGGTCT GTTCGGTGGT GCGGGTGTTG      400
55  GTAAAACAGT AAACATGATG GAGCTGATCC GTAACATCGC GATCGAGCAC      450
   TCAGGTTACT CTGTATTTGC CGGCGTGGGT GAACGTAATC GTGAGGGTAA      500
   CGACTTCTAC CACGAAATGA CCGACTCCAA CGTATTGGAC AAAGTATCAC      550
   TGGTTTATGG CCAGATGAAC GAGCCACCAG GAAACCGTCT GCGCGTTGCG      600
   CTGACCGGTC TGACTATGGC TGAGAAGTTC CGTGACGAAG GTCGTGACGT      650
60  ACTGCTGTTC ATCGATAACA TCTACCGTTA TACCTTGGCC GGTACCGAAG      700

```

TATCTGCACT GTTGGGTCGT ATGCCTTCTG CGGTAGGTTA TCAGCCAACG 750
 CTGGCGGAAG AGATGGGTGT TCTGCAAGAA CGTATCACCT CGACCAAAAC 800
 GGGTTCAATC A 811

5

2) INFORMATION FOR SEQ ID NO: 312

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Kingella kingae*
 (B) STRAIN: ATCC 23330

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312

CGCATGCTAT TCCACGCGTT TACGATGCGT TGAAACTGGT TGATGTGGAC 50
 TTGACATTAG AAGTGCAACA ACAACTGGGC GATGGCGTAG TGCGTACCAT 100
 25 TGCGATGGGT AGTACCGATG GTTTGAAACG CGGCTTAGCC GTGAACAACA 150
 CAGGCGCACC TATTACAGTG CCTGTTGGTA AAGCAACATT GGGTCGTATT 200
 ATGGACGTAT TGGGTAATCC TGTTGATGAA GCAGGTCCAA TTGGTTCTGA 250
 CCAAACGCGT GCTATTCACC AACCAGCTCC TAAATTTGAT GAACTGTCTA 300
 GCGCAACCGA ATTGCTGGAA ACAGGCATCA AAGTGATTGA CTTGCTTTCG 350
 30 CCATTTGCAA AAGGTGGTAA AGTAGGTTTG TTTGGTGGTG CAGGTGTGGG 400
 CAAAACCTGTG AACATGATGG AGTTGATTAA CAACATTGCC AAAGCGCACA 450
 GTGGTTTGTG TGTATTTGCA GGCCTGGGTG AACGTAATCG CGAAGGTAAT 500
 GACTTCTATC ACGAGATGAA AGATTCTAAG GTGTTGGATA AAGTTGCCAT 550
 GGTGTATGGT CAAATGAATG AACCTCCTGG CAACCGTTTG CGCGTTGCAT 600
 35 TGACTGGTTT GTCTATGGCA GAACACTTCC GTGATGAAAA AGACGAAAAT 650
 GGCAAAGGTC GCGATGTATT GTTCTTTGTG GACAACATCT ATCGCTACAC 700
 ATTGGCAGGT ACAGAAGTAT CGGCATTGCT GGGTCGTATG CCCTCTGCGG 750
 TAGGTTATCA ACCAACATTG GCAGAAGAAA TGGGTCGTTT GCAAGAGCGT 800
 40 ATTACTTCAA CGCAAACAGG TTCGATTACT T 831

2) INFORMATION FOR SEQ ID NO: 313

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 812 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *ozaenae*
 55 (B) STRAIN: ATCC 11296

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313

ATGCCGTACC ACGCGTGTAC GAAGCCCTTG AGGTACAGAA TGGTAATGAA 50
 60 GTTCTGGTGC TGGAAAGTTCA GCAGCAGCTG GGCGGCGGTA TCGTACGTAC 100

```

CATCGCCATG GGTTCCTTCTG ATGGTCTGCG CCGCGGTCTG GATGTAAAAAG 150
ACCTCGAGCA CCCGATCGAA GTCCCGGTAG GTAAAGCAAC GCTGGGTCGT 200
ATCATGAACG TACTGGGTCA ACCGGTTGAC ATGAAAGGCG ACATCGGCGA 250
AGAAGAGCGT TGGGCTATCC ACCGCGCGGC ACCGTCCTAT GAAGAGCTGT 300
5 CCAGCTCTCA GGAAGTGTCTG GAAACCGGCA TCAAAGTTAT CGACCTGATG 350
TGTCCGTTTCG CCAAGGGCGG TAAAGTTGGT CTGTTTCGGCG GTGCGGGTGT 400
AGGTAAAACT GTAAACATGA TGGAGCTGAT CCGTAACATC GCGATCGAGC 450
ACTCCGGTTA CTCTGTGTTT GCGGGCGTAG GTGAGCGTAC TCGTGAGGGT 500
AACGACTTCT ACCACGAAAT GACCGACTCC AACGTTATCG ATAAAGTATC 550
10 CCTGGTGTAC GGCCAGATGA ACGAGCCGCC GGGAAACCGT CTGCGCGTTG 600
CGCTGACCGG CCTGACCATG CACTGAGAAAT TCCGTGACGA AGGTCGTGAC 650
GTACTGCTGT TCGTCGATAA CATCTATCGT TACACCCTGG CCGGTACTGA 700
AGTATCCGCG CTGCTGGGTC GTATGCCTTC AGCGGTAGGT TATCAGCCGA 750
CCCTGGCGGA AGAGATGGGC GTTCTGCAGG AACGTATCAC CTCCACCAAA 800
15 ACCGGTTCTA TC 812

```

2) INFORMATION FOR SEQ ID NO: 314

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella ornithinolytica*
 30 (B) STRAIN: ATCC 31898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314

```

35 ATGCCGTACC GCGCGTGTAC GATGCTCTTG AGGTACAGAA TGGTAATGAG 50
AGCCTGGTGC TGGAAGTTCA GCAGCAGCTC GCGCGTGGTA TCGTACGTGC 100
TATCGCCATG GGTTCCTCCG ACGGTCTGCG TCGTGGTCTG GAAGTTAAAG 150
ACCTTGAGCA CCCGATCGAA GTCCCGGTTG GTAAAGCAAC GCTGGGTCGT 200
ATCATGAACG TGCTGGGTCA GCCAATCGAT ATGAAAGGCG ACATCGGCGA 250
40 AGAAGAGCGT TGGGCTATTG ACCGTGCAGC TCCGTCCTAT GAAGAGCTGT 300
CCAGCTCTCA GGAAGTGTCTG GAAACCGGCA TCAAAGTTAT CGACCTGATG 350
TGTCCGTTTCG CTAAGGGCGG TAAAGTTGGT CTGTTTCGGTG GTGCGGGTGT 400
AGGTAAAACC GTAAACATGA TGGAGCTGAT CCGTAACATC GCGATCGAGC 450
ACTCCGGTTA CTCCGTGTTT GCGGGCGTAG GTGAACGTAC TCGTGAGGGT 500
45 AACGACTTCT ACCACGAAAT GACCGACTCC AACGTTCTGG ATAAAGTATC 550
CCTGGTTTAT GGCCAGATGA ACGAGCCGCC GGGAAACCGT CTGCGCGTTG 600
CTCTGACCGG CCTGACCATG CACTGAGAAAT TCCGTGACGA AGGTCGTGAC 650
GTTCTGCTGT TCGTCGATAA CATCTATCGT TACACCCTGG CCGGTACTGA 700
AGTATCCGCA CTGCTGGGTC GTATGCCTTC AGCGGTAGGT TATCAGCCGA 750
50 CCCTGGCGGA AGAGATGGGT GTTCTGCAGG AACGTATCAC CTCCACCAAA 800
ACCGGTTCTA TC 812

```

55 2) INFORMATION FOR SEQ ID NO: 315

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 bases
 (B) TYPE: Nucleic acid
 60 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella oxytoca*

(B) STRAIN: ATCC 33496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315

```

10 GTACCGCGCG TGTACGAGGC TCTTGAGGTA CAAAATGGTA GTGAGAATCT      50
   GGTGCTGGAA GTTCAGCAGC AGCTCGGCGG CGGTATTGTT CGTACCATCG      100
   CCATGGGTTT TTCCGACGGT CTGCGTCGCG GTCTGGAAGT CAAAGACCTC      150
   GAGCATCCGA TCGAAGTCCC GGTAGGTAAA GCAACGCTGG GTCGTATCAT      200
15 GAACGTACTG GGCCAACCGG TAGACATGAA AGGCGACATC GGCGAAGAAG      250
   AGCGTTGGGC GATTCACCGC GCAGCGCCTT CCTACGAAGA GTTGTCAAAC      300
   TCTCAGGAAC TGCTGGAAAC CGGCATCAAA GTTATCGACC TGATGTGTCC      350
   GTTTGCGAAG GGCGGTAAAG TTGGTCTGTT CGGTGGTGCG GGTGTAGGTA      400
   AAACCGTAAA CATGATGGAG CTGATCCGTA ACATCGCGAT CGAGCACTCC      450
20 GGTTACTCCG TGTTTGCGGG CGTAGGTGAA CGTACTCGTG AGGGTAACGA      500
   CTTCTACCAC GAAATGACCG ACTCCAACGT TATCGATAAA GTATCCCTGG      550
   TGTATGGCCA GATGAACGAG CCGCCGGGAA ACCGTCTGCG CGTTGCGCTG      600
   ACCGGCCTGA CCATGGCTGA GAAGTTCCGT GACGAAGGTC GTGACGTTCT      650
   GCTGTTCTG GATAACATCT ATCGTTACAC CCTGGCCGGT ACTGAAGTAT      700
25 CCGCACTGCT GGGTCGTATG CCTTCAGCGG TAGGTTACCA GCCGACTCTG      750
   GCGGAAGAGA TGGGCGTTCT GCAGGAACGT ATCACCTCCA CCAAACGGG      800
   TTCTATCACT TCC
                                           813

```

2) INFORMATION FOR SEQ ID NO: 316

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 822 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella planticola*

(B) STRAIN: ATCC 33531

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316

```

50 GATCCCGTAC CGCGCGTGTA CGATGCTCTT GAGGTACAGA ATGGTAATGA      50
   GAGCCTGGTG CTGGAAGTTC AGCAGCAGCT CGGCGGTGGT ATCGTACGTG      100
   CTATCGCCAT GGGTTCCTTCT GACGGTCTGC GTCGTGGTCT GGAAGTTAAA      150
   GACCTTGAGC ACCCGATCGA AGTCCCGGTT GGTAAAGCAA CGCTGGGTCG      200
   TATCATGAAC GTGCTGGGTC AGCCGATCGA TATGAAAGGC GACATCGGCG      250
   AAGAAGAGCG TTGGGCTATT CACCGCGCAG CTCCGTCTTA TGAAGAGCTG      300
   TCCAGTTCTC AGGAACTGCT GGAAACCGGC ATCAAAGTTA TCGACCTGAT      350
   GTGTCCGTTT GCTAAGGGCG GTAAAGTAGG TCTGTTCGGT GGTGCGGGCG      400
55 TAGGTAAAC CGTAAACATG ATGGAGCTGA TCCGTAACAT CGCGATCGAG      450
   CACTCCGGTT ACTCCGTGTT TGCGGGCGTC GGTGAACGTA CTCGTGAGGG      500
   TAACGACTTC TACCACGAAA TGACCGACTC CAACGTTCTG GATAAAGTAT      550
   CCTGGTTTA TGGCCAGATG AACGAGCCG CGGGAAACCG TCTGCGCGTT      600
   GCTCTGACCG GCCTGACCAT GGCTGAGAAA TTCCGTGACG AAGGTCGTGA      650
60 CGTTCTGCTG TTCGTCGATA ACATCTATCG TTATACCCTG GCCGGTACTG      700

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AAGTATCCGC	ACTGCTGGGT	CGTATGCCTT	CAGCGGTAGG	TTATCAGCCG	750
ACCCTGGCGG	AAGAGATGGG	TGTTCTGCAG	GAACGTATCA	CCTCCACCAA	800
AACCGGTTCT	ATCACTTCCG	TA			822

5

2) INFORMATION FOR SEQ ID NO: 317

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 785 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*
 (B) STRAIN: ATCC 13883

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317

AGAATGGTAA	TGAAGTTCTG	GTGCTGGAAG	TTCAGCAGCA	GCTGGGCGGC	50
GGTATCGTAC	GTACCATCGC	CATGGGTTCT	TCTGATGGTC	TGCGCCGCGG	100
25 TCTGGATGTA	AAAGACCTCG	AGCACCCGAT	CGAAGTCCCG	GTAGGTAAAG	150
CAACGCTGGG	TCGTATCATG	AACGTACTGG	GTCAACCGGT	TGACATGAAA	200
GGCGACATCG	GCGAAGAAGA	GCGTTGGGCT	ATCCACCGCG	CGGCACCGTC	250
CTATGAAGAG	CTGTCCAGCT	CTCAGGAAGT	GCTGGAAACC	GGCATCAAAG	300
TTATCGACCT	GATGTGTCCG	TTCGCCAAGG	GCGGTAAAGT	TGGTCTGTTC	350
30 GCGGGTGGCG	GTGTAGGTAA	AACTGTAAAC	ATGATGGAGC	TGATCCGTAA	400
CATCGCGATC	GAGCACTCCG	GTTACTCTGT	GTTTGCGGGC	GTAGGTGAGC	450
GTACTCGTGA	GGGTAATGAC	TTCTACCACG	AAATGACCGA	CTCCAACGTT	500
ATCGATAAAG	TATCCCTGGT	GTACGGCCAG	ATGAACGAGC	CGCCGGGAAA	550
CCGTCTGCGC	GTTGCGCTGA	CCGGCCTGAC	CATGGCTGAG	AAATTCCGTG	600
35 ACGAAGGTCG	TGACGTACTG	CTGTTCGTCTG	ATAACATCTA	TCGTTACACC	650
CTGGCCGGTA	CTGAAGTATC	CGCACTGCTG	GGTCGTATGC	CTTCAGCGGT	700
AGGTTATCAG	CCGACCCTGG	CGGAAGAGAT	GGGCGTTCTG	CAGGAACGTA	750
TCACCTCCAC	CAAACCGGT	TCTATCACCT	CCGTA		785

40

2) INFORMATION FOR SEQ ID NO: 318

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 759 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Kluyvera ascorbata*
 (B) STRAIN: ATCC 33433

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318

CTGGTGCTGG	AAGTTCAGCA	GCAGCTCGGC	GGCGGTATCG	TACGTWCCAT	50
CGCTATGGGT	TCTTCCGACG	GTCTGCGTCG	CGGTCTGGAT	GTTAAAGATC	100
60 TCGAGCACCC	AATCGAAGTT	CCGGTMGGTA	AAGCAACMCT	GGGTCGTATC	150

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ATGAACGTAC TGGGTCACCC AGTMGACATG AAAGGCGACA TCGGTGAAGA 200
AGAGCGTTGG GCTATCCACC GCGCTGCACC TTCCTACGAA GAGCTGTCTA 250
GCTCTCAGGA ATTGCTGGAA ACCGGTATCA AAGTTATCGA CCTGATGTGT 300
CCGTTCGCTA AGGGCGGTAA AGTCGGTCTG TTCGGTGGTG CSGGTGTTGG 350
5 TAAAACCGTA AACATGATGG AGCTGATCCG TAACATCGCG ATCGAGCACT 400
CCGGTTACTC CGTGTTTGCG GCGGTAGGTG AACGTACTCG TGAGGGTAAC 450
GACTTCTACC ACGAAATGAC CGACTCCAAC GTTATCGATA AAGTATCCCT 500
GGTATATGGC CAGATGAACG AGCCACCGGG AAACCGTCTG CGCGTTGCTC 550
TGACCGGTCT GACCATGGCT GAGAAATTCC GTGACGAAGG TCGTGACGTA 600
10 CTGCTGTTTC TCGATAACAT CTATCGTTAC ACCCTGGCCG GTACTGAAGT 650
ATCTGCWCTG CTGGGTCGTA TGCCTTCAGC GGTAGGTTAC CAGCCGACCC 700
TGGCGGAAGA GATGGGCGTT CTGCAGGAAC GTATCACCTC CACCAAGACC 750
GGTTCCTATC 759

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15

2) INFORMATION FOR SEQ ID NO: 319

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(i) SEQUENCE CHARACTERISTICS:
20 (A) LENGTH: 831 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Kluyvera cryocrescens
    (B) STRAIN: ATCC 33435

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25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319

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TTCCCTCAGG ATGCCGTACC GCGTGTGTAC GAAGCCCTTG AGGTTTCAGAA 50
TGTAATGAA GTGCTGGTGC TGGAAAGTTCA GCAGCAGCTC GGCGGCGGTA 100
35 TCGTACGTAC CATCGCTATG GGTTCCTCCG ACGGTCTGCG TCGTGGTCTG 150
GATGTAAAAG ACCTCGAGCA CCCGATCGAA GTCCCGGTAG GTAAAGCAAC 200
ACTGGGTCGT ATCATGAACG TACTGGGCCA ACCGGTAGAC ATGAAAGGCG 250
ACATCGGTGA AGAAGAACGT TGGGCTATCC ACCGTGCAGC ACCTTCCTAC 300
GAAGAGCTGT CAAGCTCTCA GGAAGTGTCTG GAAACCGGCA TCAAAGTTAT 350
40 CGACCTGATG TGTCCGTTTG CGAAGGGCGG TAAAGTTGGT CTGTTTCGGTG 400
GTGCGGGTGT AGGTAAAACC GTAAACATGA TGGAGCTTAT TCGTAACATC 450
GCGATTGAGC ACTCCGGTTA TTCTGTGTTT GCGGGCGTAG GTGAACGTAC 500
TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCC AACGTTATCG 550
ATAAAGTTTC CCTGGTTTAC GGCCAGATGA ACGAGCCACC AGGAAACCGT 600
45 CTGCGCGTTG CGCTGACTGG TCTGACTATG GCTGAGAAGT TCCGTGACGA 650
AGGTGCGGAC GTACTGCTGT TCGTCGATAA CATCTATCGT TACACCCTGG 700
CCGGTACAGA AGTATCTGCA CTGCTGGGTC GTATGCCTTC AGCGGTAGGT 750
TACCAGCCGA CTCTGGCGGA AGAGATGGGC GTTCTGCAGG AACGTATCAC 800
CTCCACCAAA ACCGGTTCTA TCACCTCCGT A 831

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50

2) INFORMATION FOR SEQ ID NO: 320

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55 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 810 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

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60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Kluyvera georgiana*

(B) STRAIN: ATCC 51603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320

```

10  GCCGTACCGC GCGTGACGA AGCCCTTGAG GTACAGAATG GTAATGAAGT      50
    GCTGGTGCTG GAAGTTCAGC AGCAGCTCGG TGGCGGTATC GTGCGTACCA      100
    TCGCCATGGG TTCCTCCGAC GGTCTGCGTC GCGGTCTGGA AGTTAAAGAT      150
    CTCGAGCACC CGATCGAAGT TCCGGTAGGT AAAGCAACAC TGGGTCGTAT      200
    CATGAACGTA CTGGGTCACC CGGTAGACAT GAAAGGCGAC ATCGGTGAAG      250
    AAGAGCGTTG GGCTATCCAC CGCGCTGCGC CTTCTACGA AGAGCTGTCC      300
15  AGCTCTCAGG AACTGCTGGA AACC GGATATC AAAGTTATCG ACCTGATGTG      350
    TCCGTTTCGG AAGGGCGGTA AAGTCGGTCT GTTCGGCGGT GCGGGTGTG      400
    GTAAAACCGT AAACATGATG GAGCTGATCC GTAACATCGC GATCGAGCAC      450
    TCCGGTTACT CTGTGTTTGC GGGCGTAGGT GAACGTACTC GTGAGGGTAA      500
    CGACTTCTAC CACGAAATGA CCGACTCCAA CGTTATCGAT AAAGTATCCC      550
20  TGGTGTATGG CCAGATGAAC GAGCCGCCGG GAAACCGTCT GCGCGTTGCG      600
    CTGACCGGCC TGACCATGGC TGAGAAATTC CGTGACGAAG GTCGTGACGT      650
    ACTGCTGTTT GTCGATAACA TCTATCGTTA CACCCTGGCC GGTACTGAAG      700
    TATCTGCACT GCTGGGTCGT ATGCCTTCAG CGGTAGGTTA CCAGCCGACT      750
    CTGGCGGAAG AGATGGGCGT TCTGCAGGAA CGTATCACCT CCACCAAGAC      800
25  CGGTTCTATC                                     810

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2) INFORMATION FOR SEQ ID NO: 321

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 834 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactobacillus acidophilus*

(B) STRAIN: ATCC 4356

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321

```

45  TCGATAAGAA TTTACCTGAT ATTAACAACG CCTTACGTGT AATCAAGTCC      50
    GAAGATGAAA GCATCGTTCT TGAAGTTACA CTTGAACTCG GTGATGGTGT      100
    TTTAAGAACA ATCGCCATGG AATCTACCGA TGGTCTTCGT CGTGGTATGA      150
    AAGTCGAAGA TACTGGCGCT CCAATTTGAG TTCCAGTTGG AGAAGACACT      200
    TTAGGTCGTG TGTTTAACGT TTTAGGACAG CCTATTGATG GTGGTCCAGC      250
50  CTTTCCAAAG GATCACCAC GTGAGGGTAT CCACAAGGAA GCACCTAAAT      300
    ATGAAGATTT AACTACTAGT CGTGAAATTC TTGAACTGG TATCAAGGTT      350
    ATCGACCTTC TTGAACCATA TGTTCTGGT GGTAAAGTTG GTTTGTTTGG      400
    TGGTGCCGGT GTTGGTAAAA CTACTATTAT TCAAGAATTA ATTCACAACA      450
    TCGCTCAAGA ACACGGTGGT ATTTCCGTAT TTAGTGGTGT TGGTGAAAGA      500
55  ACTCGTGAAG GTAATGACCT TTAATTTGAA ATGAAAGCTT CAGGCGTTTT      550
    AAGTAAGACT GCCATGGTAT TTGGTCAGAT GAACGAGCCG CCTGGTGCCA      600
    GAATGCGTGT TGCATTAACC GGTTTGACAC TTGCTGAATA CTTTAGAGAT      650
    GTTGAAGGTC AAGACGTATT GCTCTTTATT GACAATATCT TTAGATTTAC      700
    TCAGGCTGGT TCAGAGGTAT CTGCTTTGCT TGGTCGTATG CCAAGTGCCG      750
60  TAGGTTATCA GCCAACTTTG GCAACAGAAA TGGGTCAATT GCAGGAAAGA      800

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ATTACTTCTA CTAAGAAGGG TTCAATTACT TCAA

834

5 2) INFORMATION FOR SEQ ID NO: 322

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Legionella pneumophila* subsp. *pneumophila*
 (B) STRAIN: ATCC 33152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322

20 TTCCTCGTGA TAGCGTGCCT AAAGTCAATG ATGCGTTAAA GCTTGTGAT 50
 AGTGATCTGG TTTTGAAGT GCAGCAGCAA CTTGGAGACG GAGTTGTGCG 100
 TACTATTGCC ATGGGAACAA CCGATGGTTT AAAGCGAGGA TTAAAAGCAG 150
 AAAATACAGG CCATCCTATT CAAGTGCCAG TAGGTAAGAA AACTTTGGGA 200
 25 CGCATTATGG ATGTTCTTGG GCGTCCTGTA GATGATGCTG GGCCTATCGA 250
 TGCTGAAGAG ACTTGGGCTA TTCATCGTAA AGCACCAAGT TATGAAGAGC 300
 AAGCTGGCAG CCAGGAATTA TTGGAAACTG GTATTAAAGT AATTGATTG 350
 CTTTGCCCTT TTGCAAGGG AGGTAAAGTT GGTCTATTCG GTGGTGCCGG 400
 TGTAGGCAAA ACCGTTAACA TGATGGAATT AATACGAAAC ATTGCAATTG 450
 30 AGCATAGCCG TTATTCAAGT TTTGCAGGGG TTGGTGAACG TACCCGTGAA 500
 GGAAACGACT TCTATCATGA GATGAAAGAC TCTAATGTAT TGGATAAAGT 550
 ATCGCTTGTT TATGGTCAGA TGAATGAGCC GCCAGGAAAC CGTTTGCGTG 600
 TTGCTCTAAC CGGTTTGACT ATGGCTGAAA AATTCCGGGA TGAAGGGCGA 650
 GACGTTCTTT TGTTTATCGA TAATATTTAT CGTTATACCT TGGCTGGGGT 700
 35 TGAAGTATCT GCGCTGTTAG GCCGTATGCC TTCTGCAGTA GGATATCAGC 750
 CGACATTAGC AGAGGAAATG GGTATGCTGC AAGAGCGCAT TACCTCCACA 800
 AAAACAGGTT CTATTACTTC CATA 824

40 2) INFORMATION FOR SEQ ID NO: 323

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leminorella grimontii*
 (B) STRAIN: ATCC 33999

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323

60 GACGCCGTAC CGAAAGTGTA CGATGCGCTT GAAGTTCAAA TTGATGCCAA 50
 GCTGGTTCTG GAAGTTCAAC AGCAGCTCGG CGGCGGCGTT GTTCGCTGCA 100
 TCGCGATGGG TACTTCAGAC GGCTTAAGCC GCGGTCTGGA CGTGCTCGAT 150
 CTGGAACACC CGATTGAAGT ACCGGTGGGC AAAGCGACGC TGGGCCGCAT 200

CATGAACGTG CTTGGTCACC CTATCGACAT GAAGGGCGAC ATCGGCGAAG 250
 AAGAGCGTTG GGCTATTCAC CGCGCAGCGC CGAGCTACGA AGACCTGTCG 300
 GGCGCAACCG AGCTGCTGGA GACCGGCATC AAGGTTATCG ACCTGATTTG 350
 TCCGTTTCGCC AAGGGCGGTA AAGTCGGCCT GTTCGGCGGC GCCGGCGTAG 400
 5 GTAAAACCGT AAACATGATG GAGCTCATTC GCAACATTGC GACCGAGCAC 450
 TCCGGTTACT CCGTGTTTGC AGGCGTAGGT GAACGTACCC GTGAGGGTAA 500
 CGACTTCTAC CACGAAATGA CTGAATCCAA CGTATTGGAC AAGGTGTCGC 550
 TGGTATACGG TCAGATGAAC GAGCCGCTG GAAACCGTCT GCGCGTAGCG 600
 TTAACGGGCT TGACCATGGC GGAGAAGTTC CGTGATGAAG GCCGTGACGT 650
 10 TCTGCTGTTT ATCGACAACA TTTACCGCTA TACCCTGGCC GGTACGGAAG 700
 TATCCGCACT GCTGGGCCGT ATGCCTTCAG CCGTAGGCTA CCAGCCGACT 750
 CTGGCTGAGG AAATGGGCGT GCTTCAAGAG CGTATTACCT CTACCAAGAC 800
 GGGGTCTATC ACCTCCGT 818

15

2) INFORMATION FOR SEQ ID NO: 324

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Listeria monocytogenes*

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324

GTGGAAACTT ACCTGAAATC TACAATGCCC TAGTTATTGA ATATAAATCT 50
 GATGCAGAAG AAGCACCAAC TAGCCAACCTT ACTTTAGAAG TAGCCATCCA 100
 ATTAGGTGAT GATGTTGTAC GTACAATCGC AATGGCATCA ACAGATGGTG 150
 35 TTCAAAGAGG TATGGAAGTT ATTGATACTG GGAGCCCAAT TACAGTTCCT 200
 GTAGGTACAG TAACTCTTGG TCGTGATTTT AATGTATTAG GAAACACCAT 250
 CGATTTGGAC GAACCACTTC CAAGCGATAT TAAACGTAAT AAAATTCACC 300
 GCGAAGCTCC AACTTTCGAT CAATTAGCAA CGACAACAGA AATTCTTGAA 350
 ACAGGAATTA AAGTAGTTGA CTTGCTAGCT CCTTACTTAA AAGGTGGTAA 400
 40 AATCGGATTG TTCGGTGGTG CCGGTGTTGG TAAAACCGTT CTAATTCAAG 450
 AGCTTATCCA TAATATCGCA CAAGAACATG GTGGTATTTT TGTGTTGCT 500
 GCGGTTGGAG AACGTACTCG TGAAGGTAAC GACCTTTACT TCGAAATGAA 550
 AGATTCAGGC GTTATTGAAA AAACAGCGAT GGTATTCCGT CAAATGAACG 600
 AGCCACCAGG TGCGCGTATG CGTGTTGCCT TAACTGGTCT AACAATTGCT 650
 45 GAATATTTCC GTGATGAAGA ACATCAAGAT GTACTTTTAT TCATTGATAA 700
 CATTTTCCGT TTCACACAAG CTGGTTCAGA GGTTCGGCT TTACTAGGTC 750
 GTATGCCATC TGCGGTAGGT TACCAACCAA CCCTAGCTAC TGAAATGGGT 800
 CAACTACAAG AACGTATTAC ATCTACTAAC GTTGG 835

50

2) INFORMATION FOR SEQ ID NO: 325

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 828 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60 (ii) MOLECULE TYPE: Genomic DNA

325

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Micrococcus lylae*
 (B) STRAIN: ATCC 27566

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325

```

5      CCCGCGTGGC GAGTTGCCGG CACTGTTCAA CGCGCTGACT GTCGAGGTCA      50
      CCCTCGAAGC AGTCGCTAAA ACCATTACCC TTGAGGTTGC TCAGCACCTC      100
10     GGCGACAAC TGGTTCGTGC CGTGTCCATG GCACCGACCG ACGGTCTCGT      150
      CCGTGGCGCT GCTGTGATCG ACAGCGGTAA GCCGATCTCA GTTCCCGTTG      200
      GTGACGTAGT CAAGGGACAC GTCTTCAACG CTCTGGGTGA TTGCCTCGAT      250
      GAGCCAGGTC TTGGCCGTGA CGGTGAGCAG TGGGGCATCC ACCGCGATCC      300
      GCCACCTTTT GACCAGCTTG AGGGTAAGAC CGAGATTCTG GAAACCGGTA      350
15     TTAAGGTCAT CGACCTGCTG ACCCCGTATG TTAAGGGCGG CAAGATCGGC      400
      CTGTTCCGGT GTGCTGGTGT GGGTAAGACC GTTCTTATCC AGGAAATGAT      450
      CACCCGTATC GCTCGCGAGT TCTCCGGTAC CTCGGTGTTC GCAGGCGTGG      500
      GTGAGCGTAT CCGTGAGGGC ACCGACCTCT TCCTGGAAAT GGAAGAGATG      550
      GGCGTTCTCC AGGACACCGC TCTTGTGTTT GGCCAGATGG ACGAGCCTCC      600
20     AGGAGTTCGT ATGCGCGTGG CGCTGTCCGG CCTGACCATG GCGGAGTACT      650
      TCCGCGATGT GCAGACCAG GACGTGCTTC TGTTTCATCGA CAACATCTTC      700
      CGTTTCACCC AGGCAGGTTT CGAGGTTTCC ACCCTCCTAG GCCGCATGCC      750
      TTCTGCCGTG GGTTACCAGC CAACGCTGGC AGACGAGATG GGTGTTCTGC      800
      AGGAGCGTAT TACCTCCACA AAGGGTAA      828
25

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2) INFORMATION FOR SEQ ID NO: 326

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Moellerella wisconsensis*
 (B) STRAIN: ATCC 35017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326

```

45     GATGCCGTAC CAAAAGTGTA CGATGCTCTT GAGGTTCTTA ACGGTAAAGA      50
      AAAATTGGTG CTGGAAGTTC AGCAACAATT AGGCGGTGGT GTTGTTTCGTT      100
      GTATCGCAAT GGGTACATCA GATGGTTTAA GCCGCGGTTT AGAAGTTAAA      150
      AATACAGATC ATCCGATCGA AGTTCCTGTC GGTGTTAAAA CGCTTGGCCG      200
      TATCATGAAC GTGCTGGGTG ACCCAATCGA CATGAAAGGT GATATCGGCG      250
      AAGAAGAACG CTGGTCAATT CACCGCGCAG CACCAAGCTA TGAAGATCTG      300
50     GCTAACTCAA CAGAACTTCT AGAAACAGGT ATCAAAGTTA TGGACCTGAT      350
      TTGCCCATTG GCTAAAGGGG GTAAAGTGGG TCTGTTCCGT GGTGCGGGTG      400
      TCGGTAAAAC AGTTAACATG ATGGAGCTTA TTCGTAATAT CGCGATTGAG      450
      CACTCAGGTT ATTCTGTATT CGCGGGTGTG GGTGAACGTA CTCGTGAAGG      500
      TAACGATTTT TACCATGAAA TGACAGACTC AAACGTTCTG GATAAAGTTT      550
      CATTGGTTTA TGGCCAGATG AATGAGCCAC CAGGAAACCG TCTGCGTGTT      600
      GCTCTGACTG GTCTGACTAT GGCAGAGAAA TTCCGTGACG AAGGTCGTGA      650
      CGTACTGTTA TTCGTAGATA ATATTTATCG TTATACCTTA GCAGGGACAG      700
      AAGTATCTGC ACTGCTGGGT CGTATGCCTT CAGCGGTGGG TTATCAGCCA      750
      ACGTGCGCGG AAGAGATGGG TGTTCTGCAA GAACGTATCA CCTCGACTAA      800
60     GACCGGCTCT ATCACTTCCG TA      822

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2) INFORMATION FOR SEQ ID NO: 327

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 854 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Branhamella catarrhalis*
 (B) STRAIN: ATCC 43628

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327

20	CCGTGGCGAT	GTCCCCCAA	TCTTTGATGC	ACTTCATGTT	GATGGTACTG	50
	AAACCACCCT	TGAAGTCCAA	CAACAGTTAG	GTGATGGTGT	GGTGCGTACC	100
	ATTGCCATGG	GTTCTACCGA	AGGCTTAAAG	CGTGGCTTGC	CTGTCTCTAA	150
	TTCAGGTGCA	CCCATTTCGG	TACCAGTCGG	TCAAGCAACA	CTGGGTCGCA	200
	TTATGGATGT	CCTAGGTCGC	CCAATCGATG	AAGCAGGTCC	GGTAAATGCT	250
25	GAACAAAAAT	GGTCCATTCA	TCGTGAAGCA	CCAAGTTATG	ATGAACAGTC	300
	AAATAGTACA	GAACTTTTCG	AAACAGGCAT	CAAAGTGATT	GATTTGCTTT	350
	GTCCATTTCG	CAAAGGTGGT	AAAGTCGGTC	TGTTTCGGTGG	TGCTGGTGTT	400
	GGTAAGACCG	TTAACATGAT	GGAGCTTATC	AATAATATCG	CCCTAAAACA	450
	CTCAGGTCTG	TCGGTTTTTG	CTGGTGTGGG	TGAGCGTACT	CGTGAGGGTA	500
30	ATGACTTCTA	CCATGAAATG	CAAGAAGCAG	GCGTTGTTAA	TACCGAAGAT	550
	TTTACTCAGT	CAAAAGTTGC	CATGGTTTAT	GGTCAGATGA	ATGAGCCACC	600
	AGGAAACCGT	CTGCGTGTTG	CCTTAACTGG	TTTGACCATG	GCAGAGTATT	650
	TCCGTGATGA	AAAAGACGAA	GCAACGGGCA	AAGGCCGTGA	TGTTCTGCTG	700
	TTTCGTTGATA	ATATTTATCG	TTACACATTG	GCAGGTAATG	AGGTATCAGC	750
35	ACTTTTAGGT	CGTATGCCAT	CTGCGGTAGG	TTATCAGCCG	ACTTTGGCCG	800
	AAGAGATGGG	CTTGCTACAA	GAGCGTATCA	CCTCCACCCA	ATCAGGCTCA	850
	ATTA					854

2) INFORMATION FOR SEQ ID NO: 328

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Moraxella osloensis*
 (B) STRAIN: ATCC 19976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328

60	CCGTCAAAGC	GTACCAAGAA	TTTATGATGC	CTTAAAAGTT	GAAGGCACAG	50
	AAACTACATT	AGAAGTACAA	CAACAATTGG	GTGATGGTAT	CGTACGTACT	100
	ATTGCCATGG	GTTCTACTGA	AGGTCTAAAA	CGTGGTCTAC	CAGTTAGCAA	150
	CACTGGCGCA	CCAATCTCTG	TACCTGTGGG	TAAAGGTACA	CTAGGTCGTA	200

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TCATGGACGT TTTAGGACAC CCAATCGATG AGGCAGGTCC GGTAGAGCAT 250
AGTAACACTT GGGCGATTCA CCGTGAAGCG CCAAGCTATG ATGAACAATC 300
AAACTCTACT GAACCTTTAG AAACCGGTAT TAAAGTAATT GACTTACTAT 350
GCCCATTTGC TAAAGGTGGT AAAGTCGGTC TGTTCGGTGG CGCGGGTGT 400
5 GGTAAAACCG TTAACATGAT GGAACTTATC AATAACATCG CAAAAGCACA 450
CTCAGGTTTA TCGGTATTTG CTGGTGTAGG TGAGCGTACT CGTGAAGGTA 500
ATGACTTCTA CCACGAGATG AAAGACTCAA ACGTACTTGA TAAAGTTGCG 550
ATGGTGTATG GTCAGATGAA TGAGCCACCA GGAAACCGTT TACGTGTTGC 600
CCTGACAGGT TTAACCATGG CAGAATACTT CCGTGACGAA AAAGATGAAA 650
10 ACGGTAAAGG TCGTGACGTA TTATTGTTCC TTGACAATAT TTATCGTTAC 700
ACGCTAGCGG GTACCGAAGT ATCAGCATTA TTAGGTCGTA TGCCATCTGC 750
AGTAGGGTAT CAGCCAACGC TTGCAGAAGA GATGGGTGTA CTACAAGAAC 800
GTATTACTTC AACCCAATCA GGCTCTATTA C 831

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2) INFORMATION FOR SEQ ID NO: 329

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20 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 835 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

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25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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    (A) ORGANISM: Morganella morganii subsp. morganii
    (B) STRAIN: ATCC 25830

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329

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CGAATTTCTT CAGGATGCAG TACCGAAAGT GTACGATGCG CTTGAGGTAA 50
CAAATGGTAA AGAAAACTG GTGCTGGAAG TTCAGCAGCA GTTAGGCGGC 100
35 GGGGTTGTCC GTTGTATCGC TATGGGTACA TCTGATGGTC TGAGCCGTAA 150
TCTGGAAGTA ACCGATTTAG GCCACCCGAT CGAAGTCCCT GTCGGCGTGA 200
AAACCTTAGG ACGTATCATG AACGTTCTGG GTGATCCGAT CGATATGAAA 250
GGTGACATCG GCGCAGAAGA AAAATGGTCT ATTACCGTG CTGCACCAAC 300
ATACGAAGAA CTGTCTAACT CCCAGGAAC GCTGGAAACA GGTATCAAAG 350
40 TAATGGACCT GATCTGCCCC TTGCGAAGG GTGGTAAAGT CGGTCTGTTC 400
GGTGGTGCGG GTGTGGGTAA AACCGTAAAC ATGATGGAAC TGATCCGTAA 450
CATCGCGATC GAGCACTCCG GTTACTCTGT ATTGCGAGGG GTCGGTGAGC 500
GTACCCGTGA AGGTAACGAC TTCTATCATG AAATGACAGA CTCCAACGTT 550
CTGGACAAAG TATCACTCGT GTACGGCCAG ATGAACGAGC CACCGGGAAA 600
45 CCGTCTGCGC GTTGCTCTGA CCGGTCTGAC CATGGCGGAA AAATTCCGTG 650
ATGAAGGCCG CGATGTACTG CTGTTGTTG ATAACATCTA CCGTTATACC 700
CTGGCCGGTA CTGAAGTATC CGCGCTGTGA GGCCGTATGC CTTCAGCGGT 750
AGGTTACCAG CCGACACTGG CGGAAGAAAT GGGTGTGCTT CAGGAACGTA 800
TCACATCGAC CAAAACAGGC TCTATCACGT CTGTA 835

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2) INFORMATION FOR SEQ ID NO: 330

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55 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 824 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

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(ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

(A) ORGANISM: *Pantoea agglomerans*

(B) STRAIN: ATCC 27155

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 330

	GACGCGGTAC	CGCAAGTGTA	CAGCGCCCTC	GAGGTTATGA	ATGGTGATGC	50
10	GCGTCTGGTG	CTGGAAGTTC	AGCAGCAGCT	CGGCGGCGGC	GTAGTACGTA	100
	CCATCGCAAT	GGGTACGTCT	GACGGCCTGA	AGCGTGGTCT	GAGCGTCAAC	150
	GACCTGCAGA	AACCGATTCA	GGTACCCGTC	GGTAAAGCGA	CCCTGGGCCG	200
	TATCATGAAC	GTTCTCGGCG	AGCCAATCGA	TATGAAAGGC	GAGCTGAAAG	250
	AAGAAGATGG	CAGCGCAGTA	GAGATCGCCT	CTATTACCCG	CGCAGCCCCT	300
15	TCTTATGAAG	ATCAGTCTAA	CTCGCAGGAA	CTGCTGGAAA	CCGGCATCAA	350
	GGTTATCGAC	CTGATGTGTC	CGTTTGCTAA	AGGCGGTAAA	GTCGGTCTGT	400
	TCGGTGGTGC	GGGTGTAGGT	AAAACCGTCA	ACATGATGGA	ACTGATCCGT	450
	AACATCGCGG	CTGAACACTC	AGGTTACTCA	GTGTTTGCCG	GTGTGGGTGA	500
	GCGTACTCGT	GAGGGTAACG	ACTTCTACCA	CGAAATGACT	GACTCTAACG	550
20	TTATCGATAA	AGTTGCACTG	GTCTATGGCC	AGATGAACGA	GCCGCCGGGT	600
	AACCGTCTGC	GCGTAGCACT	GACCGGTCTG	ACCATGGCGG	AAAAATTCCG	650
	TGATGAAGGT	CGCGACGTTT	TGCTGTTTAT	CGATAACATC	TACCGTTATA	700
	CCCTGGCCGG	TACAGAAGTT	TCTGCACTGC	TGGGTCGTAT	GCCATCTGCG	750
	GTAGGTTACC	AGCCAACGCT	GGCAGAAGAG	ATGGGTGTGT	TGCAGGAGCG	800
25	TATTACCTCC	ACCAAGACCG	GTTC			824

2) INFORMATION FOR SEQ ID NO: 331

(i)SEQUENCE CHARACTERISTICS:

(A) LENGTH: 808 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

(A) ORGANISM: *Pantoea dispersa*

(B) STRAIN: ATCC 14589

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 331

45	TATACAGCGC	TCTCGAGGTA	AAAAATGGTG	ATGCTCGTCT	GGTGCTGGAA	50
	GTACAGCAGC	AGCTGGGCGG	TGGCGTGGTG	CGTACCATCG	CCATGGGGTTC	100
	TTCTGACGGC	CTGAAGCGCG	GTCTGGAAGT	CACCGACCTG	AAAAAACCTA	150
	TCCAGGTTCC	GGTTGGTAAA	GCAACACTCG	GCCGTATCAT	GAACGTGCTG	200
	GGTGAGCCAA	TCGACATGAA	AGGCGACCTG	AAAGAAGAAG	ACGGCAGCGC	250
50	TGTAGAGGTT	TCCTCTATT	ATCGCGCAGC	GCCTTCTTAT	GAAGATCAGT	300
	CAAACCTCGCA	GGAACCTGCTG	GAAACCGGCA	TCAAGGTTAT	CGACCTGATG	350
	TGTCGGTTTCG	CGAAGGGCGG	TAAAGTCGGT	CTGTTTCGGTG	GTGCGGGTGT	400
	AGGTAAAACC	GTAACATGA	TGGAGCTGAT	CCGTAACATC	GCGGCTGAGC	450
	ACTCAGGTTA	TTCGGTCTTT	GCCGGCGTGG	GTGAGCGTAC	TCGTGAGGGT	500
55	AACGACTTCT	ACCACGAAAT	GACGGACTCC	AACGTTATCG	ATAAAGTAGC	550
	GCTGGTGTAT	GGCCAGATGA	ACGAGCCGCC	GGGTAACCGT	CTGCGCGTAG	600
	CACTGACCGG	TCTGACCATG	GCGGAAAAAT	TCCGTGATGA	AGGCCGTGAC	650
	GTTCTGCTGT	TCATCGACAA	CATCTACCGT	TACACCCTGG	CCGGTACAGA	700
	GGTTTCTGCA	CTGCTGGGTC	GTATGCCATC	GGCGGTAGGT	TATCAGCCAA	750
60	CGCTGGCTGA	AGAGATGGGT	GTGCTGCAGG	AGCGTATTAC	CTCCACCAAG	800

ACCGGTTC

808

5 2) INFORMATION FOR SEQ ID NO: 332

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 805 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pasteurella multocida*
 (B) STRAIN: NCTC 10322

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332

20 GATGCAGTAC CAAAAGTATA TGATGCCTTA AATGTTGAAA CAGGTTTAGT 50
 ACTTGAAGTT CAACAACAAT TAGGTGGTGG TGTAGTTCGC TGTATCGCAA 100
 TGGGATCATC TGATGGATTA AAACGCGGTT TAAGCGTAAC AAATACGAAT 150
 AACCCAATTT CTGTTCCAGT GGGAACGAAA ACATTGGGTC GTATCATGAA 200
 25 CGTATTGGGT GAACCAATCG ATGAGCAAGG TGAAATCGGT GCAGAAGAGA 250
 ATTGGTCTAT TCACCGTGCG CCACCAAGTT ATGAAGAACA ATCTAACAGT 300
 ACTGAACTTT TAGAAACGGG AATTAAAGTT ATCGACTTAG TTTGTCCGTT 350
 TGCGAAAGGG GGTAAAGTAG GTTTATTCGG TGGTGCGGGT GTCGGTAAAA 400
 CCGTCAATAT GATGGAATTA ATCCGTAACA TCGCAATTGA GCACTCAGGT 450
 30 TACTCTGTCT TTGCGGGGGT AGGTGAGCGT ACGCGTGAAG GTAACGACTT 500
 CTATCATGAG ATGAAAGACT CTAACGTATT AGATAAAGTG TCTCTTGTTT 550
 ATGGTCAAAT GAACGAGCCA CCAGGTAACC GTTTACGTGT GGCATTAACA 600
 GGCTTAAC TA TGGCGGAAAA ATTCCGTGAT GAAGGTCGTG ATGTCTTATT 650
 CTTCGTTGAT AATATTTATC GTTATACTCT TGCTGGTACA GAAGTTTCTG 700
 35 CATTATTAGG TCGTATGCCA TCTGCGGTAG GTTATCAACC AACCCTTGCA 750
 GAAGAAATGG GTGTTCTGCA AGAGCGTATT ACCTCAACCA AAACAGGTTC 800
 TATTA 805

40 2) INFORMATION FOR SEQ ID NO: 333

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 bases
 45 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pragia fontium*
 (B) STRAIN: ATCC 49100

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333

TTCCTCAAG ACGCCGTACC AAAAGTGTAC GACGCGCTTG AAGTTCAGAA 50
 CGATGCCAAG CTGGTGCTGG AAGTTCAACA ACAGCTCGGT GGTGGTGTCTG 100
 TCGTTGTAT CGCAATGGGT ACTTCCGATG GCTTAAGCCG CGGTTTAAAA 150
 60 GTGCTTGATT TAGAACATCC TATCGAAGTA CCGGTTGGTA CTGCGACGCT 200

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GGGCCGTATT ATGAACGTGC TCGGTCAGCC AATCGATATG AAAGGCGATA 250
TTGGTGAAGA AGAGCGTTGG GCTATTCACC GTGAAGCACC AAGTTATGAA 300
GATTTATCTG GCGCCAATGA ACTGCTGGAA ACGGGTATCA AGGTTATCGA 350
CCTGATTTGT CCGTTTGCTA AAGGTGGTAA AGTTGGTCTG TTTGGTGGTG 400
5 CGGGTGTAGG TAAAACCGTA AACATGATGG AGCTGATTCG TAACATTGCG 450
ACTGAGCACT CAGGTTACTC CGTATTCGCC GGTGTAGGGG AACGTACCCG 500
TGAAGGTAAT GACTTCTACC ACGAAATGAC CGAATCAAAC GTACTGGATA 550
AAGTATCTCT GGTTTATGGC CAGATGAACG AGCCACCAGG AAACCGTCTG 600
CGCGTGGCGT TAACGGGTTT GACCATGGCT GAAAAATTCC GTGATGAAGG 650
10 TCGTGACGTT CTGTTATTTA TCGATAACAT TTATCGCTAT ACCTTAGCCG 700
GTACCGAAGT ATCAGCACTG TTGGGGCGTA TGCCATCAGC GGTAGGTTAT 750
CAGCCAACGT TAGCAGAAGA GATGGGTGTG TTGCAGGAAC GTATTACTTC 800
AACCAAAACC GGTTCATCA CTTCTGTA 828

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2) INFORMATION FOR SEQ ID NO: 334

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20 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 807 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Proteus mirabilis
        (B) STRAIN: ATCC 25933

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334

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GTCCCTAAAG TATACGACGC TCTTGAGGTT ATGAATGGTA AAGAAAAACT 50
GGTGCTGGAA GTTCAGCAAC AGTTAGGCGG TGGTATCGTT CGTTGTATCG 100
35 CAATGGGTAC ATCAGACGGT TTAAGCCGTG GCTTAAAGGT TGAAGATTTA 150
GGCCACCCAA TTGAAGTACC AGTAGGTAAA GCGACTTTAG GACGTATCAT 200
GAACGTTCTG GGTACACCTA TTGATATGAA AGGTGAGATT GAAACCGAAG 250
AGCGTTGGTC AATCCACCGT GAAGCACCAA CTTACGAAGA GTTATCAAAC 300
TCTCAAGAAC TGCTTGAAAC CGGTATCAAA GTTATGGACT TAATCTGTCC 350
40 ATTTGCTAAAG GGTGGTAAAG TCGGTCTGTT CGGTGGTGCG GGTGTTGGTA 400
AAACAGTTAA CATGATGGAA TTGATCCGTA ATATCGCGAT CGAGCACTCA 450
GGTTACTCTG TATTTGCTGG TGTTGGTGAG CGTACTCGTG AGGGTAACGA 500
CTTCTATCAT GAAATGACAG ATTCTAACGT TCTTGACAAA GTATCGTTAG 550
TTTACGGTCA GATGAATGAG CCACCAGGAA ACCGTCTGCG TGTTGCACTG 600
45 ACTGGTCTGA CTATGGCTGA GAAATTCCGT GATGAAGGCC GTGACGTACT 650
GTTATTCGTC GATAACATCT ATCGTTACAC CTTAGCCGGT ACAGAAGTAT 700
CAGCAAGGTT AGGTCGTATG CCATCAGCGG TAGGTTACCA ACCAACATTG 750
GCTGAAGAGA TGGGTGTTCT GCAAGAGCGT ATCACTTCAA CCAAACAGG 800
TTCTATC 807

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2) INFORMATION FOR SEQ ID NO: 335

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55 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 811 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

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(ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

(A) ORGANISM: *Proteus vulgaris*

(B) STRAIN: ATCC 13315

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 335

	CCCTAAAGTA	TACGACGCTC	TTGAGGTTAT	GAATGGTAAA	GAGAAACTGG	50
10	TGCTAGAAGT	TCAGCAACAG	TTAGGCGGTG	GTATCGTTTCG	TTGTATCGCA	100
	ATGGGTACAT	CAGACGGTTT	AAGCCGTGGC	TTAAAAGTTG	AAAACCTAGG	150
	CCACCCAATT	GAAGTACCAG	TAGGTAAAGC	AACACTGGGA	CGTATCATGA	200
	ACGTTCTGGG	TACACCTATC	GATATGAAAG	GTGATATTGC	AACTGAAGAA	250
	CGTTGGTCTA	TTACCGCGCA	AGCGCCAACC	TATGAAGAGT	TATCAAGCTC	300
15	TCAAGAACTA	CTAGAAACCG	GTATCAAAGT	AATGGACTTA	ATCTGTCCGT	350
	TTGCTAAAGG	TGGTAAAGTA	GGTCTCTTCG	GTGGTGCGGG	TGTTGGTAAA	400
	ACAGTTAACA	TGATGGAATT	GATCCGTAAC	ATCGCGATTG	AGCACTCAGG	450
	TTATTCTGTA	TTTGCAAGGTG	TTGGTGAGCG	TACTCGTGAG	GGTAACGACT	500
	TCTATCATGA	AATGACAGAT	TCTAACGTTT	TTGACAAAGT	ATCGTTAGTT	550
20	TATGGTCAGA	TGAATGAGCC	ACCAGGAAAC	CGTCTACGTG	TAGCACTGAC	600
	GGGTTTAACC	ATGGCGGAAA	AATTCCGTGA	TGAAGGCCGT	GACGTACTGT	650
	TATTCGTCTGA	TAACATCTAT	CGTTACACCT	TAGCCGGTAC	CGAAGTATCA	700
	GCACTGTTAG	GCCGTATGCC	ATCAGCAGTA	GGTTACCAAC	CAACATTGGC	750
	TGAAGAGATG	GGTGTTCTGC	AAGAACGTAT	CACTTCAACC	AAAACAGGTT	800
25	CAATCACCTC	T				811

2) INFORMATION FOR SEQ ID NO: 336

(i)SEQUENCE CHARACTERISTICS:

(A) LENGTH: 806 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

(A) ORGANISM: *Providencia alcalifaciens*

(B) STRAIN: ATCC 9886

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 336

45	TCAAGATAAC	GTACCAAAAG	TGTACGATGC	TCTTGAGGTT	ATTAACGGTA	50
	AAGAAAAACT	GGTGTTGGAA	GTTCAACAAC	AGTTAGGTGG	TGGTGTGTGC	100
	CGTTGTATCG	CAATGGGTAC	ATCAGATGGT	CTGAGCCGTG	GTTTAGAAGT	150
	TGTAAACTTA	GAGCACCCAA	TCGAAGTACC	AGTCGGTAAA	GCAACTCTGG	200
	GACGTATCAT	GAACGTTCTG	GGTGAACCAA	TCGACATGAA	AGGTGATATC	250
50	GGCGAAGAAG	AGCGCTGGTC	TATTCACCGT	GCTGCACCAA	GCTACGAAGA	300
	ATTAGCTAAC	TCAACTGAAC	TGCTGGAAAC	CGGTATCAAA	GTAATGGACT	350
	TAATCTGTCC	ATTCGCGAAA	GGTGGTAAAG	TAGGTCTGTT	CGGTGGTGCG	400
	GGTGTTGGTA	AAACCGTAAA	CATGATGGAA	CTGATCCGTA	ACATCGCGAT	450
	TGAGCACTCA	GGTTACTCAG	TGTTTCGCTGG	TGTTGGTGAG	CGTACCCGTG	500
55	AAGGTAACGA	CTTCTATCAT	GAAATGACAG	ACTCAAACGT	TCTGGATAAA	550
	GTATCACTGG	TTTATGGCCA	GATGAACGAG	CCACCAGGAA	ACCGTCTGCG	600
	TGTTGCGCTG	ACTGGTCTGA	CTATGGCTGA	AAAATTCCGT	GACGAAGGTC	650
	GTGACGTACT	GCTGTTTCGT	GACAACATTT	ATCGTTATAC	ACTGGCAGGT	700
	ACTGAAGTAT	CAGCACTGTT	AGGTCGTATG	CCATCAGCGG	TAGGTTACCA	750
60	ACCAACGCTG	GCGGAAGAGA	TGGGTGTTCT	TCAAGAACGT	ATTACCTCAA	800

CTCAAA

806

5 2) INFORMATION FOR SEQ ID NO: 337

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 10 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Providencia rettgeri*
 (B) STRAIN: ATCC 9250

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337

20 TTCCCTCAAG ATGACGTACC AAAAGTGTAC GACGCTCTTG AGGTTGTTAA 50
 CGGTAAAGAA ACACTGGTGC TGGAAGTTCA GCAACAGTTA GGCGGTGGTG 100
 TTGTCCGTTG TATCGCAATG GGTACATCAG ATGGCCTGAG CCGTGGTTTA 150
 GAAGTTGTAA ACTTAGAGCA CCAATTGAA GTACCAGTAG GTAAAGCAAC 200
 25 TTTAGGACGT ATCATGAACG TTCTGGGTCA GCCTATTGAT ATGAAAGGTG 250
 ATATCGGCGA AGAAGAGCGC TGGTCAATTC ACCGTGCTGC ACCTAGCTAC 300
 GAAGAGTTAG CTAAC TCAAC AGAGCTGCTG GAAACCGGTA TCAAAGTAAT 350
 GGACTTAATC TGTCCATTCT CGAAAGGTGG TAAAGTTGGT CTGTTCTGGT 400
 GTGCGGGTGT TGGTAAACA GTAAACATGA TGGAAGTATG CCGTAACATC 450
 30 GCGATTGAGC ACTCAGGTTA CTCAGTATTC GCTGGTGTG GTGAGCGTAC 500
 TCGTGAAGGG AACGACTTCT ATCATGAAAT GACTGACTCA AACGTTCTGG 550
 ATAAAGTATC ACTGGTTTAT GGCCAGATGA ATGAGCCACC AGGAAACCGT 600
 CTGCGCGTTG CGTTGACTGG TCTGACTATG GCTGAAAAAT TCCGTGACGA 650
 AGGTCGTGAC GTACTACTGT TCGTTGACAA CATCTATCGT TATACACTGG 700
 35 CAGGTACTGA AGTATCAGCA CTGTTAGGTC GTATGCCTTC AGCGGTAGGT 750
 TATCAGCCAA CGCTGGCGGA AGAGATGGGT GTTCTGCAAG AACGTATTAC 800
 CTCAACTCAA ACGGGTTCTA TCACTTCCGT 830

40 2) INFORMATION FOR SEQ ID NO: 338

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 bases
 45 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Providencia rustigianii*
 (B) STRAIN: ATCC 33673

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338

AGCGTACCAA AAGTGTACGA TGCTCTTGAG GTTATTAACG GTAAAGAAAA 50
 ACTGGTGTTG GAAGTTCAGC AGCAGTTAGG CCGTGGTGTG GTCCGTTGTA 100
 TCGCAATGGG TACATCAGAT GGTCTGAGCC GTGGTTTAGA AGTTGTAAAC 150
 60 TTGAACACC CAATTGAAGT ACCAGTAGGT AAAGCAACTC TGGGACGTAT 200

	CATGAACGTT	CTGGGTGACC	CTATTGATAT	GAAAGGTGAT	ATCGGCGAAG	250
	AAGAGCGCTG	GTCTATTCAC	CGTTCAGCGC	CAAGCTATGA	AGAATTAGCT	300
	AACTCAACAG	AACTGCTAGA	AACCGGTATC	AAAGTAATGG	ACTTAATCTG	350
	TCCATTGCGG	AAAGGTGGTA	AAGTTGGTCT	GTTCGGTGGT	GCGGGTGTG	400
5	GTA AACAGT	AAACATGATG	GAAC TGATCC	GTAACATCGC	GATTGAGCAC	450
	TCAGGTTACT	CAGTATTCGC	TGGTGTGTTGGT	GAGCGTACCC	GTGAAGGTAA	500
	CGACTTCTAT	CATGAAATGA	CTGATTCTAA	CGTTCTGGAT	AAAGTATCAC	550
	TGGTTTATGG	CCAGATGAAC	GAGCCACCAG	GAAACCGTCT	GCGTGTGTCG	600
	CTGACTGGTC	TGACTATGGC	TGAAAAATTC	CGTGACGAAG	GTCGTGACGT	650
10	ACTGCTGTTC	GTTGACAACA	TTTATCGTTA	TACACTGGCA	GGTACTGAAG	700
	TATCAGCACT	GTTAGGTCGT	ATGCCCTTCAG	CGGTAGGTTA	TCAGCCAACA	750
	TTGGCAGAAG	AGATGGGTGT	TCTACAAGAA	CGTATCACTT	CTACCAAAAC	800
	CGGTTCTATC	AC				812

15

2) INFORMATION FOR SEQ ID NO: 339

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Providencia stuartii*
 (B) STRAIN: ATCC 33672

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339

	TCAAGATGCA	GTACCAAAAG	TGTACGATGC	GCTTGAGGTT	GTTAACGGTA	50
	AAGAAAAACT	GGTGCTGGAA	GTT CAGCAAC	AGTTAGGCGG	TGGTGTGTC	100
35	CGTTGTATCG	CAATGGGTAC	ATCAGATGGC	CTAAGCCGTG	GTTTAGAAGT	150
	TAAAAATTTA	GAACACCCAA	TTGAAGTACC	AGTAGGTAAA	GCAACACTCG	200
	GACGTATCAT	GAACGTTCTG	GGTGACCCTA	TTGATATGAA	AGGTGATATC	250
	GGCGAAGAAG	AGCGTTGGTC	TATTCACCGC	GCTGCACCAA	GCTACGAAGA	300
	GCTATCGAGC	TCAACTGAAC	TGCTAGAGAC	AGGTATCAAA	GTCATGGACT	350
40	TGATCTGTCC	ATTCGCGAAA	GGTGGTAAAG	TTGGTCTGTT	CGGTGGTGCG	400
	GGTGTTGGTA	AAACGGTAAA	CATGATGGAA	CTTATCCGTA	ACATCGCGAT	450
	TGAGCACTCA	GGTTACTCAG	TATTCGCAGG	TGTTGGTGAG	CGTACCCGTG	500
	AAGGTAACGA	CTTCTATCAT	GAAATGACAG	ATTCAAACGT	TCTTGACAAA	550
	GTATCACTGG	TTTATGGTCA	GATGAATGAG	CCACCAGGAA	ACCGTCTACG	600
45	CGTAGCATTG	ACTGGTTTGA	CTATGGCTGA	GAAATTCCGT	GACGAAGGCC	650
	GTGATGTTCT	GTTGTTCGTG	GATAACATCT	ATCGTTATAC	ACTGGCAGGT	700
	ACAGAAGTAT	CGGCTCTGTT	AGGTCGTATG	CCATCAGCAG	TAGGTTATCA	750
	GCCAACATTG	GCAGAAGAGA	TGGGTGTTCT	TCAAGAACGT	ATCACTTCTA	800
50	CTAAGACAGG	TTCTATCAC				819

2) INFORMATION FOR SEQ ID NO: 340

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 907 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Psychrobacter phenylpyruvicus*

(B) STRAIN: ATCC 23333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340

	AACCGCACTG	ACGTGCCTCA	AATTTATGAC	GCGTTAGTTG	TAGATGGTAC	50
10	CGAAACCACC	CTAGAAGTTC	AGCAGCAGCT	GGGCGATGGT	GTGGTACGTA	100
	CTATTGCAAT	GGGATCTACT	GAAGGTCTTA	AGCGTGGTTT	ACCAGTAACA	150
	AACACTGGTG	CCCCAATTAC	AGTTCCAGTA	GGTGATGCGA	CTTTAGGTCG	200
	TATTATGGAC	GTTTTAGGTC	GTCCAATTGA	CGAACAAGGT	CCAGTTAATT	250
	GCTAAGACCA	TTGGTCAATC	CACCGTCAAG	CGCCATCATA	TGATGAGCAA	300
15	GCTAACAGTA	CTGACCTATT	AGAGACAGGT	ATTAAAGTAA	TTGACTTACT	350
	TTGTCCGTTT	GCTAAAGGGG	GTAAAGTTGG	TCTGTTCCGT	GGTGCCGGTG	400
	TTGGTAAAAC	CGTAAACATG	ATGGAATTGA	TTAATAACAT	CGCTCTTAAG	450
	CACTCAGGTT	TATCAGTATT	CGCTGGTGTG	GGTGAGCGTA	CTCGTGAAGG	500
	TAACGACTTC	TACCACGAGA	TGCAAGAAGC	GGGTGTTGTT	GACGTTGAAA	550
20	ACTTCACCAA	CTCAAAAGTT	GCGATGGTTT	ATGGTCAGAT	GAATGAGCCA	600
	CCAGGTAAAC	GTTTACGTGT	TGCGTTAACC	GGTCTGACTA	TGGCTGAGTA	650
	CTTCCGTGAT	CAAAAAGATG	AAAACGGTAA	AGGTAAAGAC	GTTCTATTAT	700
	TCGTTGATAA	CATCTACCGC	TACACGCTAG	CCGGTACTGA	AGTATCAGCA	750
	CTTCTAGGTC	GTATGCCATC	AGCAGTAGGT	TATCAGCCAA	CACTAGCGGA	800
25	AGAGATGGGT	GTACTACAAG	AGCGTATTAC	TTCAACTCAG	ACTGGTTCTA	850
	TTACTTC					907

30 2) INFORMATION FOR SEQ ID NO: 341

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 832 bases

(B) TYPE: Nucleic acid

35 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Rahnella aquatilis*

(B) STRAIN: DSM 4594

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341

45	GTTCCCTCAG	GATGCAGTAC	CGAACGTGTA	CAATGCTCTT	GAGGTAGAAA	50
	ACGGTACCTC	CAAACCTGGT	CTGGAAGTTC	AGCAACAGTT	AGGCGGCGGC	100
	GTTGTTCGTT	GTATCGCAAT	GGGTACCTCA	GACGGCCTGC	GTCGCGGTCT	150
	GAAAGTGAAC	AACCTGGAAC	ACCCAATTGA	AGTACCGGTA	GGTAAAGCGA	200
50	CTCTGGGTCG	TATCATGAAC	GTATTGGGTG	AACCAATCGA	CATGAAAGGT	250
	GAAATCGGCG	AAGAAGAACG	TCGTGCTATT	CACCGTGCTG	CGCCTTCTTA	300
	TGAAGAGCTG	GCAAACCTCC	AGGAATTGCT	GGAAACCGGT	ATCAAAGTTA	350
	TGGACCTGAT	GTGTCCGTTT	GCTAAGGGCG	GTAAAGTTGG	TCTGTTCCGT	400
	GGTGCGGGTG	TAGGTAAAAC	TGTGAACATG	ATGGAGCTGA	TCCGTAACAT	450
55	TGCGATCGAG	CACTCCGGTT	ATTCTGTGTT	TGCAGGCGTG	GGTGAACGTA	500
	CTCGTGAGGG	TAACGACTTC	TACCACGAAA	TGACTGATTC	CAACGTTATC	550
	GACAAAGTTT	CCCTGGTGTA	TGGCCAGATG	AATGAGCCAC	CAGGTAACCG	600
	TCTGCGCGTT	GCACTGACCG	GCCTGACCAT	GGCGGAAAAA	TTCCGTGATG	650
	AAGGTCGTGA	CGTACTGCTG	TTCGTTGACA	ACATTTACCG	TTACACCCTG	700
60	GCCGGTACCG	AAGTGTCCCG	ACTTCTGGGC	CGTATGCCAT	CGGCGGTAGG	750

TTATCAGCCA ACGCTGGCGG AAGAGATGGG CGCTCTGCAA GAACGTATCA 800
 CCTCGACCAA AAGTGGTTCT ATCACCTCCG TA 832

5

2) INFORMATION FOR SEQ ID NO: 342

(i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 824 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *arizonae*
- (B) STRAIN: ATCC 13314

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342

TTCCCTCAGG ATGCCGTACC ACGCGTGTAC GATGCTCTTG AGGTGCAGAA 50
 TGGTAATGAG AAGCTGGTGC TGGAAAGTTCA GCAGCAGCTT GGCGGCGGTA 100
 TCGTGCGTAC CATCGCGATG GGGTCTTCTG ACGGTCTGCG TCGCGGTCTT 150
 25 GATGTAAAAG ATCTCGAACA CCCGATCGAA GTCCCGGTAG GTAAAGCCAC 200
 GCTGGGTTCG ATCATGAACG TCCTGGGCGA ACCGGTCGAT ATGAAAGGCG 250
 AGATCGGCGA AGAAGAGCGT TGGGCTATTC ACCGCGCGGC GCCGTCTTAC 300
 GAAGAGTTGT CAAACTCTCA GGAAGTGTCTG GAAACCGGTA TAAAAGTTAT 350
 CGACCTGATG TGTCCGTTTCG CGAAGGGCGG TAAAGTCGGT CTGTTTCGGT 400
 30 GCGCGGGTGT AGGTAAAACC GTAAACATGA TGGAGCTTAT CCGTAACATC 450
 GCGATCGAGC ACTCCGGTTA CTCTGTGTTT GCGGGCGTAG GTGAACGTAC 500
 TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCT AACGTTATCG 550
 ATAAAGTATC CCTGGTGTAT GGCCAGATGA ACGAGCCACC GGGAAACCGT 600
 CTGCGCGTTG CATTGACCGG CCTGACCATG GCGGAAAAAT TCCGTGATGA 650
 35 AGGTCGTGAC GTTCTGCTGT TCGTCGACAA CATCTACCGT TATACCCTCG 700
 CCGGTACGGA AGTATCCGCA CTGCTGGGTC GTATGCCTTC CGCGGTAGGT 750
 TAYCASCAGA CTCTGGCGGA AGAGATGGGC GTTCTGCAGG AACGTATCAC 800
 CTCCACCAAA ACCGGTTCTA TCAC 824

40

2) INFORMATION FOR SEQ ID NO: 343

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 820 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype *choleraesuis*
- (B) STRAIN: ATCC 7001

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343

GATGCCGTAC CACGCGTGTA CGATGCCCTT GAGGTGCAGA ATGGTAATGA 50
 60 GAAGCTGGTG CTGGAAGTTC AGCAGCAGCT TGGCGGCGGT ATCGTGCGTA 100


```

CCATCGCGAT GGGGTCTTCT GACGGTCTGC GTCGCGGTCT GGATGTAAAA 150
GATCTCGAAC ACCCGATCGA AGTCCCAGTA GGTAAGCCA CGCTGGGTCG 200
TATCATGAAC GTCCTGGGCG AACCAGTCTGA CATGAAAGGC GAGATCGGCG 250
AAGAAGAGCG TTGGGCGATT CACCGCGCAG CACCTTCCTA CGAAGAGTTG 300
5 TCAAACCTCTC AGGAACCTGCT GGAAACCGGT ATCAAAGTTA TCGACCTGAT 350
GTGTCCGTTT GCGAAGGGCG GTAAAGTCGG TCTGTTCCGGT GGTGCGGGTG 400
TAGGTAAAAC CGTAAACATG ATGGAGCTTA TTCGTAACAT CGCGATCGAG 450
CACTCCGGTT ACTCAGTGTT TGCGGGCGTA GGGGAACGTA CTCGTGAGGG 500
TAACGACTTC TACCACGAAA TGACCGACTC CAACGTTATC GATAAAGTAT 550
10 CCCTGGTGTA TGGCCAGATG AACGAGCCCG CGGGAACCG TCTGCGCGTT 600
GCACTGACCG GCCTGACCAT GGCGGAGAAA TTCCGTGACG AAGGTCGTGA 650
TGTACTGCTG TTCGTCGATA ACATCTATCG TTACACCCTG GCCGGTACGG 700
AAGTATCCGC ACTGCTGGGC CGTATGCCTT CCGCAGTAGG TTACCAGCCG 750
ACTCTGGCGG AAGAGATGGG CGTTCTGCAG GAACGTATCA CCTCCACCAA 800
15 AACCGGTTCT ATCACCTCCG 820

```

2) INFORMATION FOR SEQ ID NO: 344

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 30 (A) ORGANISM: *Salmonella choleraesuis* subsp. *diarizonae*
 (B) STRAIN: ATCC 43973

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344

```

35 TTCCCTCAGG ATGCCGTACC ACGCGTGTAC GATGCTCTTG AGGTGCAGAA 50
TGGTAATGAG AAGCTGGTGC TGGAAGTTCA GCAGCAGCTT GGCGGCGGTA 100
TCGTGCGTAC CATCGCGATG GGGTCTTCTG ACGGTCTGCG TCGCGGTCTT 150
GATGTAAAAG ATCTCGAACA CCCGATCGAA GTCCCAGTAG GTAAAGCAAC 200
GCTGGGTCGT ATCATGAACG TCCTGGGTGA ACCGGTCGAT ATGAAAGGCG 250
40 AGATCGGCGA AGAAGAGCGT TGGCGGATTG AACGCGCGGC GCCGTCCTAC 300
GAAGAGTTGT CAAACTCTCA GGAACCTGCTG GAAACCGGTA TCAAAGTTAT 350
CGACCTGATG TGTCCGTTCT CGAAGGGCGG TAAAGTCGGT CTGTTCGGTG 400
GCGCGGGTGT AGGTAAACCC GTAAACATGA TGGAGCTTAT CCGTAACATC 450
GCGATCGAGC ACTCCGGTTA CTCTGTGTTT GCGGGCGTAG GTGAACGTAC 500
45 TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCT AACGTTATCG 550
ATAAAGTATC CCTGGTGTAT GGCCAGATGA ACGAGCCACC GGGAAACCGT 600
CTGCGCGTTG CATTGACCGG CCTGACCATG GCGGAAAAAT TCCGTGATGA 650
AGGTCGTGAC GTTCTGCTGT TCGTCGACAA CATCTACCGT TATACCTCG 700
CCGGTACGGA AGTATCCGCA CTGCTGGGTC GTATGCCTTC CGCGGTAGGT 750
50 TATCAGCCGA CTCTGGCTGA AGAAATGGGC GTTCTGCAGG AACGTATCAC 800
CTCCACCAA ACCGGTTCTA TCACCTCCGT A 831

```

55 2) INFORMATION FOR SEQ ID NO: 345

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 60 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Salmonella choleraesuis* subsp. *houtenae*

(B) STRAIN: ATCC 43974

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345

```

10 TTCCCTCAGG ATGCCGTACC ACGCGTGTAC GATGCTCTTG AGGTGCAGAA      50
   TGGTAATGAG AAGCTGGTGC TGGAAGTTCA GCAGCAGCTT GGCGGCGGTA      100
   TCGTACGTAC CATCGCGATG GGGTCTTCTG ACGGTCTGCG TCGCGGTCTG      150
   GATGTAAAAG ATCTCGAACA CCCGATCGAA GTCCCAGGTAG GTAAAGCTAC      200
15 GCTGGGTCGT ATCATGAACG TCCTGGGCGA ACCGGTCGAT ATGAAAGGCG      250
   AGATCGGCGA AGAAGAGCGT TGGGCGATTC ACCGCGCTGC GCCGTCTTAC      300
   GAAGAGTTGT CAAACTCTCA GGAAGTGTCT GAAACCGGTA TCAAAGTTAT      350
   CGACCTGATG TGTCCGTTCG CGAAGGGCGG TAAAGTCGGT CTGTTCCGGT      400
   GCGCGGGTGT AGGTAAAACC GTAAACATGA TGGAGCTTAT CCGTAACATC      450
20 GCGATCGAGC ACTCCGGTTA CTCCGTGTTT GCGGGCGTAG GTGAACGTAC      500
   TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCC AACGTTATCG      550
   ATAAAGTATC CCTGGTGTAT GGTCAGATGA ACGAGCCGCC GGGAAACCGT      600
   CTGCGCGTTG CATTGACCGG CCTGACCATG GCGGAAAAAT TCCGTGACGA      650
   AGGTCGTGAC GTTCTGCTGT TCGTCGATAA CATCTATCGT TACACCCTGG      700
25 CCGGTACGGA AGTATCCGCA CTGCTGGGTC GTATGCCTTC CGCGGTAGGT      750
   TATCAGCCGA CGCTGGCGGA AGAGATGGGC GTTCTGCAGG AACGTATCAC      800
   CTCCACCAAG ACCGGTTCTA TCACCTCCGT A                          831

```

30

2) INFORMATION FOR SEQ ID NO: 346

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 829 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Salmonella choleraesuis* subsp. *indica*

(B) STRAIN: ATCC 43974

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346

```

   TTCCCTCAGG ATGCCGTACC ACGCGTGTAC GATGCCCTTG AGGTGCAGAA      50
   TGGTAATGAG AAGCTCGTGC TGGAAGTTCA GCAGCAGCTT GGCGGCGGTA      100
   TCGTGCGTAC CATCGCGATG GGGTCTTCTG ACGGTCTGCG TCGCGGTCTG      150
50 GATGTAAAAG ATCTCGAACA CCCGATCGAA GTCCCAGGTAG GTAAAGCCAC      200
   GCTGGGTCGT ATCATGAACG TCCTGGGCGA ACCGGTCGAT ATGAAAGGCG      250
   AGATCGGCGA AGAAGAGCGT TGGGCGATTC ACCGCGCGGC GCCGTCTTAT      300
   GAAGAGTTGT CAAACTCTCA GGAAGTGTCT GAAACCGGTA TCAAAGTTAT      350
   CGACCTGATG TGTCCGTTCG CGAAGGGCGG TAAAGTCGGT CTGTTCCGGT      400
55 GTGCGGGCGT AGGTAAAACC GTAAACATGA TGGAGCTTAT CCGTAACATC      450
   GCGATCGAGC ACTCCGGTTA CTCTGTGTTT GCGGGCGTAG GTGAACGTAC      500
   TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCC AACGTTATCG      550
   ACAAAGTATC CCTGGTGTAT GGCCAGATGA ACGAGCCGCC GGGAAACCGT      600
   CTGCGCGTTG CACTGACCGG CCTGACCATG GCGGAGAAGT TCCGTGACGA      650
60 AGGTCGTGAC GTACTGCTGT TCGTCGATAA CATCTATCGT TATACCCTGG      700

```

CCGGTACGGA	AGTTTCCGCA	CTGCTGGGTC	GTATGCCTTC	CGCGGTAGGT	750
TATCAGCCAA	CTCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	800
CTCCACCAA	ACCGGTTCTA	TCACCTCCG			829

5

2) INFORMATION FOR SEQ ID NO: 347

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 817 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype *paratyphi* A
 (B) STRAIN: ATCC 9150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347

25	GCCGTACCAC	GCGTGTACGA	TGCCCTTGAG	GTGCAGAATG	GTAATGAGAA	50
	GCTGGTGCTG	GAAGTTCAGC	AGCAGCTTGG	CGGCGGTATC	GTGCGTACCA	100
	TCGCGATGGG	GTCTTCTGAC	GGTCTGCGTC	GCGGTCTGGA	TGTAAAAGAT	150
	CTCGAACACC	CGATCGAAGT	CCCGGTAGGT	AAAGCTACGC	TGGGTCGTAT	200
	CATGAACGTC	CTGGGCGAAC	CGGTCGACAT	GAAAGGCGAG	ATCGGCGAAG	250
	AAGAGCGTTG	GCGGATTAC	CGCGCAGCGC	CTTCCTACGA	AGAGTTGTCA	300
30	AACTCTCAGG	AACTGCTGGA	AACCGGTATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTCCGG	AAGGGCGGTA	AAGTCGGTCT	GTTTCGGTGGT	GCGGGTGTAG	400
	GTAAAACCGT	AAACATGATG	GAGCTTATCC	GTAACATCGC	GATCGAGCAC	450
	TCCGGTTACT	CTGTGTTTGC	GGGCGTAGGT	GAACGTA	GTGAGGGTAA	500
	CGACTTCTAC	CATGAAATGA	CCGACTCCAA	CGTTATCGAT	AAAGTATCCC	550
35	TGGTGTATGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCA	600
	ATGACCGGCC	TGACCATGGC	GGAGAAATTC	CGTGACGAAG	GTCGTGACGT	650
	ACTGCTGTTC	GTCGATAACA	TCTATCGTTA	CACCCTGGCC	GGTACGGAAG	700
	TATCCGCACT	GCTGGGTCGT	ATGCCTTCCG	CGGTAGGTTA	CCAGCCGACT	750
	CTGGCGGAAG	AGATGGGCGT	TCTGCAGGAA	CGTATCACCT	CCACCAAGAC	800
40	CGGTTCTATC	ACCTCCG				817

2) INFORMATION FOR SEQ ID NO: 348

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype *paratyphi* B
 (B) STRAIN: ATCC 8759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348

60

```

GCCGTACCAC GCGTGTACGA TGCCCTTGAG GTGCAGAATG GTAATGAGAA      50
GCTGGTGTCTG GAAAGTTCAGC AGCAGCTTGG CGGCGGTATT GTGCGTACCA      100
TCGCGATGGG GTCTTCTGAC GGTCTGCGTC GCGGTCTGGA TGTAAGAGAT      150
CTCGAACACC CGATCGAAGT CCCGGTAGGT AAAGCCACGC TGGGTCTGAT      200
5 CATGAACGTC CTGGGCGAAG CGGTTCGACAT GAAAGGCGAG ATCGGCGAAG      250
AAGAGCGTTG GCGGATTACG CGCGCAGCGC CTTCTCTACGA AGAGTTGTCA      300
AACTCTCAGG AACTGCTGGA AACCAGGTATC AAAGTTATCG ACCTGATGTG      350
TCCGTTTCGCG AAGGGCGGTA AAGTCGGTCT GTTCGGTGGT GCGGGTGTGG      400
GTAAAACCGT AAACATGATG GAGCTTATCC GTAACATCGC GATCGAGCAC      450
10 TCCGGTTACT CTGTGTTTGC GGGCGTAGGT GAACGTACTC GTGAGGGTAA      500
CGACTTCTAC CACGAAATGA CCGACTCCAA CGTTATCGAT AAAGTATCCC      550
TGGTGTATGG CCAGATGAAG GAGCCGCGG GAAACCGTCT GCGCGTTGCA      600
TTGACCGGTC TGACCATGGC GGAGAAATTC CGTGACGAAG GTCGTGACGT      650
ACTGCTGTTC GTCGATAACA TCTATCGTTA CACCCTGGCC GGTACGGAAG      700
15 TATCCGCACT GCTGGGCCGT ATGCCTCCG CAGTAGGTTA CCAGCCGACT      750
CTGGCGGAAG AGATGGGCGT TCTGCAGGAA CGTATCACCT CCACCAAAC      800
CGGTTC      806

```

20

2) INFORMATION FOR SEQ ID NO: 349

(i) SEQUENCE CHARACTERISTICS:

```

25 (A) LENGTH: 831 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Salmonella choleraesuis subsp. salamae
    (B) STRAIN: ATCC 43972

```

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349

```

TTCCCTCAGG ATGCCGTACC ACGCGTGTAC GATGCCCTTG AGGTGCAGAA      50
TGGTAATGAG AAGCTGGTGC TGGAAGTTCA GCAGCAGCTT GGCGGCGGTA      100
TCGTGCGTAC CATCGCGATG GGGTCTTCTG ACGGTCTGCG TCGKGGTCTG      150
40 GATGTAAAAG ATCTCGAACA CCCGATCGAA GTCCCAGTAG GTAAAGCAAC      200
GCTGGGCCGT ATCATGAACG TACTGGGCGA ACCGGTCGAC ATGAAAGGCG      250
AGATTGGTGA AGAAGAGCGT TGGGCTATTC ACCGTGCTGC GCCGTCCTAC      300
GAAGAGTTGT CAAACTCTCA GGAAGTGTCT GAAACCGGTA TCAAAGTTAT      350
CGACCTGATG TGTCCGTTCT CGAAGGGCGG TAAAGTCGGT CTGTTCCGGT      400
45 GCGCGGGTGT AGGTAAAACC GTAAACATGA TGGAGCTCAT CCGTAACATC      450
GCGATCGAGC ACTCCGGTTA CTCCGTGTTT GCGGGCGTAG GTGAACGTAC      500
TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCC AACGTTATCG      550
ATAAAGTATC CCTGGTGTAT GGCCAGATGA ACGAGCCGCC GGGAAACCGT      600
CTGCGCGTTG CACTGACCGG CCTGACCATG GCGGAAAAAT TCCGTGACGA      650
50 AGGTCGTGAC GTACTGCTGT TCGTCGATAA CATCTATCGT TATACCCTGG      700
CCGGTACGGA AGTATCCGCA CTGCTGGGTC GTATGCCTTC CGCGGTAGGT      750
TATCAGCCGA CGCTGGCGGA AGAGATGGGC GTTCTGCAGG AACGTATCAC      800
CTCCACTAAA ACCGGTTCTA TCACCTCCGT A      831

```

55

2) INFORMATION FOR SEQ ID NO: 350

(i) SEQUENCE CHARACTERISTICS:

```

60 (A) LENGTH: 823 bases

```

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype *typhi*

10 (B) STRAIN: ATCC 10749

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350

	TTCCCTCAGG	ATGCCGTACC	ACGCGTGTAC	GATGCCCTTG	AGGTGCAGAA	50
15	TGGTAATGAG	AAGCTGGTGC	TGGAAGTTCA	GCAGCAGCTT	GGCGGCGGTA	100
	TCGTGCGTAC	CATCGCGATG	GGGTCTTCTG	ACGGTCTGCG	TCGCGGTCTG	150
	GATGTAAAAG	ATCTCGAACA	CCCGATCGAA	GTCCCGGTAG	GTAAAGCTAC	200
	GCTGGGTCGT	ATCATGAACG	TCCTGGGCGA	ACCGGTCGAC	ATGAAAGGCG	250
	AGATCGGCCA	AGAAGAGCGT	TGGGCGATTG	ACCGCGCAGC	GCCTTCCTAC	300
20	GAAGAGTTAT	CAAACTCTCA	GGAAGTGTCTG	GAAACCGGTA	TCAAAGTTAT	350
	CGACCTGATG	TGTCCGTTTCG	CGAAGGGCGG	TAAAGTCGGT	CTGTTCGGTG	400
	GTGCGGGTGT	AGGTAAAACC	GTAAACATGA	TGGAGCTTAT	CCGTAACATC	450
	GCGATCGAGC	ACTCCGGTTA	CTCTGTGTTT	GCGGGCGTAG	GTGAACGTAC	500
	TCGTGAGGGT	AACGACTTCT	ACCATGAAAT	GACCGACTCC	AACGTTATCG	550
25	ATAAAGTATC	CCTGGTGTAT	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	600
	CTGCGCGTTG	CACTGACCGG	CCTGACCATG	GCGGAGAAAT	TCCGTGACGA	650
	AGGTCGTGAC	GTAAGTGTCTG	TGCTCGATAA	CATCTATCGT	TACACCCTGG	700
	CCGGTACGGA	AGTATCCGCA	CTGCTGGGTC	GTATGCCTTC	CGCGGTAGGT	750
	TACCAGCCGA	CTCTGGCGGA	AGAGATGGGC	GTTCTGCAGG	AACGTATCAC	800
30	CTCCACCAAG	ACCGGTTCTA	TCA			823

2) INFORMATION FOR SEQ ID NO: 351

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

45 (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype *typhimurium*

(B) STRAIN: ATCC 14028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351

50

	TTCCCTCAGG	ATGCCGTACC	ACGCGTGTAC	GATGCCCTTG	AGGTGCAGAA	50
	TGGTAATGAG	AAGCTGGTGC	TGGAAGTTCA	GCAGCAGCTT	GGCGGCGGTA	100
	TTGTGCGTAC	CATCGCGATG	GGGTCTTCTG	ACGGTCTGCG	TCGCGGTCTG	150
	GATGTAAAAG	ATCTCGAACA	CCCGATCGAA	GTCCCGGTAG	GTAAAGCTAC	200
55	GCTGGGTCGT	ATCATGAACG	TCCTGGGCGA	ACCGGTCGAC	ATGAAAGGCG	250
	AGATCGGCCA	AGAAGAGCGT	TGGGCGATTG	ACCGCGCAGC	GCCTTCCTAC	300
	GAAGAGTTGT	CAAACTCTCA	GGAAGTGTCTG	GAAACCGGTA	TCAAAGTTAT	350
	CGACCTGATG	TGTCCGTTTCG	CGAAGGGCGG	TAAAGTCGGT	CTGTTCGGTG	400
	GTGCGGGTGT	AGGTAAAACC	GTAAACATGA	TGGAGCTTAT	CCGTAACATC	450
60	GCGATCGAGC	ACTCCGGTTA	CTCAGTGTTC	GCGGGCGTAG	GGGAACGTAC	500

```

TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCC AACGTTATCG      550
ATAAAGTATC CCTGGTGTAT GGCCAGATGA ACGAGCCGCC GGGAAACCGT      600
CTGCGCGTTG CATTGACCGG TCTGACCATG GCGGAGAAAT TCCGTGACGA      650
AGGTCGTGAC GTACTGCTGT TCGTCGATAA CATCTATCGT TACACCCTGG      700
5 CCGGTACGGA AGTATCCGCA CTGCTGGGCC GTATGCCTTC CGCAGTAGGT      750
TACCAGCCGA CTCTGGCGGA AGAGATGGGC GTTCTGCAGG AACGTATCAC      800
CTCCACCAAA ACCGGTTCTA TCACCTCCGT A                          831

```

10

2) INFORMATION FOR SEQ ID NO: 352

(i) SEQUENCE CHARACTERISTICS:

```

15 (A) LENGTH: 810 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Salmonella choleraesuis subsp. choleraesuis
        serotype virchow
    (B) STRAIN: ATCC 51955

```

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352

```

GCCGTACCAC GCGTGACGA TGCCCTTGAG GTGCAGAATG GTAATGAGAA      50
GCTGGTGCTG GAAGTTCAGC AGCAGCTTGG CGGCGGTATC GTGCGTACCA      100
30 TCGCGATGGG GTCTTCTGAC GGTCTGCGTC GCGGTCTGGA TGTAAGAGAT      150
CTCGAACACC CGATCGAAGT CCCGGTAGGT AAAGCCACGC TGGGTCGTAT      200
CATGAACGTC CTGGGCGAAC CGGTCGACAT GAAAGGCGAG ATCGGCGAAG      250
AAGAGCGTTG GCGGATTAC CCGCGAGCAC CTTCTACGA AGAGTTGTCA      300
AACTCTCAGG AACTGCTGGA AACCGGTATC AAAGTTATCG ACCTGATGTG      350
35 TCCGTTTCGG AAGGGCGGTA AAGTCGGTCT GTTCGGTGGT GCGGGTGTAG      400
GTAAACCGGT AAACATGATG GAGCTTATTC GTAACATCGC GATCGAGCAC      450
TCCGTTTACT CTGTGTTTGC GGGCGTAGGG GAACGTACTC GTGAGGGTAA      500
CGACTTCTAC CACGAAATGA CCGACTCCAA CGTTATCGAT AAAGTCTCCC      550
TGGTGTATGG CCAGATGAAC GAGCCGCCGG GAAACCGTCT GCGCGTTGCA      600
40 TTGACCGGTC TGACCATGGC GGAGAAATTC CGTGACGAAG GTCGTGACGT      650
ACTGCTGTTT GTCGATAACA TCTATCGTTA CACCCTGGCC GGTACGGAAG      700
TATCCGCACT GCTGGGCCGT ATGCCTTCCG CAGTAGGTTA CCAGCCGACT      750
CTGGCGGAAG AGATGGGCGT TCTGCAGGAA CGTATCACCT CCACCAAAC      800
45 CCGTTCTATC                                         810

```

2) INFORMATION FOR SEQ ID NO: 353

50 (i) SEQUENCE CHARACTERISTICS:

```

    (A) LENGTH: 820 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Serratia ficaria
60    (B) STRAIN: ATCC 33105

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353

	GATGCCGTAC	CAAAAGTGTA	CGATGCCCTT	GAGGTAGAAA	ACGGTACCGA	50
5	GAAACTGGTG	CTGGAAGTTC	AGCAGCAGCT	GGGCGGTGGC	GTCGTTTCGCT	100
	GTATCGCAAT	GGGGACCTCT	GACGGTCTGC	GTCGCGGTCT	GAAAGTGAAC	150
	AACCTGGAAC	ACCCGATTGA	AGTGCCGGTG	GGTAAAGCTA	CCCTGGGCCG	200
	TATCATGAAC	GTATTGGGCG	AACCAATCGA	CATGAAAGGC	GAGATCGGCG	250
	AAGAAGAGCG	TTGGGCGATT	CACCGTCCTG	CGCCAAGCTA	CGAAGAGCTG	300
10	TCCAACCTCCC	AGGACCTGCT	GGAAACCGGT	ATCAAGGTAA	TGGACCTGAT	350
	TTGTCCGTTT	GCCAAGGGCG	GTAAAGTCGG	TCTGTTTCGGT	GGTGCGGGCG	400
	TGGGCAAAAC	CGTAAACATG	ATGGAGCTGA	TCCGTAACAT	CGCGATCGAG	450
	CACTCCGGTT	ATTCCGTGTT	TGCGGGCGTG	GGCGAGCGTA	CTCGTGAGGG	500
	TAACGACTTC	TACCACGAAA	TGAACGACTC	CAACGTTCTG	GACAAAGTAT	550
15	CCCTGGTTTA	CGGCCAGATG	AACGAGCCGC	CGGGTAACCG	TCTGCGCGTT	600
	GCATTGACCG	GCCTGACCAT	GGCGGAGAAA	TTCCGTGACG	AAGGCCGCGA	650
	CGTTCTGCTG	TTCGTTGACA	ACATTTACCG	TTACACCCTG	GCCGGTACCG	700
	AAGTGTCGCG	ACTTCTGGGC	CGTATGCCAT	CCGCGGTAGG	TTATCAGCCA	750
	ACGCTGGCGG	AAGAGATGGG	CGTTCTGCAA	GAACGTATCA	CCTCGACCAA	800
20	GACCGGTTCC	ATCACCTCCG				820

2) INFORMATION FOR SEQ ID NO: 354

25

(i) SEQUENCE CHARACTERISTICS:

- | | | |
|----|-----|----------------------|
| | (A) | LENGTH: 816 bases |
| | (B) | TYPE: Nucleic acid |
| | (C) | STRANDEDNESS: Double |
| 30 | (D) | TOPOLOGY: Linear |

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- | | | |
|----|-----|-------------------------------------|
| 35 | (A) | ORGANISM: <i>Serratia fonticola</i> |
| | (B) | STRAIN: ATCC 29844 |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354

40	GATGCCGTAC	CGAAAGTGTA	CAACGCTCTT	GAGGTTGCAA	ACGGCACCGA	50
	GAAATTGGTG	CTGGAAGTTC	AGCAACAGCT	GGGTGGCGGC	GTGGTTTCGCT	100
	GTATCGCAAT	GGGGACCTCA	GACGGTCTGC	GTCGTGGTCT	GGCCGTAACC	150
	GACCTGCAGC	ACCCAATTGA	AGTACCGGTA	GGTAAAGCTA	CCCTGGGCCG	200
	TATCATGAAC	GTATTGGGTG	AACCAATCGA	CATGAAGGGC	GACATCGGCG	250
45	AAGAAGAACG	TTGGGCTATT	CACCGCCCTG	CGCCAAGCTA	CGAAGAGCTG	300
	TCCAGCTCCC	AGGATCTGCT	GGAAACCGGT	ATCAAGGTAA	TGGACCTGAT	350
	CTGCCCCTTC	GCCAAGGGTG	GTAAAGTTGG	TCTGTTTCGGT	GGTGCTGGTG	400
	TAGGTAAAAC	CGTAAACATG	ATGGAGCTGA	TCCGTAACAT	CGCGATCGAG	450
	CACTCCGGTT	ATTCTGTGTT	TGCGGGCGTG	GGTGAACGTA	CTCGTGAGGG	500
50	TAACGACTTC	TACCACGAAA	TGACCGATTG	CAACGTAAGT	GACAAAGTTT	550
	CCCTGGTTTA	CGGCCAGATG	AACGAGCCAC	CAGGTAACCG	TCTGCGCGTT	600
	GCGCTGACCG	GCCTGACCAT	GGCTGAGAAG	TTCCGTGACG	AAGGTCGTGA	650
	CGTACTGCTG	TTCGTGATA	ACATCTACCG	TTATACCCTG	GCCGGTACCG	700
	AAGTGTCGCG	ACTTCTGGGC	CGTATGCCAT	CGGCGGTAGG	TTATCAGCCA	750
55	ACGCTGGCGG	AAGAGATGGG	TGTTCTGCAA	GAACGTATCA	CCTCTACCAA	800
	GACTGGTTCA	ATCACC				816

60 2) INFORMATION FOR SEQ ID NO: 355

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia grimesii*
 (B) STRAIN: ATCC 14460

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355

```

15 GATGCCGTAC CAAAAGTGTA CAACGCTCTT GAGGTAGAAA ACGGTGCCAA      50
   TAAGCTGGTG CTGGAAGTTC AGCAACAGTT GGGCGGTGGC GTGGTTCGCT      100
   GTATCGCAAT GGGGACCTCT GATGGTCTGC GTCGCGGTCT GAAAGTCACA      150
   GACCTGGACC ACCCAATTGA AGTACCGGTA GGTAAAGCTA CTCTGGGCCG      200
20 TATCATGAAC GTATTGGGTG AACCAATCGA CATGAAGGGC GATATCGGCG      250
   AAGAAGAACG TTGGGCGATT CACCGTCCGG CGCCAAGCTA CGAAGATTG      300
   GCCAACTCCC AGGATCTGCT GGAAACCGGT ATCAAGGTAA TGGACCTGAT      350
   CTGCCCGTTC GCCAAGGGTG GTAAAGTCGG TCTGTTCCGG GTTGCGGGTG      400
   TTGGTAAAAC CGTAAACATG ATGGAGCTGA TCCGTAACAT CGCGATCGAG      450
25 CACTCCGGTT ATTCTGTGTT TGCGGGCGTG GGTGAGCGTA CTCGTGAGGG      500
   TAACGACTTC TACCACGAAA TGAACGACTC CAACGTA CTG GACAAAGTAT      550
   CCCTGGTTTA CGGCCAGATG AACGAGCCAC CGGGTAACCG TCTGCGCGTT      600
   GCTCTGACCG GTCTGACCAT GGCTGAGAAA TTCCGTGACG AAGGCCGTGA      650
   CGTTCTGCTG TTCGTTGATA ACATCTACCG TTATACCCTG GCCGGTACCG      700
30 AAGTGTCCGC ACTTCTGGGC CGTATGCCAT CGGCGGTAGG TTATCAGCCA      750
   ACGCTGGCGG AAGAGATGGG TGTCTGCAA GAACGTATCA CCTCTACCAA      800
   GACTGGTTCA ATCACCTCCG TA                                     822

```

2) INFORMATION FOR SEQ ID NO: 356

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia liquefaciens*
 (B) STRAIN: ATCC 27592

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356

```

ATGCCGTACC AAAAGTGTA AATGCTCTTG AGGTAGAAAA CCGTACCGAG      50
AAGCTGGTGC TGGAGTTCA GCAGCAGTTG GGCGGTGGCG TAGTTCGCTG      100
TATCGCGATG GGGACCTCAG ATGGTCTGCG CCGCGGTCTG AAAGTGAACG      150
55 ATCTGGAACA CCCAATTGAA GTACCGGTAG GTAAAGCTAC CCTGGGCCGT      200
ATCATGAACG TATTGGGTGA ACCAATCGAC ATGAAAGGCG ACATCGGCGA      250
AGAAGAACGT TGGGCGATTC ACCGTCCAGC GCCAAGCTAC GAAGATTTGT      300
CAAACCTCCA GGATCTGCTG GAAACCGGTA TCAAGGTTAT GGACCTGATT      350
TGTCGGTTCC CTAAGGGCGG TAAAGTTGGT CTGTTCCGGT GTGCTGGTGT      400
60 TGGTAAAACC GTAAACATGA TGGAGCTGAT CCGTAACATC GCGATCGAGC      450

```



```

ACTCCGGTTA TTCCGTGTTT GCAGGCGTGG GTGAGCGTAC TCGTGAGGGT 500
AACGACTTCT ACCACGAAAT GAACGACTCC AACGTACTGG ACAAAGTATC 550
CCTGGTTTAC GGCCAGATGA ACGAGCCACC GGGTAACCGT CTGCGCGTTG 600
CTCTGACCGG TCTGACCATG GCGGAGAAAT TCCGTGACGA AGGCCGCGAC 650
5 GTTCTGCTGT TCGTTGATAA CATTTACCGT TATACCCTGG CCGGTACCGA 700
AGTGTCCGCA CTTCTGGGCC GTATGCCATC TCGGGTAGGT TATCAGCCAA 750
CGCTGGCGGA AGAGATGGGC GTTCTGCAAG AACGTATCAC CTCTACCAAG 800
ACCGTTCTA TCACTTCCG 819

```

10

2) INFORMATION FOR SEQ ID NO: 357

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 805 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia marcescens*
 (B) STRAIN: ATCC 13880

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357

```

TCAGGATGCC GTACCGAAAG TGTACGACGC CCTTGAGGTA GAAAACGGCA 50
CCGAAAAACT GGTGTTGGAA GTTCAGCAAC AGCTGGGCGG TGGCGTGGTT 100
30 CGCTGTATCG CAATGGGGAC CTCCGACGGT CTGCGTCGCG GTCTGAAAGT 150
GAACAACCTG GACCACCCGA TTGAAGTGCC GGTGGGTAAA GCTACCCTGG 200
GTCGTATCAT GAACGTATTG GGTCAACCGA TCGACATGAA AGGCGACATC 250
GGCGAAGAAG AGCGTTGGGC GATTCAACGC GCGGCGCCAA GCTACGAAGA 300
GCTGTCAAGC TCTCAGGAAC TGCTGGAAAC CGGTATCAAG GTAATGGACC 350
35 TGATTTGTCC GTTCGCCAAG GCGGTTAAAG TCGGTCTGTT CGGCGGTGCG 400
GGCGTAGGTA AAACCGTAAA CATGATGGAG CTGATCCGTA ACATCGCGAT 450
CGAGCACTCC GGTTATTCCG TGTTTGCGGG CGTGGGCGAG CGTACTCGTG 500
AGGGTAACGA CTTCTACCAC GAAATGACCG ACTCCAACGT TCTGGACAAA 550
GTATCCCTGG TTTACGGCCA GATGAACGAG CCACCAGGTA ACCGTCTGCG 600
40 CGTTGCGCTG ACCGGTCTGA CCATGGCGGA GAAATTCCGT GACGAAGGCC 650
GTGACGTTCT GCTGTTTCGT GACAACATCT ACCGTTACAC CCTGGCCGGT 700
ACCGAAGTGT CCGCACTTCT GGGCCGTATG CCATCCGCGG TAGGTTATCA 750
GCCAACGCTG GCGGAAGAGA TGGGCGTTCT GCAAGAACGT ATCACCTCGA 800
CCAAG 805
45

```

2) INFORMATION FOR SEQ ID NO: 358

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 822 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia odorifera*
 (B) STRAIN: ATCC 33077

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358

```

5  GATGCCGTAC CAAAAGTGTA CGATGCCCTT GAGGTAGAAA ACGGTACCGA 50
   AACTCTGGTG CTGGAAGTTC AGCAGCAGCT GGGCGGTGGC GTGGTTCGTT 100
   GTATCGCTAT GGGCACCTCC GACGGTTTGC GTCGCGGCCT GAAAGTGAAC 150
   GATCTGCAAC ACCCAATCGA AGTCCCGGTT GGCAAGGCAA CGCTGGGTCG 200
   TATCATGAAC GTATTGGGTC AACCAATCGA CATGAAAGGC GACATCGGCG 250
   AAGAAGAGCG TTGGGCGATT CACCGCGCGG CGCCAAGCTA CGAAGAACTG 300
10  TCCAAC TCCC AGGATCTGCT GGAAACCGGT ATCAAGGTTA TGGACCTGAT 350
   CTGCCC GTTT GCCAAGGGTG GTAAAGTCGG TCTGTTCCGT GGTGCGGGTG 400
   TTGGTAAAC CGTAAACATG ATGGAGCTGA TCCGTAAACAT CGCGATCGAG 450
   CACTCCGGTT ATTCAGTGTT TCGGGGCGTG GGTGAGCGTA CTCGTGAGGG 500
   TAACGACTTC TACCACGAAA TGACCGACTC CAACGTA CTG GACAAGGTTT 550
15  CCCTGGTTTA CGGCCAGATG AACGAGCCAC CGGGTAACCG TCTGCGCGTT 600
   GCGCTGACCG GTCTGACCAT GGCCGAGAAA TTCCGTGACG AAGGTCGTGA 650
   CGTTCTGCTG TTCGTTGACA ACATTTACCG TTACACCCTG GCCGGTACCG 700
   AAGTGTCTGC ACTTCTGGGC CGTATGCCAT CGGCGGTAGG TTATCAGCCA 750
   ACGCTGGCGG AAGAGATGGG CGTTCTGCAA GAACGTATCA CCTCGACCAA 800
20  GACCGGTTCT ATCACCTCCG TA 822

```

2) INFORMATION FOR SEQ ID NO: 359

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 805 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia plymuthica*
 (B) STRAIN: ATCC 183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359

```

40  GTGTACAACG CTCTTGAGGT AGAAAACGGT GCCAATAAGC TGGTGCTGGA 50
   AGTTCAGCAA CAGCTGGGCG GTGGCGTGGT TCGCTGTATC GCGATGGGGA 100
   CCTCTGATGG TCTGCGTCGC GGTCTGAAAG TGATCGACCT GGATCACCCG 150
   ATTGAAGTAC CGGTAGGTAA AGCTACCCTG GGCCGTATCA TGAACGTATT 200
   GGGTGAACCA ATCGACATGA AAGGCGACAT CGGCGAAGAA GAACGTTGGG 250
45  CAATTCACCG TCCAGCGCCA AGCTACGAAG ATTTGGCCAA CTCCCAGGAT 300
   CTGCTGGAAA CCGGTATCAA GGTATGGAC CTGATCTGTC CGTTCGCTAA 350
   GGGCGGTAAA GTGGGTCTGT TCGGCGGTGC GGGCGTGGGT AAAACCGTAA 400
   ACATGATGGA GCTGATCCGT AACATCGCGA TCGAACACTC CGGTTATTCC 450
   GTGTTTGCGG GCGTGGGTGA GCGTACTCGT GAGGGTAACG ACTTCTACCA 500
50  CGAAATGAAC GACTCCAACG TACTGGACAA AGTATCCCTG GTTTACGGCC 550
   AGATGAACGA GCCACCGGGT AACCGTCTGC GCGTTGCTCT GACCGGTCTG 600
   ACCATGGCGG AGAAATTCCG TGACGAAGGC CGCGACGTTT TGCTGTTCGT 650
   TGATAACATC TACCGTTATA CCCTGGCCCG TACCGAAGTG TCCGCACTTC 700
   TGGGCCGTAT GCCATCTGCG GTAGGTTATC AGCCAACGCT GGCGGAAGAG 750
55  ATGGGCGTTC TGCAAGAACG TATCACCTCT ACCAAGACCG GTTCTATCAC 800
   CTCCG 805

```

2) INFORMATION FOR SEQ ID NO: 360

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Serratia rubidaea*
 (B) STRAIN: ATCC 27593

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360

```

15  TTCCCTCAGG ATGCCGTACC AAAAGTGTAC GATGCCCTTG AGGTAGAGAA      50
    CGGTAACGAA AACTGGTGC TGGAAAGTTCA GCAGCAGCTG GCGGGCGGCG      100
    TTGTACGCTG TATCGCCATG GGTACTTCCG ACGGTCTGCG TCGCGGTCTG      150
    AAAGTTAACG ACCTCGAGCA CCCAATCGAA GTGCCAGTTG GTAAAGCAAC      200
20  GCTGGGTCGT ATCATGAACG TATTGGGTCA GCCAATCGAC ATGAAAGGCG      250
    ACATCGGCGA AGAAGAGCGT TGGGCGATTG ACCGCGCGGC GCCAAGCTAC      300
    GAAGAGCTGT CCAGCTCCCA AGAGCTGCTG GAAACCGGTA TCAAGGTAAT      350
    GGACCTGATC TGCCCGTTCG CCAAGGGTGG TAAAGTTGGT CTGTTCTGGTG      400
    GTGCGGGCGT AGGTAAACC GTAAACATGA TGGAGCTGAT CCGTAACATC      450
25  GCGATCGAGC ACTCCGGTTA CTCTGTGTTT GCGGGCGTGG GTGAGCGTAC      500
    TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCC AACGTACTGG      550
    ACAAAGTATC CCTGGTTTAC GGCCAGATGA ACGAGCCGCC GGGTAACCGT      600
    CTGCGCGTTG CACTGACCGG CCTGACCATG GCGGAAAAAT TCCGTGATGA      650
    AGGCCGCGAC GTTCTGCTGT TCGTGATAA CATCTACCGT TACACCTGG      700
30  CCGGTACCGA AGTGTCGCA CTGCTCGGCC GTATGCCATC TGCGGTAGGT      750
    TATCAGCCAA CGCTGGCGGA AGAGATGGGC GTTCTGCAAG AACGTATCAC      800
    CTCGACCAAG ACCGGTTCAA TCACCTCCGT A                        831
  
```

2) INFORMATION FOR SEQ ID NO: 361

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shewanella putida*
 (B) STRAIN: LCDC D7179

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361

```

55  CCGTAAACAT GATGGAAGT ATCCGTAACA TCGCCATCGA GCACAGCGGT      50
    TATTCGGTGT TCGCCGGTGT GGGTGAGCGT ACTCGTGAGG GTAACGACTT      100
    CTACCACGAG ATGAAGGACT CCAACGTTCT CGACAAGGTA GCGCTGGTCT      150
    ACGGTCAGAT GAACGAGCCA CAGGAAACC GTCTGCGCGT AGCGCTGACC      200
    GGCCTGACCA TGGCCGAGAA GTTCCGTGAC GAAGGTAACG ACGTTCTGCT      250
    GTTCGTCGAC AACATCTATC GTTACACCTT GGCCGGTACC GAAGTATCCG      300
    CACTGCTGGG CCGTATGCCT TCGGCGGTAG GTTACCAGCC GACCCTGGCT      350
    GAAGAGATGG GCGTTCTGCA AGAACGTATC ACTTCGACCA AGGAAGGTTC      400
60  GATCAC                                         406
  
```

2) INFORMATION FOR SEQ ID NO: 362

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shigella boydii*
 (B) STRAIN: ATCC 9207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362

```

20  TTCCCTCAGG ATGCCGTACC GCGCGTGTAC GATGCTCTTG AGGTGCAAAA      50
    TGGTAATGAG CGTCTGGTGC TGGAAAGTTCA GCAGCAGCTC GGCGGCGGTA      100
    TCGTGCGTAC CATCGCAATG GGTTCCTCCG  ACGGTCTGCG TCGCGGTCTG      150
    GATGTAAAAG ACCTCGAACA CCCGATCGAA  GTCCCGGTAG GTAAAGCGAC      200
    TCTGGGCCGT ATCATGAACG TACTGGGTGA ACCGGTCGAC ATGAAAGGCG      250
25  AGATCGGTGA AGAAGAGCGT TGGGCGATTG ACCGCGCAGC ACCTTCCTAC      300
    GAAGAGCTGT CAAACTCTCA GGAAGTGTG GAAACCGGTA TCAAAGTTAT      350
    CGACCTGATG TGTCCGTTCT CTAAGGGCGG TAAAGTTGGT CTGTTTCGGT      400
    GTGCGGGTGT AGGTAAAACC GTAAACATGA TGGAGCTCAT TCGTAACATC      450
    GCGATCGAGC ACTCCGGTTA CTCTGTGTTT GCGGGCGTAG GTGAACGTAC      500
30  TCGTGAGGGT AACGACTTCT ACCACGAAAT GACCGACTCC AACGTTATCG      550
    ACAAAGTATC CCTGGTGTAT GGCCAGATGA ACGAGCCGCC GGGAAACCGT      600
    CTGCGCGTTG CTCTGACCGG TCTGACCATG GCTGAGAAAT TCCGTGACGA      650
    AGGTCGTGAC GTTCTGCTGT TCGTTGACAA CATCTATCGT TACACCCTGG      700
    CCGGTACGGA AGTATCCGCA CTGCTGGGCG GTATGCCTTC AGCGGTAGGT      750
35  TATCAGCCGA CCCTGGCGGA AGAGATGGGC GTTCTGCAGG AACGTATCAC      800
    CTCCACCAAA ACTGGTTCTA TCACCTCCGT  A                          831
  
```

2) INFORMATION FOR SEQ ID NO: 363

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shigella dysenteriae*
 (B) STRAIN: ATCC 11835

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363

```

55  GCCGTACCGC GCGTGTACGA TGCTCTTGCG GTGCAAAATG GTAATGAGCG      50
    TCTGGTGCTG GAAGTTCAGC AGCAGCTCGG CGGCGGTATC GTGCGTACCA      100
    TCGCAATGGG TTCCTCCGAC GGTCTGCGTC GCGGTCTGGA TGTAAGAGAC      150
    CTCGAACACC CGATCGAAGT CCCGGTAGGT AAAGCGACTC TGGGCCGTAT      200
60  CATGAACGTA CTGGGTGAAC CGGTCGACAT GAAAGGCGAG ATCGGTGAAG      250
  
```

```

AAGAGCGTTG GGCTATTCAC CGCGCAGCAC CTTCTACGA AGAGCTGTCA 300
AACTCTCAGG AACTGCTGGA AACCAGGTATC AAAGTTATCG ACCTGATGTG 350
TCCGTTTCGCT AAGGGCGGTA AAGTTGGTCT GTTCGGTGGT GCGGGTGTAG 400
GTAAAACCGT AAACATGATG GAGCTCATTC GTAACATCGC GATCGAGCAC 450
5 TCCGTTTACT CTGTGTTTGC GGGCGTAGGT GAACGTACTC GTGAGGGTAA 500
CGACTTCTAC CACGAAATGA CCGACTCCAA CGTTATCGAC AAAGTATCCC 550
TGGTGTATGG CCAGATGAAC GAGCCGCCGG GAAACCGTCT GCGCGTTGCT 600
CTGACCGGTC TGACCATGGC TGAGAAATTC CGTGACGAAG GTCGTGACGT 650
TCTGCTGTTT GTTGACAACA TCTATCGTTA CACCCTGGCC GGTACGGAAG 700
10 TATCCGCACT GCTGGGCCGT ATGCCTTCAG CCGTAGGTTA TCAGCCGACC 750
CTGGCGGAAG AGATGGGCGT TCTGCAGGAA CGTATCACCT CCACCAAAAC 800
CG 802

```

15

2) INFORMATION FOR SEQ ID NO: 364

(i) SEQUENCE CHARACTERISTICS:

```

20 (A) LENGTH: 819 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Shigella flexneri
    (B) STRAIN: ATCC 12022

```

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364

```

ATGCCGTACC GCGCGTGTAC GATGCTCTTG AGGTGCAAAA TGGTAATGAG 50
CGTCTGGTGC TGGAAGTTCA GCAGCAGCTC GCGGGCGGTA TCGTGCGTAC 100
CATCGCAATG GGTTCCTCCG ACGGTCTGCG TCGCGGTCTG GATGTAAAAG 150
35 ACCTCGAACA CCCGATCGAA GTCCCAGTAG GTAAAGCGAC TCTGGGCCGT 200
ATCATGAACG TACTGGGTGA ACCGGTCGAC ATGAAAGGCG AGATCGGTGA 250
AGAAGAGCGT TGGGCGATTC ACCGCGCAGC ACCTTCCTAC GAAGAGCTGT 300
CAAACCTCTC GGAAGTGCTG GAAACCGGTA TCAAAGTTAT CGACCTGATG 350
TGTCCGTTTC CTAAGGCGCG TAAAGTTGGT CTGTTTCGGT GTGCGGGTGT 400
40 AGGTAAAACC GTAAACATGA TGGAGCTCAT TCGTAACATC GCGATCGAGC 450
ACTCCGGTTA CTCTGTGTTT GCGGGCGTAG GTGAACGTAC TCGTGAGGGT 500
AACGACTTCT ACCACGAAAT GACCGACTCC AACGTTATCG ACAAAGTATC 550
CCTGGTGTAT GGCCAGATGA ACGAGCCGCC GGGAAACCGT CTGCGCGTTG 600
CTCTGACCGG TCTGACCATG GCTGAGAAAT TCCGTGACGA AGGTCGTGAC 650
45 GTTCTGCTGT TCGTTGACAA CATCTATCGT TACACCCTGG CCGGTACGGA 700
AGTATCCGCA CTGCTGGGCC GTATGCCTTC AGCGGTAGGT TATCAGCCGA 750
CCCTGGCGGA AGAGATGGGC GTTCTGCAGG AACGTATCAC CTCCACCAA 800
ACTGGTTCTA TCACCTCCG 819

```

50

2) INFORMATION FOR SEQ ID NO: 365

(i) SEQUENCE CHARACTERISTICS:

```

55 (A) LENGTH: 802 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Shigella sonnei*

(B) STRAIN: ATCC 29930

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365

5
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GTACCGCGCG	TGTACGATGC	TCTTGAGGTG	CAAAATGGTA	ATGAGCGTCT	50
GGTGCTGGAA	G TTCAGCAGC	AGCTCGGCGG	CGGTATCGTG	CGTACCATCG	100
CAATGGGTTC	CTCCGACGGT	CTGCGTCGCG	GTCTGGATGT	AAAAGACCTC	150
GAACACCCGA	TCGAAGTCCC	GGTAGGTAAA	GCGACTCTGG	GCCGTATCAT	200
GAACGTA CTG	GGTGAACCGG	TCGACATGAA	AGGCGAGATC	GGTGAAGAAG	250
AGCGTTGGGC	GATTCACCGC	GCAGCACCTT	CCTACGAAGA	GCTGTCAAAC	300
TCTCAGGAAC	TGCTGGA AAC	CGGTATCAAA	GTTATCGACC	TGATGTGTCC	350
GTTCGCTAAG	GGCGGTAAAG	TTGGTCTGTT	CGGTGGTGCG	GGTGTAGGTA	400
AAACCGTAAA	CATGATGGAG	CTCATTCGTA	ACATCGCGAT	CGAGCACTCC	450
GGTTACTCTG	TGTTTGCGGG	CGTAGGTGAA	CGTACTCGTG	AGGGTAACGA	500
CTTCTACCAC	GAAATGACCG	ACTCCAACGT	TATCGACAAA	GTATCCCTGG	550
TGTATGGCCA	GATGAACGAG	CCGCCGGGAA	ACCGTCTGCG	CGTTGCTCTG	600
ACCGGTCTGA	CCATGGCTGA	GAAATTCCGT	GACGAAGGTC	GTGACGTTCT	650
GCTGTTCGTT	GACAACATCT	ATCGTTACAC	CCTGGCCGGT	ACGGAAGTAT	700
CCGCACTGCT	GGGCCGTATG	CCTTCAGCGG	TAGGTTATCA	GCCGACCCTG	750
GCGGAAGAGA	TGGGCGTTCT	GCAGGAACGT	ATCACCTCCA	CCAAA ACTGG	800
TT					802

2) INFORMATION FOR SEQ ID NO: 366

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 785 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366

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TAACGCCTTG	GTTATTGATG	TGCCTAAAGA	AGAAGGTACA	ATACAACTAA	50
CATTAGAAGT	TGCGCTGCAA	TTAGGTGACG	ACGTTGTTTCG	TACAATTGCG	100
ATGGATTCAA	CTGATGGTGT	CCAAAGAGGC	ATGGATGTAA	AAGATACAGG	150
CAAAGAAATT	AGTGTACCTG	TTGGTGATGA	AACATTAGGT	CGTGTATTTA	200
ATGTACTAGG	TGAAACAATT	GACCTTAAAG	AAGAAATTAG	TGATTCTGTT	250
CGCCGCGATC	CTATCCATCG	TCAAGCACCA	GCATTCGATG	AACTTTCAAC	300
AGAAGTTCAA	ATTTTAGAAA	CAGGTATTAA	AGTAGTAGAT	TTACTAGCAC	350
CTTATATTAA	AGGTGGTAAA	ATCGGATTGT	TCGGTGGTGC	CGGTGTAGGT	400
AAAACAGTAT	TAATCCAAGA	ATTAATTAAC	AACATCGCTC	AAGAGCACGG	450
TGGTATTTCT	GTATTGCGCG	GTGTAGGTGA	ACGTACTCGT	GAAGGTAACG	500
ATTTATACTT	CGAAATGAGT	GATAGTGGTG	TAATTAAGAA	AACAGCCATG	550
GTATTGCGGC	AAATGAATGA	GCCACCTGGT	GCACGTATGC	GTGTTGCATT	600
ATCTGGTTTA	ACAATGGCTG	AATATTTCCG	TGACGAACAA	GGTCAAGACG	650
TATTATTATT	CATCGATAAC	ATTTTCAGAT	TTACACAAGC	TGGTTCTGAG	700
GTATCTGCAT	TATTAGGTCT	TATGCCTTCT	GCAGTAGGTT	ACCAACCAAC	750
ACTTGCTACT	GAAATGGGAC	AATTACAAGA	ACGTA		785

2) INFORMATION FOR SEQ ID NO: 367

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 843 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus auricularis*
 (B) STRAIN: ATCC 33753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367

```

GAACATAACG AAGTGCCTAA TATTAATAAC GCCTTAGTAC TCGATGTTGA      50
AAGAGAAGAC GGAACAGTGT CTTTAACTTT AGAAGTAGCT TTACAATTAG      100
20 GCGATGACGT TGTTTCGTACC ATTGCAATGG ATTCAACTGA TGGTGTAA      150
CGTGGTAAACG AAGTCAAAGA TACTGGTAAT AGCATTAGCG TACCAGTCGG      200
AGACGAAACT TTAGGACGTG TCTTCAACGT TCTAGGTGAA ACAATTGATT      250
TAGAAGATAA ACTTGATGAT TCTGCGCGAC GTGACCCTAT ACATAGAGAA      300
GCGCCAGCGT TTGATCAATT ATCAACTCAA GTTGAAATTT TAGAAACAGG      350
25 AATTAAAGTT GTTGACTTAT TAGCACCTTA TATTAAAGGT GGTAAGTTG      400
GACTCTTCGG TGGTGCCGGT GTTGGTAAAA CCGTTTTAAT CCAAGAATTA      450
ATCAACAACA TCGCTCAAGA ACACGGTGGT ATTCAGTCT TTGCCGGTGT      500
AGGTGAACGT ACACGTGAAG GTAACGACTT GTACTATGAA ATGAGCGACA      550
GTGGTGTAAT CAAGAAAACA GCCATGGTCT TCGGACAAAT GAACGAACCA      600
30 CCTGGCGCAC GTATGCGTGT TGCTTTATCT GGTTTAACAA TGGCTGAATA      650
TTTCCGTGAT GAACAAGGAC AAGACGTATT GTTATTCATC GACAATATTT      700
TCCGTTTCAC ACAAGCCGGT TCAGAAGTTT CTGCCTTACT AGGTCGTTTA      750
CCATCAGCCG TTGGTTATCA ACCTACATTA GCAACAGAAA TGGGACAATT      800
ACAAGAACGT ATTACTTCAA CAACAAAAGG ATCAGTTACT TCA          843
35

```

2) INFORMATION FOR SEQ ID NO: 368

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 849 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus capitis* subsp. *capitis*
 (B) STRAIN: ATCC 27840

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368

```

GCTTTGAACA TAATGAAGTT CCTGATATTA ACAATGCCTT ACACATCGAA      50
55 GTTCCTAAAG AAGATAGCAC ACTTCATTTA ACTTTAGAAG TTGCACTTCA      100
ATTAGGTGAC GATGTAGTAC GTACAATCGC AATGGACTCA ACTGACGGCG      150
TTCAAAGAGG TATGGAAGTT AAAGATACAG GTAAAGATAT TAGCGTACCT      200
GTTGGTGATG CAACTTTAGG AAGAGTATTT AACGTATTAG GAGAAACAAT      250
CGATTTAGAT GAAAAGATTG ATGATTCACT ACGTCGTGAT CCTATTCTA      300
60 GACAGGCACC TGGCTTCGAT GAATTATCTA CTAAAGTAGA AATCTTAGAA      350

```

	ACAGGTATCA	AAGTAGTAGA	CTTATTAGCA	CCTTACATTA	AAGGTGGTAA	400
	AATTGGATTA	TTCGGTGGTG	CCGGTGTG	TAAGACAGTT	TTAATCCAAG	450
	AACTTATCAA	TAATATCGCT	CAAGAGCATG	GTGGTATTTT	AGTATTCGCC	500
	GGTGTGGTG	AACGTACACG	TGAAGGTAAC	GACCTTTACT	ATGAAATGAG	550
5	CGATAGTGGT	GTAATTAAGA	AAACAGCGAT	GGTATTCGGT	CAGATGAACG	600
	AGCCACCTGG	TGCTCGTATG	CGTGTTCAT	TATCAGGTTT	AACAATGGCA	650
	GAATATTTCC	GTGATGAAGA	AGGCCAAGAC	GTATTATTAT	TCATTGATAA	700
	TATCTTCAGA	TTCACACAAG	CTGGTTCTGA	AGTTTCAGCA	TTACTTGGAC	750
	GTATGCCTTC	AGCCGTTGGT	TATCAACCAA	CACTTGCTAC	TGAAATGGGT	800
10	CAATTACAAG	AACGTATTAG	TTCAACTAAT	AAAGGTTCTG	TTACTTCAA	849

2) INFORMATION FOR SEQ ID NO: 369

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus cohnii*
 (B) STRAIN: DSM 20260

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369

30	GAAGTTCCAG	AAATTAATAA	TGCCTTAGTT	CTCGATATAG	AAAGAGAAGA	50
	AGGTACTGTT	GAATTAACGT	TAGAAGTTGC	ATTACAACCTT	GGTGATGACG	100
	TAGTACGAAC	AATCGCAATG	GATTCAACTG	ATGGTGTTAA	ACGTGGTACA	150
	GAAGTTAGAG	ATAGCGGAAA	TAGTATCAGC	GTACCAGTTG	GTAATGAAAC	200
	ATTAGGTAGA	GTATTTAATG	TATTAGGTGA	TACGATAGAT	TTAGATGAAG	250
35	ACATAGATGA	CTCAGTGCCT	CGTGACCCAA	TTCATAGAGA	AGCACCTGCA	300
	TTTGATCAGT	TATCTACTAA	AGTTGAAATT	TTAGAAACAG	GTATCAAAGT	350
	CATTGATTTA	TTAGCACCAT	ATATCAAAGG	TGGTAAAGTT	GGATTATTCG	400
	GTGGTGCCGG	TGTTGGTAAA	ACTGTATTAA	TTCAAGAATT	AATCAATAAT	450
	ATCGCTCAAG	AGCATGGTGG	TATATCCGTA	TTTGCTGGTG	TAGGTGAGCG	500
40	TACGCGTGAA	GGTAATGACC	TATACTTTGA	AATGAGTGAT	AGTGGTGTTA	550
	TTAAAAAGAC	AGCTATGGTA	TTTGACAAA	TGAACGAACC	ACCTGGTGCG	600
	CGTATGCGAG	TAGCACTTTC	TGGTTTAACA	ATGGCTGAAT	ATTTCCGGGA	650
	TGAACAAGGA	CAAGATGTTC	TATTATTCAT	AGATAACATC	TTTAGATTTA	700
	CTCAAGCTGG	TTCAGAAGTT	TCTGCGTTAT	TAGGTCGTAT	GCCTTCAGCT	750
45	GTTGGTTACC	AACCAACGTT	AGCAACTGAA	ATGGGACAAT	TACAAGAACG	800
	TATTACTTCT	ACAACATAAG	GTTCAGTAAC			830

50 2) INFORMATION FOR SEQ ID NO: 370

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 787 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

60

(A) ORGANISM: *Staphylococcus epidermidis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370

```

5  AATAATGCAT TACACATCGA AGTTCCTAAA GAAGATGGAG CGCTTCAATT 50
   AACATTAGAA GTTGCACCTC AACTAGGTGA CGATGTAGTT CGTACAATTG 100
   CAATGGACTC AACTGACGGC GTTCAAAGAG GAATGGAAGT TAAAGATACA 150
   GGTAGAGACA TAAGTGTACC TGTCCGTGAC GTAACCTAG GAAGAGTGTT 200
   TAACGTACTA GGAGAACTA TTGACTTAGA TGAAAAAATT GATGATTCAG 250
10  TACGACGTGA CCCTATCCAT AGACAAGCTC CAGGATTCGA CGAATTATCA 300
   ACAAAGTAG AAATCTTAGA AACTGGTATT AAAGTAGTAG ACTTATTAGC 350
   ACCTTACATA AAAGGTGGTA AAATTGGATT ATTTGGTGGT GCCGGTGTAG 400
   GTAAAACCGT ACTAATCCAA GAACTTATTA ATAACATCGC TCAAGAACAC 450
   GGTGGTATCT CAGTATTCGC TGGTGTGGT GAACGTACAC GTGAAGGTAA 500
15  TGATCTTTAC TATGAAATGA GTGACAGTGG TGTATCAAG AAAACTGCAA 550
   TGGTCTTTGG TCAAATGAAT GAGCCACCTG GTGCACGTAT GCGTGTAGCA 600
   TTATCCGGAT TAACAATGGC CGAATATTTT CGAGATGAAG AAGGCCAAGA 650
   TGTGTTATTA TTCATTGATA ACATTTTCAG ATTCACTCAA GCTGGTTCAG 700
   AAGTTTCTGC GTTATTAGGT CGTATGCCAT CAGCTGTTGG TTATCAACCT 750
20  ACACTTGCTA CAGAAATGGG TCAATTACAA GAACGTA 787

```

2) INFORMATION FOR SEQ ID NO: 371

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

35

- (A) ORGANISM: *Staphylococcus haemolyticus*
- (B) STRAIN: ATCC 29970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371

```

40  GAAGTACCTG AAATTAATAA CGCCTTAATC ATCGAAGTTC CCAAAGAAGA 50
   TGGTACTTTT GAATTAACGC TTGAAGTTGC ATTACAATA GGTGATGACG 100
   TTGTTTCGTAC AATTGCTATG GATTCAACAG ATGGTGTTCA ACGTGGTATG 150
   GAAGTTCAGA AACTTGGAAA AGACATTTCA GTACCAGTTG GCGAAGTAAC 200
   TTTAGGACGT GTATTTAACG TATTAGGTGA CACAATTGAT TTAGAAGATA 250
45  AATTAGATGG TTCAGTAAGA CGTGATCCAA TTCATAGACA ATCACCTAAC 300
   TTTGACGAAT TATCTACTGA AGTAGAAATT CTTGAAACTG GAATCAAAGT 350
   TGTAGACTTA TTAGCACCAT ACATCAAAGG TGGTAAAATC GGTCTATTTG 400
   GTGGTGCCGG TGTGGTAAA ACCGTTTTAA TCCAAGAATT GATTAATAAT 450
   ATCGCACAAG AACATGGTGG TATCTCAGTA TTTGCTGGTG TAGGTGAACG 500
50  TACACGTGAA GGTAACGACC TATATTATGA AATGAGAGAT AGTGGTGTTA 550
   TTAAGAAAAC AGCAATGGTA TTTGGTCAAA TGAACGAGCC ACCTGGTGCA 600
   CGTATGCGTG TGGCACTTTC TGCATTGACA ATGGCTGAGT ATTTCCGTGA 650
   TGAACAAGGA CAAGACGTTT TGTATTTCAT CGATAACATT TTCAGATTTA 700
   CTCAAGCAGG TTCAGAAAGTA TCAGCATTAT TGGGACGTAT GCCTTCAGCT 750
55  GTAGGTTATC AACCTACTTT AGCTACAGAA ATGGGTCAAT TACAAGAACG 800
   TATTACATCA ACGAATAAAG GTTCAGTAAC 830

```

60 2) INFORMATION FOR SEQ ID NO: 372

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus hominis* subsp. *hominis*
 (B) STRAIN: ATCC 27844

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372

```

TCGAACATAA TGAAGTCCCT GAAATTAATA ATGCCCTAAT TATTGAAGTA      50
CCCAAAAATG ATGGCACATT TAAATTAACA TTAGAAGTTG CATTGCAACT      100
AGGTGATGAT GTTGTTTCGT CTATTGCAAT GGATTCAACT GATGGTGTTT      150
AACGTGGTAT GCAAGTTGTG AATACTGGTA AAGATATTAG TGTTCTGTGTA      200
GGTGAAGAAA CACTTGGACG TGTGTTTAAC GTTTTAGGAG AAACAATAGA      250
TTTAAACGAA AAAATAGATA GTTCTGTTAG ACGTGATCCA ATTCATCGTC      300
GTCAACCTAA TTTTGATGAA TTATCTACTG AAGTAGAAAT TCTTGAAACA      350
GGTATTAAAG TTGTAGACTT ATTAGCACCT TATATTAAAG GTGGTAAGAT      400
TGGTTTATTC GGTGGTGCCG GCGTAGGTAA AACTGTATTA ATTCAAGAAT      450
TAATCAATAA TATCGCTCAA GAACATGGTG GTATTTCTGT ATTCGCTGGT      500
GTAGGTGAAC GTACTCGTGA AGGTAACGAT TTATACTATG AAATGAGCGA      550
TAGTGGCGTT ATCAATAAAA CAGCCATGGT ATTTGGGCAA ATGAATGAGC      600
CGCCAGGTGC GCGTATGCGT GTTGCTTTAT CAGCATTGAC AATGGCTGAA      650
TATTTCCGTG ATGAACAAGG TCAAGATGTA CTTTTATTCA TTGACAATAT      700
TTTCCGCTTT ACTCAAGCTG GTTCTGAAGT TTCAGCATTG TTAGGACGTA      750
TGCCTTCAGC TGTAGGTTAT CAACCTACAT TAGCAACTGA AATGGGTCAA      800
TTACAAGAAC GTATTACATC TACTAATAAA GGTTTCAGTCA CTTCAA          846

```

2) INFORMATION FOR SEQ ID NO: 373

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus hominis*
 (B) STRAIN: CSG 175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373

```

TCGAACATAA TGAAGTCCCT GAAATTAATA ATGCCCTAAT TATTGAAGTA      50
CCCAAAAATG ATGGCACATT CAAATTAACA TTAGAAGTTG CATTGCAACT      100
AGGTGATGAT GTTGTTTCGT CTATTGCAAT GGATTCAACT GATGGTGTTT      150
AACGTGGTAT GCAAGTTGTG AATACTGGTA AAGATATTAG TGTTCTGTGTA      200
GGTGAAGAAA CACTTGGACG TGTGTTTAAC GTTTTAGGAG AAACAATAGA      250
TTTAAACGAA AAAATAGATA GTTCTGTTAG ACGTGATCCA ATTCATCGTC      300
GTCAACCTAA TTTTGATGAA TTATCTACTG AAGTAGAAAT TCTTGAAACA      350
GGTATTAAAG TTGTAGACTT ATTAGCACCT TATATTAAAG GTGGTAAGAT      400
TGGTTTATTC GGTGGTGCCG GCGTAGGTAA AACTGTATTA ATTCAAGAAT      450

```

	TAATCAATAA	TATCGCTCAA	GAACATGGTG	GTATTTCTGT	ATTCGCTGGT	500
	GTAGGTGAAC	GTA CTCTGTA	AGGTAACGAT	TTATACTATG	AAATGAGCGA	550
	TAGTGGCGTT	ATCAATAAAA	CAGCCATGGT	ATTTGGGCAA	ATGAATGAGC	600
	CGCCAGGTGC	GCGTATGCGT	GTTGCTTTAT	CAGCATTGAC	AATGGCTGAA	650
5	TATTTCCGTG	ATGAACAAGG	TCAAGATGTA	CTTTTATTCA	TTGACAATAT	700
	TTTCCGCTTT	ACTCAAGCTG	GTTCTGAAGT	TTCAGCATT	TTAGGACGTA	750
	TGCCTTCAGC	TGTAGGTTAT	CAACCTACAT	TAGCAACTGA	AATGGGTCAA	800
	TTACAAGAAC	GTATTACATC	TACTAATAAA	GGTTCAGTCA	CTTCAA	846

10

2) INFORMATION FOR SEQ ID NO: 374

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus lugdunensis*
 (B) STRAIN: ATCC 43809

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374

	ATAATGAAGT	GCCTGAAATA	AATAATGCGC	TCATTGTTGA	AATTCCTAAA	50
	AGTGATACAA	CAATCAGTTT	AACACTTGAA	GTTGCTTTGC	AATTAGGTGA	100
30	CGATGTTGTA	CGTACTATTG	CAATGGATTTC	AACTGATGGC	GTTCAACGTG	150
	GTATGGAAGT	TCAAAACACA	GGTAAAGACA	TCAGTGTACC	TGTTGGAGAT	200
	GAAACATTAG	GAAGAGTATT	TAACGTTTTTA	GGAGAATCTA	TTGATTTAGA	250
	AGAAAAGCTA	GATGACTCTG	TGCGTAGAGA	TCCAATTCAT	AGACTAGCAC	300
	CTAAATTTGA	TGAATTATCT	ACAGAAGTAG	AAATTCTTGA	AACTGGTATT	350
35	AAAGTTGTTG	ATTTATTAGC	ACCATATATT	AAAGGTGGTA	AAGTTGGATT	400
	GTTTGGTGGT	GCCGGAGTAG	GTAAAACGGT	ATTAATTCAA	GAATTAATCA	450
	ACAATATTGC	TCAAGAACAT	GGTGGTATTT	CTGTGTTTGC	CGGAGTAGGT	500
	GAACGTACAC	GTGAAGGTAA	TGACTTATAT	TATGAAATGA	GCGATAGTGG	550
	CGTAATTAAG	AAAACAGCGA	TGGTATTTGG	CCAAATGAAT	GAACCACCTG	600
40	GTGCACGTAT	GAGAGTTGCG	TTATCTGCCT	TAACAATGGC	TGAATATTTT	650
	CGTGACGAGC	AAGGACAAGA	CGTATTGCTG	TTTATCGATA	ATATATTCCG	700
	TTTTACACAA	GCAGGTTTCA	AAGTATCTGC	ATTACTTGGA	CGTATGCCAT	750
	CTGCCGTTGG	TTATCAACCA	ACATTGGCTA	CAGAAATGGG	ACAATTGCAA	800
	GAAAGAATTA	CATCTACAAA	TAAAGTTTCT	GTAAC		835

45

2) INFORMATION FOR SEQ ID NO: 375

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 842 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*
 (B) STRAIN: ATCC 15305

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375

```

5  GAGCACAATG AAGTTCCAGA AATTAACAAT GCCTTAGTCG TAGACGTTGA      50
   AAGAGATGAA GGTACAGTAT CTCTTACATT AGAAGTGGCA TTACAACTTG      100
   GCGATGATGT CGTACGTACA ATTGCAATGG ATTCTACTGA TGGTGTAAAA      150
   CGTGGTACAG AAGTTCGAGA TAGCGGAGAT AGCATCAGTG TTCCAGTTGG      200
   TGATGCTACG TTAGGACGTG TGTTTAATGT TCTTGGTGAT ACAATTGACT      250
   TAGACGAGAA GCTTGATACT TCTGTCAAAC GTGATCCAAT TCATAGAGAA      300
10  GCACCTGCAT TCGATCAATT ATCAACAAAA GTTGAAATCT TAGAAACAGG      350
   TATTAAAGTA ATTGATTTAC TTGCACCATA TATTAAAGGT GGTAATAATCG      400
   GTTTATTCCG TGGCGCTGGT GTAGGTAAAA CAGTATTAAT TCAAGAATTA      450
   ATTAATAATA TAGCTCAAGA ACATGGTGGT ATTTTCAGTAT TTGCCGGCGT      500
   AGGTGAACGT ACGCGTGAAG GTAATGACTT ATACTACGAA ATGAGTGATA      550
15  GTGGTGTTAT TAAGAAAACA GCTATGGTCT TCGGACAAAT GAATGAGCCA      600
   CCTGGTGCGC GTATGCGTGT TGCTTTATCA GGCTTAACAA TGGCTGAACA      650
   CTTCCGTGAT GTACAAGGAC AAGATGTTTT ACTATTTATT GATAACATAT      700
   TCAGATTTAC GCAAGCTGGT TCAGAAAGTAT CAGCACTATT AGGTCGTATG      750
   CCATCAGCCG TTGGTTATCA ACCTACCCTT GCTACTGAAA TGGGTCAATT      800
20  ACAAGAACGT ATTACATCAA CAACTAAAGG ATCTGTAACG TC              842

```

2) INFORMATION FOR SEQ ID NO: 376

25

(i) SEQUENCE CHARACTERISTICS:

```

   (A) LENGTH: 842 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
30  (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

```

35  (A) ORGANISM: Staphylococcus simulans
   (B) STRAIN: ATCC 27848

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376

```

40  TGATGAACTG CCTAAGATTA ATAACGCATT AGTGCTAGAT GTACCTAAGA      50
   AAGATGGCAC GACTGAATCT CTTACATTAG AAGTAGCACT TGAATTAGGC      100
   GACGACGTAG TTAGAACTAT CGCCATGGAC TCTACAGACG GAATTAAACG      150
   TGGTGACGAC GTTAAAGACA CTGGTCGTCC AATCAGTGTA CCTGTCGGTG      200
   AAGATACGTT AGGAAGAGTA TTTAACGTTT TAGGTGATCC AATCGATAAT      250
45  GATGGACCGA TTTCTGAATC AGTTCCACGT GAACCAATTC ATAGACAACC      300
   ACCTAAATTT GATGAATTAT CAACAAAAGT TGAAC TACTT GAAACTGGTA      350
   TCAAAGTAGT AGACTTATTA GCACCATATA TCAAAGGTGG TAAAGTTGGT      400
   TTATTCGGTG GTGCCGGAGT AGGTAAAAC TATTTAATCC AAGAATTAAT      450
   TAATAACATC GCTCAAGAAC ACGGCGGTAT TTCAGTATTC GCAGGTGTTG      500
50  GTGAACGTAC ACGTGAAGGT AACGACTTGT ACTTCGAAAT GAGCGACAGT      550
   GGTGTTATCA AGAAAACAGC GATGGTATTC GGACAAATGA ACGAACCACC      600
   TGGTGACGCT ATGCGTGTAG CTTTATCAGG TTTAACAATG GCTGAATACT      650
   TCCGTGATGT TAAAGGACAA GACGTTCTTT TATTCATCGA TAACATTTTC      700
   CGCTTCACAC AAGCAGGTTT TGAGGTATCA GCATTGCTTG GCCGTATGCC      750
55  ATCAGCCGTT GGTACCAAC CAACATTGGC AACAGAAATG GGTCAATTAC      800
   AAGAACGTAT CACTTCTACA ATGAAAGGTT CTATCACATC TA              842

```

60 2) INFORMATION FOR SEQ ID NO: 377

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 841 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus warneri*
 (B) STRAIN: ATCC 27836

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377

```

15  CATAACGAAG TCCCTGATAT TAATAATGCC CTTATTATTG AAGTTCCAAA      50
    AGAAGATGGA ACGTTAAACT TAACATTAGA AGTTGCACTA CAATTAGGTG      100
    ATGATGTTGT ACGTACAATT GCAATGGATT CAACTGATGG TGTTCAAAGA      150
    GGCATGGATG TTAAAGACAC AGGTAAAGAT ATTAGTGTAC CTGTAGGCGA      200
20  TGAAACGCTT GGAAGAGTGT TTAATGTACT AGGTGAAACA ATTGACTTGG      250
    AAGAGAAAAT TGATGATTCC GTACGTCGTG ATCCAATCCA TAGACAATCA      300
    CCAGGTTTCG ATGAATTATC TACTGAAGTA GAAATCTTAG AAACAGGTAT      350
    TAAAGTAGTA GACTTATTAG CACCTTACAT TAAAGGTGGT AAAGTTGGAC      400
    TATTCGGTGG TGCCGGAGTA GGTAAAACCG TTTTAATCCA AGAATTAATT      450
25  AACAAATATT CACAAGAACA TGGTGGTATT TCAGTATTCT CGGGTGTAGG      500
    TGAACGTACT CGTGAAGGTA ATGATTTATA CTATGAAATG AGTGATAGTG      550
    GTGTAATTAA GAAAACAGCG ATGGTATTTG GACAAATGAA TGAACCACCT      600
    GGCGCACGTA TGCCTGTAGC TTTATCTGGT TTAACATGG CTGAATACTT      650
    CCGTGATGAA CAAGGACAAG ACGTACTTTT ATTCATCGAT AATATTTTCA      700
30  GATTTACACA AGCTGGTTCT GAAGTTTCTG CATTACTTGG TCGTATGCCT      750
    TCAGCCGTTG GTTACCAACC AACATTAGCA ACTGAAATGG GTCAATTACA      800
    AGAACGAATT ACATCTACAA ATAAAGGTTC TGTAACATCT A              841
  
```

2) INFORMATION FOR SEQ ID NO: 378

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus acidominimus*
 (B) STRAIN: ATCC 51726

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378

```

55  TTTAACACGA ATGAACCGCT TCCTGAGATA AATAATGCAC TTGTTGTTTA      50
    CAAAGACAGT GAGAAAAAAC ATAAAATCGT TCTTGAAGTA GCTCTTGAAC      100
    TTGGTGAAGG CCTCGTTCGT ACCATTGCTA TGGAATCAAC TGATGGTTTG      150
    ACACGTGGTC TAGAAGTTCT TGATACAGGC CGTGCAATCA GTGTACCAGT      200
    TGGTAAAGAA ACGCTTGGAC GTGTCTTCAA CGTTCTTGGT GATGCTATCG      250
    ATCTTGAAGA ACCATTTGGA GAAGATGCAG AACGTCACCC CATTCATAAG      300
    AGTGCCCCAA CTTTTGATGA ATTATCAACG TCAACAGAAA TCCTTGAAAC      350
    AGGGATTAAA GTTATCGACC TACTTGCCCC TTACTTAAAA GGAGGGAAGG      400
60  TTGGACTTTT CGGTGGTGCC GGAGTTGGTA AGACCGTTCT TATCCAAGAG      450
  
```

```

TTGATTCATA ACATTGCTCA AGAGCATGGT GGTATTTTCAG TATTTACCGG      500
AGTTGGTGAA CGTACACGTG AAGGTAATGA CCTCTATTGG GAAATGAAAG      550
AATCAGGCGT TATTGAAAAA ACAGCTATGG TATTTGGTCA GATGAATGAG      600
CCACCTGGTG CACGTATGCG TGTAGCCCTT ACTGGTTTGA CAATCGCTGA      650
5 ATATTTCCGT GATGTTGAAG GACAGGACGT GCTTCTCTTT ATTGATAACA      700
TTTTTCGTTT CACACAAGCA GGTTCCTGAAG TTTCAGCTCT TCTTGGACGT      750
ATGCCATCAG CCGTTGGTTA TCAACCAACC TTGGCAACTG AAATGGGTCA      800
ATTGCAAGAA CGTATCACGT CAACTAAAAA AGGTTCTGTT ACATCA          846

```

10

2) INFORMATION FOR SEQ ID NO: 379

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 846 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*
 (B) STRAIN: ATCC 12403

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379

```

TTGCAAGTGG CGACAAACTT CCTGAGATTA ATAATGCATT GATTGTCTAT      50
AAAAATGGCG ATAAGTCACA AAAAGTAGTA CTTGAAGTTA CTCTTGAAC      100
30 TGGTGACGGC CTCGTTCTGTA CAATCGCTAT GGAATCAACT GATGGGCTTA      150
CACGTGGTTT GGAAGTATTA GATACTGGTC GCGCAATTAG TGTGCCGGTT      200
GGTAAGGATA CTTTGGGTCG TGTCTTCAAC GTTCTTGAGG ATGCTATTGA      250
CCTTGAAGAG CCTTTTGCAG AAGATGCAGA ACGTCAACCA ATCCATAAAA      300
AAGCACCATC GTTTGATGAA TTATCAACAT CATCAGAAAT CTTAGAAACA      350
35 GGTATTAAAG TTATTGACTT ATTAGCACCT TACTTAAAAG GTGGTAAAGT      400
TGGACTTTTC GGTGGTGCGA GTGTTGGTAA AACCGTTCTT ATTCAAGAAT      450
TAATCCACAA CATCGCCCAA GAACATGGTG GTATTTTCAGT ATTTACTGGT      500
GTAGGAGAAC GTACTCGTGA AGGGAATGAC CTTTATTGGG AAATGAAAGA      550
ATCTGGCGTT ATTGAAAAAA CGGCTATGGT CTTTGGTCAA ATGAATGAAC      600
40 CACCAGGAGC ACGTATGCGT GTGGCACTTA CTGGTCTTAC AATAGCTGAG      650
TACTTCCGTG ATGTAGAAGG ACAAGATGTG CTTCTCTTCA TTGATAATAT      700
CTTCCGTTTC ACACAAGCTG GGTCAAGAAG GTCAGCGCTT TTAGGTCGTA      750
TGCCTTCAGC CGTTGGTTAT CAACCAACAC TTGCTACAGA AATGGGACAA      800
TTACAAGAGC GTATCACTTC AACTAAAAAA GGTTCCTGTT CCTCAA          846

```

45

2) INFORMATION FOR SEQ ID NO: 380

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 846 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*
 (B) STRAIN: ATCC 13813

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380

	TTGCAAGTGG	CGACAAACTT	CCTGAGATTA	ATAATGCATT	GATTGTCTAT	50
5	AAAAATGGCG	ATAAGTCACA	AAAAGTAGTA	CTTGAAGTTG	CTCTTGAACT	100
	TGGTGACGGC	CTCGTTCGTA	CAATCGCTAT	GGAATCAACT	GATGGGCTTA	150
	CACGTGGTTT	GGAAGTATTA	GATACTGGTC	GCGCAATTAG	TGTGCCGGTT	200
	GGTAAGGATA	CTTTGGGTCG	TGTCTTCAAC	GTTCTTGGAG	ATGCTATTGA	250
	TCTTGAAGAG	CCTTTTGCAG	AAGATGCAGA	ACGTCAACCA	ATCCATAAAA	300
10	AAGCACCATC	GTTTGATGAA	TTATCAACAT	CATCAGAAAT	CTTAGAAACT	350
	GGTATTAAAG	TTATTGACTT	ATTAGCACCT	TACTTAAAAG	GTGGTAAAGT	400
	TGGACTTTTC	GGTGGTGCGG	GTGTTGGTAA	AACCGTTCTT	ATTCAAGAAT	450
	TAATCCACAA	CATCGCCCAA	GAACATGGTG	GTATTTTCAGT	ATTTACTGGT	500
	GTAGGAGAAC	GTACTCGTGA	AGGGAATGAC	CTTTATTGGG	AAATGAAAGA	550
15	ATCTGGCGTT	ATTGAAAAAA	CGGCTATGGT	CTTTGGTCAA	ATGAATGAAC	600
	CACCAGGAGC	ACGTATGCGT	GTGGCACTTA	CTGGTCTTAC	AATAGCTGAG	650
	TACTTCCGTG	ATGTAGAAGG	ACAAGATGTG	CTTCTCTTCA	TTGATAATAT	700
	CTTCCGTTTC	ACACAAGCTG	GGTCAGAAGT	GTCAGCGCTT	TTAGGTCGTA	750
	TGCCTTCAGC	CGTTGGTTAT	CAACCAACAC	TTGCTACAGA	AATGGGACAA	800
20	TTACAAGAGC	GTATCACTTC	AACTAAAAAA	GGTTCTGTTA	CCTCAA	846

2) INFORMATION FOR SEQ ID NO: 381

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 845 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

35

- (A) ORGANISM: *Streptococcus agalactiae*
 (B) STRAIN: ATCC 12973

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381

40	TTGCAAGTGG	CGACAAACTT	CCTGAGATTA	ATAATGCATT	GATTGTCTAT	50
	AAAAATGGCG	ATAAGTCACA	AAAAGTAGTA	CTTGAAGTTG	CTCTTGAACT	100
	TGGTGACGGC	CTCGTTCGTA	CAATCGCTAT	GGAATCAACT	GATGGGCTTA	150
	CACGTGGTTT	GGAAGTATTA	GATACTGGTC	GTGCAATTAG	TGTGCCGGTT	200
	GGTAAGGATA	CTTTGGGTCG	TGTCTTCAAC	GTTCTTGGAG	ATGCTATTGA	250
45	CCTTGAAGAG	CCTTTTGCAG	AAGATGCAGA	ACGTCAACCA	ATCCATAAAA	300
	AAGCACCATC	ATTTGATGAA	TTATCAACAT	CATCAGAAAT	CTTAGAAACA	350
	GGTATTAAAG	TTATTGACTT	ATTAGCACCT	TACTTAAAAG	GTGGTAAAGT	400
	TGGACTTTTC	GGTGGTGCGG	GTGTTGGTAA	AACCGTTCTT	ATTCAAGAAT	450
	TAATCCACAA	CATCGCCCAA	GAACATGGTG	GTATTTTCAGT	ATTTACTGGT	500
50	GTAGGAGAAC	GTACTCGTGA	AGGGAATGAC	CTTTATTGGG	AAATGAAAGA	550
	ATCTGGCGTT	ATTGAAAAAA	CGGCTATGGT	CTTTGGTCAA	ATGAATGAAC	600
	CACCAGGAGC	ACGTATGCGT	GTGGCACTTA	CTGGTCTTAC	AATAGCTGAG	650
	TACTTCCGTG	ATGTAGAAGG	ACAAGATGTG	CTTCTCTTCA	TTGATAATAT	700
	CTTCCGTTTC	ACACAAGCTG	GGTCAGAAGT	GTCAGCGCTT	TTAGGTCGTA	750
55	TGCCTTCAGC	CGTTGGTTAT	CAACCAACAC	TTGCTACAGA	AATGGGACAA	800
	TTACAAGAGC	GTATCACTTC	AACTAAAAAA	GGTTCTGTTA	CCTCA	845

60 2) INFORMATION FOR SEQ ID NO: 382

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 845 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*
 (B) STRAIN: ATCC 27591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382

```

15 TTGCAAGTGG CGACAAACTT CCTGAGATTA ATAATGCATT GATTGTCTAT      50
   AAAAATGGCG ATAAGTCACA AAAAGTAGTA CTTGAAGTTG CTCTTGAACT      100
   TGGTGACGGC CTCGTTTCGTA CAATCGCTAT GGAATCAACT GATGGGCTTA      150
   CACGTGGTTT GGAAGTATTA GATACTGGTC GCGCAATTAG TGTGCCGGTT      200
20 GGTAAGGATA CTTTGGGTCG TGTCTTCAAC GTTCTTGGAG ATGCTATTGA      250
   CCTTGAAGAG CCTTTTGCAG AAGATGCAGA ACGTCAACCA ATCCATAAAA      300
   AAGCACCATC GTTTGATGAA TTATCAACAT CATCAGAAAT CTTAGAAACT      350
   GGTATTAAAG TTATTGACTT ATTAGCACCT TACTTAAAAG GTGGTAAAGT      400
   TGGACTTTTC GGTGGTGCAG GTGTTGGTAA AACCGTTCTT ATTCAAGAAT      450
25 TAATCCACAA CATCGCCCAA GAACATGGTG GTATTTCAGT ATTTACTGGT      500
   GTAGGAGAAC GTACTCGTGA AGGGAATGAC CTTTATTGGG AAATGAAAGA      550
   ATCTGGCGTT ATTGAAAAAA CGGCTATGGT CTTTGGTCAA ATGAATGAAC      600
   CACCAGGAGC ACGTATGCGT GTGGCACTTA CTGGTCTTAC AATAGCTGAG      650
   TACTTCCGTG ATGTAGAAGG ACAAGATGTG CTTCTCTTCA TTGATAATAT      700
30 CTTCCGTTTC ACACAAGCTG GGTGAGAAGT GTCAGCGCTT TTAGGTCGTA      750
   TGCCTTCAGC CGTTGGTTAT CAACCAACAC TTGCTACAGA AATGGGACAA      800
   TTACAAGAGC GTATCACTTC AACTAAAAAA GGTTCGTGTA CATCA          845

```

2) INFORMATION FOR SEQ ID NO: 383

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 845 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*
 (B) STRAIN: CDC ss1073

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383

```

55 TTGCAAGTGG CGACAAACTT CCTGAGATTA ATAATGCATT GATTGTCTAT      50
   AAAAATGGCG ATAAGTCACA AAAAGTAGTA CTTGAAGTTG CTCTTGAACT      100
   TGGTGACGGC CTCGTTTCGTA CAATCGCTAT GGAATCAACT GATGGGCTTA      150
   CACGTGGTTT GGAAGTATTA GATACTGGTC GCGCAATTAG TGTGCCGGTT      200
   GGTAAGGATA CTTTGGGTCG TGTCTTCAAC GTTCTTGGAG ATGCTATTGA      250
   CCTTGAAGAG CCTTTTGCAG AAGATGCAGA ACGTCAACCA ATCCATAAAA      300
   AAGCACCATC GTTTGATGAA TTATCAACAT CATCAGAAAT CTTAGAAACT      350
   GGTATTAAAG TTATTGACTT ATTAGCACCT TACTTAAAAG GTGGTAAAGT      400
60 TGGACTTTTC GGTGGTGCAG GTGTTGGTAA AACCGTTCTT ATTCAAGAAT      450

```



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5  TAATCCACAA CATCGCCCAA GAACATGGTG GTATTTTCAGT ATTTACTGGT 500
   GTAGGAGAAC GTACTCGTGA AGGGAATGAC CTTTATTGGG AAATGAAAGA 550
   ATCTGGCGTT ATTGAAAAAA CGGCTATGGT CTTTGGTCAA ATGAATGAAC 600
   CACCAGGAGC ACGTATGCGT GTGGCACTTA CTGGTCTTAC AATAGCTGAG 650
   TACTTCCGTG ATGTAGAAGG ACAAGATGTG CTTCTCTTCA TTGATAATAT 700
   CTTCCGTTTC ACACAAGCTG GGTGAGAAGT GTCAGCGCTT TTAGGTCGTA 750
   TGCCTTCAGC CGTTGGTTAT CAACCAACAC TTGCTACAGA AATGGGACAA 800
   TTACAAGAGC GTATCACTTC AACTAAAAAA GGTCTGTGTA CATCA 845

```

10

2) INFORMATION FOR SEQ ID NO: 384

(i) SEQUENCE CHARACTERISTICS:

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15  (A) LENGTH: 845 bases
     (B) TYPE: Nucleic acid
     (C) STRANDEDNESS: Double
     (D) TOPOLOGY: Linear

```

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

```

     (A) ORGANISM: Streptococcus dysgalactiae
     (B) STRAIN: ATCC 43078

```

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384

```

30  TTGCTAGTGG GGACAAACTT CCAGAGATTA ATAATGCATT GATTGTTTAT 50
   AAAGATAGTG ATAAAAAGCA AAAAATCGTC CTTGAAGTTG CTCTGGAACT 100
   TGGTGACGGT ATGGTGCGAA CAATCGCTAT GGAATCAACT GATGGGCTTA 150
   CACGTGGGTT AGAAGTTCTT GACACTGGTC GTGCGATTAG TGTACCAGTA 200
   GGTAAGAGAA CTTTGGGACG CGTCTTTAAT GTACTTGGAG AAACCATTGA 250
   CTTGGAAGAA CCATTTGCAG AAGACGTTGA CCGTCAGCCA ATCCATAAAA 300
   AAGCACCATC GTTTGATGAA TTATCAACAT CATCAGAAAT TCTTGAAACT 350
   GGTATCAAGG TAATTGACCT TCTTGCCCCT TACCTTAAAG GTGGTAAAGT 400
   TGGACTTTTC GGGGGTGCCG GAGTTGGTAA GACTGTCCTT ATCCAAGAAT 450
   TAATCCACAA TATCGCCCAA GAACACGGAG GTATTTTCAGT ATTTACCGGT 500
   GTTGGTGAGC GAACACGTGA AGGAAATGAC CTTTACTGGG AAATGAAAGA 550
   ATCAGGCGTT ATTGAGAAAA CTGCCATGGT TTTTGGTCAG ATGAATGAGC 600
   CGCCTGGGGC ACGTATGCGT GTAGCCCTTA CTGGTTTAAC CATTGCTGAG 650
   TATTTCCGTG ATGTAGAAGG CCAAGATGTT TTGCTCTTTA TTGATAATAT 700
   CTTCCGTTTC ACTCAGGCAG GTTCAGAAGT ATCAGCCCTC TTAGGCCGTA 750
   TGCCTTCTGC TGTTGGTTAC CAACCGACCC TTGCTACTGA AATGGGACAA 800
   TTGCAAGAAC GTATTACGTC AACTCAAAAA GGATCTGTGA CTTCT 845

```

45

2) INFORMATION FOR SEQ ID NO: 385

(i) SEQUENCE CHARACTERISTICS:

```

50  (A) LENGTH: 846 bases
     (B) TYPE: Nucleic acid
     (C) STRANDEDNESS: Double
     (D) TOPOLOGY: Linear

```

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

```

60  (A) ORGANISM: Streptococcus equi subsp. equi
     (B) STRAIN: ATCC 9528

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385

	TTGCGAGTGG	GGACAAACTA	CCAGAGATTA	ATAATGCGTT	GATAGTTTAT	50
5	AAAGATGGCG	ATAAAAAGCA	AAAAATCGTT	CTCGAGGTTG	CCCTAGAGCT	100
	TGGAGACGGT	ATGGTACGTA	CAATTGCTAT	GGAATCAACC	GATGGGCTTA	150
	CACGTGGATT	AGAGGTTCTT	GATACTGGTC	GTGCCATTAG	TGTACCAGTT	200
	GGTAAAGAGA	CTCTAGGTCG	TGTTTTCAAC	GTTCTTGGTG	AAACCATCGA	250
	CCTAGAAGCA	CCATTTGCAG	ATGATGTTAA	TCGTGAACCG	ATCCATAAAA	300
10	AAGCACCAGC	CTTTGATGAA	TTGTCAACAT	CATCAGAAAT	TCTTGAAACA	350
	GGTATCAAGG	TTATTGACCT	GCTTGCCCCCT	TACTTAAAGG	GTGGTAAGGT	400
	CGGTCTTTTC	GGTGGTGCCG	GAGTTGGTAA	AACCGTTCTT	ATCCAAGAAT	450
	TAATCCACAA	TATCGCTCAA	GAGCATGGTG	GGATCTCGGT	ATTTACCGGT	500
	GTTGGTGAGC	GTACGCGTGA	AGGAAATGAC	CTTTACTGGG	AAATGAAGGA	550
15	ATCAGGCGTT	ATTGAAAAAA	CAGCCATGGT	TTTTGGTCAG	ATGAATGAAC	600
	CACCAGGAGC	CCGTATGCGT	GTTGCCTTGA	CCGGCTTGAC	AATTGCTGAA	650
	TATTTCCGCG	ATGTTGAAGG	CCAAGACGTC	CTGCTCTTCA	TTGACAATAT	700
	TTTCCGCTTT	ACTCAAGCAG	GCTCAGAGGT	ATCAGCCCTT	CTAGGTCGTA	750
	TGCCTTCAGC	CGTTGGTTAC	CAGCCAACAC	TTGCCACTGA	AATGGGACAA	800
20	TTGCAAGAGC	GTATCACCTC	AACGAAAAAA	GGCTCTGTTA	CCTCTA	846

2) INFORMATION FOR SEQ ID NO: 386

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus anginosus*
- (B) STRAIN: ATCC 27335

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386

40	TTGCAGCTGG	TGATAAATTA	CCTGAGATAA	ATAATGCACT	TGTAGTCTAT	50
	AAAAATGACG	AAAATAAATC	AAAAATCGTC	CTTGAAGTAG	CTCTTGAGCT	100
	TGGTGATGGA	GTGGTTCGAA	CTATTGCCAT	GGAATCCACT	GATGGGTTGA	150
	CTCGTGGCAT	GGAAGTTCTA	GATACTGGTC	GACCAATTTC	TGTTCCAGTT	200
	GGGAAAGAAA	CACTTGGTGCG	CGTCTTTAAC	GTTTTAGGCG	ATACCATTGA	250
45	TTTGGATACT	CCATTGCGCG	AAGATGCAGA	ACGTCAACCA	ATCCATAAAA	300
	AAGCTCCAAC	TTTTGATGAG	TTATCTACTT	CATCAGAAAT	CTTAGAAACA	350
	GGAATAAAGG	TTATTGACCT	TTTAGCCCCC	TACCTCAAAG	GTGGGAAAGT	400
	CGGCCTCTTC	GGTGGTGCTG	GCGTTGGGAA	AACTGTCTTG	ATTCAAGAGT	450
	TGATTCATAA	TATCGCCCAA	GAACACGGCG	GGATTTTCAGT	CTTTACTGGT	500
50	GTTGGGGAAC	GAATCTCGTGA	AGGGAATGAC	CTGTACTGGG	AAATGAAAGA	550
	ATCTGGTGTT	ATCGAAAAGA	CGGCTATGGT	CTTTGGGCAA	ATGAATGAAC	600
	CGCCTGGAGC	ACGTATGCGT	GTAGCTTTGA	CTGGGTTAAC	GATTGCAGAG	650
	TATTTCCGTG	ATGTGGAAGG	TCAAGATGTT	CTTTTGTTTA	TTGATAATAT	700
	TTTCCGTTTC	ACTCAAGCTG	GTTCTGAAGT	GTCAGCCCTT	CTTGGTCGTA	750
55	TGCCATCAGC	TGTTGGTTAC	CAACCAACCT	TGGCTACTGA	AATGGGGCAA	800
	TTACAAGAAC	GTATTACATC	AACGAAAAAA	GGTTCTGTTA	CCTCAA	846

60 2) INFORMATION FOR SEQ ID NO: 387

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 843 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus salivarius*
 (B) STRAIN: ATCC 7073

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387

```

15 GCAGCTGGTG ATAAACTTCC TGAGATTAAC AATGCATTGG TCGTTTATAC      50
   TGATGAACAA AAGTCTAAAC GTATCGTGCT CGAAGTAGCT CTTGAACTTG      100
   GAGAAGGTGT GGTTCTGTACC ATTGCCATGG AATCTACTGA TGGATTGACT      150
   CGTGGACTAG AAGTTCTGGA CACTGGTCGT CCAATCAGCG TTCCTGTTGG      200
20 TAAAGATACC CTTGGACGTG TCTTTAACGT TCTTGGTGAT ACCATTGACT      250
   TGGAAGCACCC TTTTGCAGAC GATGCAGAGC GTGAACCAAT TCACAAAAAA      300
   GCACCAACTT TCGATGAATT GTCAACATCT ACTGAAATCC TTGAAACAGG      350
   GATTAAAGTT ATCGACTTGC TAGCCCCTTA CCTTAAGGGT GGTAAGTCG      400
   GACTCTTCGG TGGTGCCGGT GTTGGTAAAA CCGTTCCTTAT TCAAGAGTTG      450
25 ATTCACAACA TTGCCAAGA GCACGGTGGT ATTTCCTGTG TTACAGGTGT      500
   TGGTGAACGT ACACGTGAAG GTAATGACCT TTACTGGGAA ATGAAAGAAT      550
   CTGGCGTTAT CGAGAAAACA GCCATGGTCT TCGGTCAAAT GAACGAACCA      600
   CCTGGAGCAC GTATGCGTGT TGCCCTTACT GGTTCGACAA TTGCGGAATA      650
   CTTCCGTGAT GTCGAGGGTC AAGACGTTCT TCTCTTCATC GATAACATCT      700
30 TCCGTTTCAC TCAAGCAGGT TCTGAGGTTT CTGCCCTTCT TGGTCGTATG      750
   CCATCAGCCG TTGGTTACCA ACCTACACTT GCTACTGAAA TGGGTCAATT      800
   GCAAGAACGT ATCACATCAA CTAAAAAAGG TTCTGTTACA TCT              843

```

2) INFORMATION FOR SEQ ID NO: 388

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 841 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus suis*
 (B) STRAIN: ATCC 43765

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388

```

   TTGCAGCAGA AGATAAACTT CCTGAGATTA ACAACGCACT CGTTGTATAT      50
   AAAAATGATG ATTCCAAACA AAAAGTCGTG CTTGAAGTGG CTTTGGAAC      100
   TGGTGATGGC GTTGACGGA CCATTGCCAT GGAATCAACG GATGGATTGA      150
55 CACGTGGGAT GGAAGTTCTC GATACAGGTC GTCCCATCTC TGTTCAGTC      200
   GGTAAGAAA CGCTGGGTCG TGTCTTCAAT GTGTTGGGAG ATACCATTGA      250
   CTTGAAGAG TCTTTCCGG CAGATTTTGA ACGTGAGCCT ATCCATAAGA      300
   AAGCGCCGGC TTTTGACGAA TTATCTACTT CAAGCGAAAT TTTGGAAACA      350
   GGGATTAAGG TTATCGACCT CCTAGCACCT TATCTAAAAG GTGGTAAGGT      400
60 TGGTCTCTTC GGTGGTGCTG GTGTTGGTAA AACCGTTCTT ATCCAAGAAT      450

```

	500
	550
	600
	650
5	700
	750
	800
	841

10

2) INFORMATION FOR SEQ ID NO: 389

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 844 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus uberis*
 (B) STRAIN: ATCC 19436

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389

	50
	100
30	150
	200
	250
	300
	350
35	400
	450
	500
	550
	600
40	650
	700
	750
	800
45	844

2) INFORMATION FOR SEQ ID NO: 390

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 896 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tatumella ptyseos*
 (B) STRAIN: ATCC 33301

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390

	TTCCCTCAGG	ACGCTGTACC	ACAGGTGTAC	AACGCTCTTG	AGGTTGAAAA	50
5	TGGTGATACC	CGTCTGGTGC	TGGAAGTTCA	GCAGCAGCTG	GGCGGTGGTG	100
	TCGTTCGTAC	GATTGCAATG	GGAACCTCTG	ACGGCCTGAA	ACGTGGCCTT	150
	AAGGTGACCG	ATCTGCAAAA	ACCGATTTCAG	GTACCGGTCTG	GTAAAGCGAC	200
	GCTGGGCCGT	ATCATGAACG	TACTGGGTCA	GCCAATCGAT	ATGAAAGGCG	250
	ACCTGAAGAA	CGAAGATGGT	AGCAATGTTG	AGGTGAACTC	TATTCACCGT	300
10	GCAGCGCCAA	GCTACGAAGA	ACTGGCTAAC	TCTACTGAGC	TGCTGGAAAC	350
	GGGTATCAAG	GTTATCGACC	TGATCTGTCC	GTTTGCAAAA	GGCGGTAAAG	400
	TGGGTCTGTT	CGGTGGTGCG	GGTGTAGGTA	AGACCGTCAA	CATGATGGAA	450
	CTGATCCGTA	ACATCGCTAT	CGAGCACTCT	GGTTACTCTG	TATTTGCAGG	500
	GGTGGGTGAG	CGTACCCGTG	AAGGTAACGA	CTTCTACCAC	GAAATGACCG	550
15	AGTCTAACGT	TCTGGATAAA	GTTGCTCTGG	TTTATGGCCA	GATGAACGAG	600
	CCACCAGGAA	ACCGTCTGCG	CGTTGCGCTG	ACCGGTCTGA	CTATGGCTGA	650
	AAAATTCCGT	GACGAAGGCC	GTGACGTACT	GCTGTTCGTT	GATAACATCT	700
	ATCGTTATAC	CCTGGCCGGT	ACTGAAGTTT	CAGCACTGCT	GGGTCGTATG	750
	CCTTCTGCGG	TAGGTTATCA	GCCAACTACTG	GCCGAAGAAA	TGGGTGTTCT	800
20	TCAGGAACGT	ATCACGTCAA	CCAAAACCGG	TTCAATCACT	TCCGTA	896

2) INFORMATION FOR SEQ ID NO: 391

25

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 829 bases
	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
30	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

35	(A)	ORGANISM: <i>Trabulsiella guamensis</i>
	(B)	STRAIN: ATCC 49490

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391

40	TTCCCTCAGG	ATGCCGTACC	GCGCGTGTAC	GATGCTCTTG	AGGTTATGAA	50
	TGGTAGTGAG	CGTCTGGTGC	TGGAAGTTCA	GCAGCAGCTC	GGTGGTGGTA	100
	TCGTACGTAC	TATCGCCATG	GGTTCTTCCG	ACGGTCTGCG	TCGTGGTCTG	150
	GATGTAAAAG	ATCTCGAGCA	TCCGATCGAA	GTCCCAGTAG	GTAAAGCAAC	200
	GCTGGGTCGT	ATCATGAACG	TGCTGGGTCA	GCCGATCGAT	ATGAAAGGCG	250
45	ACATCGGCGA	AGAAGAGCGT	TGGGCTATCC	ACCGCGCAGC	ACCGTCCTAC	300
	GAAGAGCTGT	CCAGCTCTCA	GGAAGTCTG	GAAACCGGCA	TCAAAGTTAT	350
	CGACCTGATG	TGTCCGTTTC	CGAAGGGCGG	TAAAGTCGGT	CTGTTCCGGT	400
	GTGCGGGTGT	AGGTAAAACC	GTAAACATGA	TGGAGCTGAT	TCGTAACATC	450
	GCGATCGAGC	ACTCCGGTTA	CTCTGTGTTT	GCGGGCGTGG	GTGAACGTAC	500
50	TCGTGAGGGT	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTTCTGG	550
	ACAAAGTATC	CCTGGTGTAT	GGACAGATGA	ACGAGCCGCC	GGGAAACCGT	600
	CTGCGCGTTG	CACTGACCGG	TCTGACCATG	GCTGAGAAGT	TCCGTGACGA	650
	AGGTCGTGAC	GTTCTGCTGT	TCGTGATAAA	CATCTACCGT	TACACCCTGG	700
	CGGGTACTGA	AGTATCTGCA	CTGCTGGGCC	GTATGCCTTC	AGCGGTAGGT	750
55	TACCAGCCGA	CCCTGGCGGA	AGAGATGGGT	GTTCTTCAGG	AACGTATCAC	800
	CTCAACCAAA	ACCGTTTCTA	TCACCTCCG			829

60 2) INFORMATION FOR SEQ ID NO: 392

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia bercovieri*
 (B) STRAIN: ATCC 43970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392

```

15  CGAATTCCCC CAAGACGCTG TACCAAAAGT GTACAACGCC CTTGAGGTTG      50
    AAGGCACAGC TCAGAAAGCTG GTGCTGGAAG TTCAGCAACA GCTGGGCGGT      100
    GGTGTTGTTC GTTGATATCGC AATGGGCTCT TCCGATGGTC TGAGCCGCGG      150
    GTTGAAAGTC ATCAACCTGG AACACCCAAT TGAAGTGCCG GTGGGTAAAT      200
20  CAACTCTGGG CCGTATCATG AACGTATTGG GTGACCCAAT CGACATGAAA      250
    GGTCCATATCG GTGAAGAAGA GCGTTGGGCA ATCCACCGCG AAGCGCCTTC      300
    TTACGAAGAG CTTGCCAGCT CGCAAGATCT GTTAGAAACC GGTATCAAGG      350
    TAATGGATCT GATTTGTCCG TTCGCTAAGG GCGGTAAAGT CGGTCTGTTC      400
    GGTGGTGCGG GTGTGGGTAA AACAGTCAAC ATGATGGAGC TGATTCGTAA      450
25  TATTGCGATT GAGCACTCAG GTTATTCTGT ATTTGCCGGT GTGGGTGAGC      500
    GTACTCGTGA GGGTAACGAC TTCTACCACG AGATGACTGA CTCCAACGTT      550
    CTGGACAAAG TATCCTTGGT TTATGGCCAG ATGAATGAGC CACCAGGTAA      600
    CCGTCTGCGC GTTGCACTGA CCGGCTTGAC CATGGCGGAG AAATTCCGTG      650
    ATGAAGGTCG TGATGTACTG TTATTCATCG ATAACATCTA TCGTTATACC      700
30  CTGGCCGGTA CAGAGGTATC TGCATGCTA GGTCTGATGC CATCAGCGGT      750
    AGGCTATCAG CCAACGCTGG CAGAAGAGAT GGGTGTGTTG CAGGAACGTA      800
    TCACTTCCAC CAAGACGGGT TCAATCACCT CCGTA                      835
  
```

2) INFORMATION FOR SEQ ID NO: 393

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia enterocolitica*
 (B) STRAIN: ATCC 9610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393

```

    GCTGTACCAA AAGTGTACAA CGCCCTTGAG GTTGAAGGCG CAGCTGAGAA      50
    GCTGGTGCTG GAAGTTCAGC AACAGCTGGG CGGTGGTGTT GTTCGTTGTA      100
    TCGCAATGGG CTCTTCCGAT GGTCTGAGCC GTGGGTTGAA AGTCATCAAC      150
55  CTGGAACACC CAATTGAAGT GCCTGTGGGC AAGTCAACTC TGGGCCGTAT      200
    CATGAACGTA TTGGGTGACC CAATCGACAT GAAAGGTCCT ATCGGCGAAG      250
    AAGAGCGTTG GGCAATCCAT CGTGAAGCGC CTTCTTACGA AGATCTTGCC      300
    AGCTCGCAAG ACTTGTTAGA AACC GGATATC AAGGTAATGG ACTTGATTG      350
    TCCGTTTCGCT AAGGGCGGTA AAGTCGGTCT GTTCGGTGGT GCGGGTGTAG      400
60  GTAAACGGT AAACATGATG GAGCTTATTC GTAACATTGC GATTGAGCAC      450
  
```

```

TCAGGTTATT CCGTATTTGC TGGCGTGGGT GAGCGTACTC GTGAGGGTAA 500
CGACTTCTAC CACGAGATGA CTGACTCCAA CGTTCTGGAC AAAGTATCCT 550
TGGTTTATGG CCAAATGAAT GAGCCACCAG GTAACCGTCT GCGCGTTGCA 600
CTGACCGGCT TGACCATGGC GGAGAAATTC CGTGATGAAG GTCGTGACGT 650
5 ATTGCTGTTC ATCGATAACA TCTATCGCTA TACCTTAGCC GGTACGGAAG 700
TTTCCGCACT GCTGGGTCGT ATGCCATCTG CCGTAGGTTA CCAGCCAACG 750
CTGGCAGAAG AGATGGGTGT GTTGACAGAA CGTATTACTT CCACCAAGAC 800
GGGTTCAATC AC 812

```

10

2) INFORMATION FOR SEQ ID NO: 394

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 802 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia frederiksenii*
 (B) STRAIN: ATCC 33641

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394

```

AAAGTGATACA ACGCCCTTGA GGTTGAAGGT ACTGCTGAGA AGTTAGTACT 50
GGAAGTTCAG CAACAGCTGG GCGGTGGTGT TGCTCGTTGT ATCGCCATGG 100
30 GCTCTTCCGA TGGTTTGAGC CGCGGGTTGA AAGTTGTCAA CCTGGAACAC 150
CCAATTGAAG TACCGGTTGG TAAATCAACT CTGGGCCGTA TCATGAACGT 200
ATTGGGTGAC CCAATCGACA TGAAAGGTCC TATCGGTGAA GAAGAGCGTT 250
GGGCAATCCA CCGCGAAGCG CTTCTTACG AAGAGCTTGC CAGCTCGCAA 300
GATCTGTTAG AAACCGGTAT CAAGGTAATG GATCTGATTT GCCCGTTCGC 350
35 TAAAGGCGGT AAAGTCGGTC TGTTCCGTGG TGCGGGTGTA GGTAACACGG 400
TAAACATGAT GGAGCTGATC CGTAATATCG CGATCGAGCA CTCAGGTTAT 450
TCCGTATTTG CGGGTGTTGG TGAACGTACC CGTGAGGGTA ACGACTTCTA 500
CCACGAGATG ACTGACTCCA ACGTTCTGGA CAAAGTATCC TTGGTTTATG 550
GCCAGATGAA TGAGCCACCA GGTAACCGTC TTCGCGTTGC ACTGACCGGT 600
40 CTGACCATGG CCGAGAAATT CCGTGATGAA GGTCGTGACG TATTGCTGTT 650
CATCGATAAC ATCTATCGTT ATACCTTGGC CCGTACGGAA GTATCCGCAC 700
TGCTGGGTCG TATGCCATCT GCGGTAGGCT ATCAGCCAAC GCTGGCAGAA 750
GAGATGGGTG TGTTGCAGGA ACGTATTACT TCCACCAAGA CGGGTTCAAT 800
CA 802

```

45

2) INFORMATION FOR SEQ ID NO: 395

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia intermedia*
 (B) STRAIN: ATCC 29909

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395

```

5   GCTGTACCAA GAGTGTACAA CGCCCTTGAG GTTGAAGGCA CTGCTGAGAA      50
    GCTGGTGCTG GAAGTTCAGC AACAGCTAGG CGGTGGTGTT GTTCGTTGTA      100
    TCGCAATGGG CTCTTCCGAT GGTCTGAGCC GCGGGTTGAA AGTCATCAAC      150
    CTGGAACACC CAATTGAAGT GCCGGTTGGT AAATCAACTC TGGGCCGTAT      200
    CATGAACGTA TTGGGTGACC CAATCGACAT GAAAGGTCCT ATCGGTGAAG      250
    AAGAGCGTTG GGCAATCCAC CGCGAAGCGC CTTCTTACGA AGAGCTTGCC      300
10  AGCTCACAAG ATTTGTTAGA AACCGGTATC AAAGTAATGG ACTTGATTTG      350
    CCCGTTTCGCT AAGGGCGGTA AAGTGGGTCT GTTCGGTGGT GCGGGTGTAG      400
    GTAAAACAGT AAACATGATG GAGCTTATTC GTAACATCGC GATTGAGCAC      450
    TCAGGTTATT CTGTATTTGC TGGTGTGGGT GAGCGTACTC GTGAGGGTAA      500
    CGACTTCTAC CACGAGATGA CTGACTCCAA CGTTCTGGAC AAAGTATCCT      550
15  TGGTGTATGG CCAGATGAAT GAGCCACCAG GTAACCGTCT GCGCGTTGCA      600
    CTGACCGGCC TGACCATGCG GGAGAAATTC CGTGATGAAG GTCGTGACGT      650
    ACTGTTGTTC ATCGATAACA TCTATCGCTA TACCTTGGCC GGTACGGAAG      700
    TATCCGCACT GCTGGGTCGT ATGCCATCAG CGGTAGGCTA CCAGCCAACG      750
    CTGGCAGAAG AGATGGGTGT GTTGCAGGAA CGTATTACGT CCACCAAGAC      800
20  GGGTTC

```

2) INFORMATION FOR SEQ ID NO: 396

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia pseudotuberculosis*
 (B) STRAIN: ATCC 29833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396

```

40  GCTGTACCAA AAGTGTACAA CGCCCTTGAG GTAGAAGGCA CAACTGAAAA      50
    GTTAGTGCTG GAAGTTCAGC AACAGTTGGG CGGTGGTGTT GTTCGTTGTA      100
    TCGCAATGGG CTCTTCCGAT GGTCTGAGCC GTGGGTGAA AGTAACCAAC      150
    CTGGAACACC CGATCGAAGT ACCGGTTGGT AAAGCGACCC TTGGCCGTAT      200
    CATGAACGTA TTGGGTGAAC CAATCGACAT GAAAGGTCCT ATCGGTGAAG      250
45  AAGAGCGTTG GGCAATCCAT CGCGAAGCGC CTTCTTATGA AGAGCTTGCT      300
    AGCTCAAG ATCTGTTAGA AACCGGTATC AAGGTTATGG ACCTGATTTG      350
    TCCGTTTGCT AAGGGCGGTA AAGTCGGTCT GTTCGGTGGT GCGGGTGTAG      400
    GTAAAACAGT AAACATGATG GAGCTGATCC GTAACATCGC GATCGAGCAC      450
    TCTGGGTATT CTGTATTTGC CGGTGTAGGT GAGCGTACCC GTGAGGGTAA      500
50  TGACTTCTAC CATGAAATGA CTGACTCCAA CGTTTTGGAC AAAGTATCCT      550
    TGGTTTACGG CCAGATGAAT GAGCCACCAG GTAACCGTCT ACGCGTTGCA      600
    CTGACCGGCC TGACCATGGC GGAGAAATTC CGTGATGAAG GTCGTGACGT      650
    ACTGCTGTTC ATCGATAATA TCTATCGTTA TACCTAGCT GGTACGGAAG      700
    TATCCGCATT GCTGGGTCGT ATGCCATCAG CGGTAGGTTA TCAGCCAACA      750
55  CTGGCTGAAG AGATGGGTGT GTTGCAGGAA CGTATTACTT CCACTAAGAC      800
    GGGTTC

```

60 2) INFORMATION FOR SEQ ID NO: 397

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 829 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia rohdei*
 (B) STRAIN: ATCC 43380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397

```

15  TTCCCCCAAG ACGCTGTACC AAAAGTGTAC AACGCCCTTG AGGTTGAAGG      50
    TGCAGCTGAG AAGCTTGTGC TGGAAAGTTCA GCAGCAGCTG GCGGGTGGTG      100
    TTGTTTCGTTG TATCGCAATG GGCTCTTCCG ATGGTTTGAG CCGTGGGTTG      150
    AAAGTTATCA ACCTGGAACA CCCAATTGAA GTGCCAGTTG GTAAATCAAC      200
20  TCTGGGCCGT ATCATGAACG TATTGGGTGA CCCAATCGAC ATGAAAGGCC      250
    CTATCGGTGA AGAAGAGCGT TGGGCAATCC ACCGTGAAGC GCCTTCTTAC      300
    GAAGAGCTTG CCAGCTCGCA AGATCTGTTA GAAACCGGTA TCAAGGTAAT      350
    GGATCTGATT TGTCCGTTCT CTAAGGGCGG TAAAGTCGGT CTGTTCCGGT      400
    GTGCGGGTGT TGGTAAACA GTAAACATGA TGGAGCTTAT TCGTAACATC      450
25  CCGATTGAGC ACTCAGGTTA TTCTGTATTT GCCGGGGTAG GTGAACGTAC      500
    TCGTGAGGGT AACGACTTCT ACCACGAGAT GACTGACTCC AACGTTCTGG      550
    ACAAAGTATC CTTGGTTTAT GGCCAGATGA ATGAGCCACC AGGTAACCGT      600
    CTGCGCGTTG CACTGACCGG CTTGACCATG GCGGAAAAAT TCCGTGATGA      650
    AGGCCGTGAC GTATTGCTGT TCATCGATAA CATTTATCGT TATACCCTAG      700
30  CCGGTACGGA AGTATCCGCA CTGCTGGGTC GTATGCCATC TGCGGTAGGC      750
    TATCAGCCAA CACTGGCAGA AGAGATGGGT GTGTTGCAGG AACGTATTAC      800
    TTCCACTAAG ACGGGTTCAA TCACCTCCG      829
  
```

2) INFORMATION FOR SEQ ID NO: 398

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yokenella regensburgei*
 (B) STRAIN: ATCC 35313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398

```

50  ATGCCGTACC GCGCGTGTAC GATGCTCTTG AGGTACAAAA TGGTAACGAG      50
    AAAGTGGTGC TGGAAAGCTCA GCAGCAGCTC GCGGGCGGTA TCGTGCGTAC      100
    TATCGCCATG GGTTCCTTCCG ACGGTCTGCG TCGTGGTCTG GAAGTTAAAG      150
55  ACCTCGAGCA CCCGATCGAA GTCCCGGTAG GTAAAGCAAC CCTGGGCCGT      200
    ATCATGAACG TCCTGGGTCA GCCGATCGAC ATGAAAGGCG ACATCGGTGA      250
    AGAAGAGCGT TGGGCTATCC ACCGCGCAGC ACCTTCCTAT GAAGAGCTGT      300
    CCAGCTCTCA GGAAGTCTG GAAACCGGTA TCAAAGTAAT GGATCTGATC      350
    TGCCCGTTCT CTAAGGGTGG TAAAGTCGGT CTGTTCCGGT GTGCGGGTGT      400
60  AGGTAAAACT GTAAACATGA TGGAGCTTAT CCGTAACATC GCGATTGAGC      450
  
```

	ACTCCGGTTA	CTCTGTGTTT	GCAGGCGTGG	GTGAACGTAC	TCGTGAGGGT	500
	AACGACTTCT	ACCACGAAAT	GACCGACTCC	AACGTACTGG	ATAAAGTATC	550
	CCTGGTGTAC	GGCCAGATGA	ACGAGCCGCC	GGGAAACCGT	CTGCGCGTTG	600
	CGCTGACCGG	CCTGACCATG	GCTGAGAAAT	TCCGTGACGA	AGGCCGTGAC	650
5	GTTCTGCTGT	TCGTCGATAA	CATCTACCGT	TATACCCTGG	CCGGTACGGA	700
	AGTATCCGCA	CTGCTGGGTC	GTATGCCTTC	TGCGGTAGGT	TATCAGCCAA	750
	CTCTGGCGGA	AGAGATGGGT	GTTCTTCAGG	AACGTATCAC	CTCTACCAA	800
	ACCGGTTCTA	TCACCTCCG				819

10

2) INFORMATION FOR SEQ ID NO: 399

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 1097 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yarrowia lipolytica*
 (B) STRAIN: ATCC 38295

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399

	AAGCTTAAGG	CTGAGCGAGA	GCGAGGTATC	ACCATTGATA	TCGCTCTCTG	50
	GAAGTTCCAG	ACCCCTAAGT	ACTACGTCAC	CGTTATTGAT	GCTCCCGGTC	100
30	ACCGAGATTT	CATCAAGAAC	ATGATTACCG	GTACTTCCCA	GGCTGACTGC	150
	GCCATCCTCA	TCATTGCTGG	TGGTGTGGT	GAGTTCGAGG	CTGGTATCTC	200
	CAAGGATGGT	CAGACCCGAG	AGCACGCCCT	GCTCGCTTTC	ACCCTCGGTG	250
	TTAAGCAGCT	CATTGTTGCT	ATCAACAAGA	TGGACTCCGT	CAAGTGGTCT	300
	CAGGATCGAT	ACCTCGAGAT	TTGCAAGGAG	ACTGCCAACT	TCGTCAAGAA	350
35	GGTCGGTTAC	AACCCCAAGG	CTGTCCCCTT	CGTCCCCATT	TCCGGATGGA	400
	ACGGTGACAA	CATGATCGAG	CCCTCTACCA	ACTGTGACTG	GTACAAGGGA	450
	TGGACCAAGG	AGACCAAGGC	CGGCGAGATC	AAGGGTAAGA	CCCTCCTCGA	500
	GGCCATTGAT	GCCATTGAGC	CCCCCGTGCG	ACCCACGAC	AAGCCCCCTC	550
	GACTTCCCCT	CCAGGATGTC	TACAAGATCG	GTGGTATCGG	CACAGTGCCC	600
40	GTTGGCCGAG	TCGAGACCGG	TGTTATCAAG	GCCGGTATGG	KTGTTACCTT	650
	CGTCCCCGCC	AACGTGACCA	CTGAGGTCAA	GTCTGTCTGAG	ATGCACCACG	700
	AGATCCTCCC	CGATGGAGGT	TTCCCCGGTG	ACAACGTCGG	TTTCAACGTC	750
	AAGAACGTTT	CCGTCAAGGA	TATCCGACGA	GGTAACGTTG	CTGGTGAATC	800
	CAAGAACGAC	CCCCCAAGG	GCTGCGACTC	TTTCAACGCT	CAGGTCATTG	850
45	TTCTTAACCA	CCCCGGTCAG	ATCGGTGCTG	GTTACGCTCC	CGTCCTTGAT	900
	TGCCACACTG	CCCACATTGC	TTGCAAGTTC	GACACCCTGA	TCGAGAAGAT	950
	CGACCGACGA	ACCGGTAAGA	AGATGGAGGA	CTCCCCAAG	TTCATCAAGT	1000
	CTGGTGATGC	TGCCATTGTC	AAGATGGTTC	CCTCCAAGCC	CATGTGTGTC	1050
	GAGGCCTTCA	CTGAGTACCC	CCCTCTTGGT	CGATTCGCCG	TCCGAGA	1097

50

2) INFORMATION FOR SEQ ID NO: 400

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 1233 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Absidia corymbifera*

(B) STRAIN: ATCC 46775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400

```

10 CAAGCTTAAG GCTGAACGTG AGCGTGGTAT CACCATCGAT ATCGCTCTCT 50
   GGAAGTTCGA GACTCCCAAG TACCACGTTA CCGTCATTGA TGCCCCCTGGC 100
   CATCGTGATT TCATCAAGAA CATGATTACT GGTACTTCCC AAGCTGACTG 150
   CGGTATCTTG ATTATTGCTG CTGGTACTGG TGAATTCGAA GCTGGTATCT 200
   CCAAGGATGG TCAAACCCGT GAACACGCTT TGCTTGCTTT CACCCTTGGT 250
   GTCCGTCAAT TGATTGTCGC TATCAACAAG ATGGATTCCA CCAAGTACTC 300
15 TGAGGCCCCG TACAACGAAA TTGTCAAGGA AGTCTCCACC TTCATCAAGA 350
   AGATTGGTTT CAACCCCAAG TCCGTTCCCT TCGTCCCTAT CTCTGGCTGG 400
   AACGGTGACA ACATGTTGGA GGARTCCACC AACATGCCTT GGTTCAAGGG 450
   ATGGAACAAG GAGACTAAGG CTGGTGCCAA GACYGGCAAG ACCCTTCTTG 500
   AAGCCATTGA CAACATTGAT CCCCCTGTTT GCCTTCCGA CAAGCCCCTT 550
20 CGTCTTCCCC TTCAAGATGT CTACAAGATC GGTGGTATTG GTACAGTTCC 600
   TGTCGGTTCG GTTGAGACTG GTGTCATCAA GCCTGGTATG GTTGTACCT 650
   TCGCTCCCGC TAACGTCACC ACTGAAGTCA AGTCCGTYGA AATGCACCAC 700
   GAGCAACTTG CTGAAGGTGT TCCCGGTGAC AACGTCGGTT TCAACGTCAG 750
   GAACGTTTCC GTCAAGGATA TCCGCCGTGG TAACGTYTGC TCTGACTCCA 800
25 AGAACGACCC CGCCAAGGAA TCCGCTTCCT TCACCGCTCA AGTTATTGTC 850
   TTGAACCACC CTGGTCARAT TGGTGCTGGT TACTCTCCTG TCTTGGATTG 900
   CCACACTGCT CACATTGCAT GCAAGTTCTY TKAGCTTCTT KAGAAGATCG 950
   ATYGTCTGTT CGGTAAGTAA ATANTTTGGT TTRGGATATG GGTATTGGGC 1000
   TTAATCTYTG GATTTTGCCT CAATTGCTCC TTCCTTGATC TTTCTCGATT 1050
30 ACTTTTTGAT CATTTGCTAA TCCAAACCCT TTCCATTTYA TTGAAAACAG 1100
   GTAAGAAGTT GGAAGACTCC CCCAAGTTCC TCAAGWSYGG TGACTCTGCT 1150
   ATCGTCAAGA TGGTTCCCTC CAAGCCCATG TCGGTTGAAG CCTACACTGA 1200
   ATATCCTCCT CTTGGTCGTT TCGCTGTCCG TGA 1233

```

35

2) INFORMATION FOR SEQ ID NO: 401

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1151 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Alternaria alternata*

(B) STRAIN: ATCC 62099

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401

```

55 CAAGTTGAAG GCCGAGCGTG AGCGTGGTAT CACCATCGAC ATTGCTCTCT 50
   GGAAGTTCGA GACTCCCAAG GTTAGTACCC CTCTGCCTAC TACATCAAGT 100
   TCTTTACAAT GCTAACATGT TGTAATCAGT ACTATGTCAC CGTCATTGAC 150
   GCCCCCGGTC ACCGTGATTT CATCAAGAAG ATGATCACTG GTACCTCCCA 200
   GGCCGACTGC GCTATTCTCA TCATTGCCGC CGGTACTGGT GAGTTCGAGG 250
   CTGGTATCTC CAAGGATGGC CAGACTCGTG AGCACGCTCT CCTCGCTTAC 300
   ACCCTCGGTG TCAAGCAGCT CATCGTTGCC ATCAACAAGA TGGACACCAC 350
60 CAAGTGGTCC GAGGAGCGTT ACCAGGAGAT CATCAAGGAG ACCTCCAAC 400

```

	TCATCAAGAA	GGTCGGCTAC	AACCCCAAGC	ACGTTCCCTT	CGTCCCCATC	450
	TCCGGTTTCA	ACGGTGACAA	CATGATTGAG	GCCTCATCCA	ACTGCCCCTG	500
	GTACAAGGGT	TGGGAGAAGG	AGACCAAGGC	CAAGGCCACT	GGTAAGACCC	550
5	TCCTCGAGGC	CATCGACGCC	ATCGACCCTY	CCAGCCGTCC	CACCGACAAG	600
	CCCCTCCGTC	TTCCCCTYCA	GGATGTTTAC	AAGATTGGTG	GTATTGGCAC	650
	GGTGCCCGTC	GGTCGTGTCG	AGACCGGTAT	CATCAAGGCC	GGTATGGTCG	700
	TCACCTTCGC	CCCCGCTGGT	GTCACCACTG	AAGTCAAGTC	CGTCGAGATG	750
	CACCACGAGC	AGCTCACC GA	GGGTGTCCCC	GGTGACAACG	TCGGCTTCAA	800
	CGTCAAGAAC	GTCTCCGTCA	AGGAGATCCG	TCGTGGTAAC	GTTGCCGGTG	850
10	ACTCCAAGAA	CGACCCCCCC	AAGGGTGCCG	AGTCCTTCAA	CGCCCAGGTC	900
	ATCGTCCCTCA	ACCACCCTGG	TCAGGTCGGT	GCTGGTTACG	CCCCAGTCCT	950
	CGACTGCCAC	ACCGCCCACA	TTGCTTGCAA	GTTCTCTGAG	CTCCTCGAGA	1000
	AGATTGACCG	CCGTACCGGA	AAGTCTGTTG	AGAACTCTCC	CAAGTTCATC	1050
	AAGTCCGGTG	ACGCCGCCAT	CGTCAAGATG	GTTCCCTCCA	AGCCCATGTG	1100
15	CGTTGAGGCT	TTCACTGACT	ACCCTCCTCT	CGGTCGTTTC	GCTGTCCGTG	1150
	A					1151

20 2) INFORMATION FOR SEQ ID NO: 402

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1283 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus flavus*
 (B) STRAIN: ATCC 26947

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402

35	CAAGCTCAAG	TCCGAGCGTG	AGCGTGGTAT	CACCATCGAT	ATCGCCCTCT	50
	GGAAGTTCCA	GACCTCCAAG	TATGAGGTCA	CCGTCATTGG	TAAGCATTTG	100
	AGTTCCAAC	TACGTTGCCC	AACATTTACA	GTCATCTAAC	AAAGTTCAAT	150
	AGATGCCCCC	GGTCACCGTG	ACTTCATCAA	GAACATGATC	ACTGGTACTT	200
40	CCCAGGCTGA	CTGCGCTATC	CTCATCATTG	CCTCCGGTAC	TGGTGAATTC	250
	GAGGCTGGTA	TCTCCAAGGA	TGGTCAGACC	CGTGAGCACG	CTCTGCTCGC	300
	TTTCACCCTC	GGTGTCCGTC	AGCTCATCGT	TGCCCTCAAC	AAGATGGACA	350
	CCTGCAAGTG	GTCTCAGGAT	CGTTACAACG	AAATCGTTAA	GGAGACTTCC	400
	AACTTCATCA	AGAAGGTCGG	ATACAACCCC	AAGAGCGTTC	CTTTCGTCCC	450
45	CATCTCCGGT	TTCAACGGTG	ACAACATGAT	TGAGGCCTCC	ACCAACTGCC	500
	CCTGGTACAA	GGGTTGGGAG	AAGGAGACCA	AGGCTGGCAA	GTCCACCGGT	550
	AAGACCCTTC	TCGAGGCCAT	CGATGCCATC	GAGCCCCCCG	TCCGTCCCAC	600
	CGACAAGCCT	CTCCGTCTTC	CCCTYCAGGA	TGTCTACAAG	ATCTCTGGTA	650
	TCGGTACTGT	GCCCGTCGGT	CGTGTGAGGA	CTGGTGTCAT	CAAGCCTGGT	700
50	ATGGTCGTTA	CTTTCGCTCC	TGCCAACGTG	ACCACTGAAG	TCAAGTCCGT	750
	TGAAATGCAC	CACCAGCAGC	TCCAGGCCGG	TAACCCCGGT	GACAACGTTG	800
	GTTTCAACGT	CAAGAACGTC	TCCGTCAAGG	AAGTCCGCCG	TGGTAACGTT	850
	GCCGGTGACT	CCAAGAACGA	CCCCCTGCT	GGCTGCGATT	CCTTCAACGC	900
	CCAGGTCATC	GTCCTTAACC	ACCCCGGTCA	GGTCGGCAAC	GGTTACGCTC	950
55	CCGTCCCTGA	CTGCCACACC	GCTCACATTG	CTTGCAAGTT	CGCTGAGCTC	1000
	CTTGAGAAGA	TTGACCGCCG	TACCGGTAAA	TCTGTTGAGG	ACAAGCCCAA	1050
	GTTTCATCAAG	TCTGGTGATG	CTGCCATCGT	CAAGATGATT	CCCTCCAAGC	1100
	CCATGTGTGT	GGAGTCTTTT	ACTGACTTCC	CCCCTCTTGG	TCGTTTCGCT	1150
	GTCCGTGACG	TAAGTTTTC	CCTCTTGACT	ATCTTCACAA	TTTTTCACAT	1200
60	ATTTTCACGC	CTCGTCCCAC	TCTTTTTTCT	CCCTTCCTCT	TTGGTTCCCC	1250

TTTTTGCCTG CAAGTTCTCT ATAGCTAACA TGA

1283

5 2) INFORMATION FOR SEQ ID NO: 403

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1103 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus fumigatus*
 (B) STRAIN: DAL95

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403

20 TCCGAGCGTG AGCGTGGTAT CACCATCGAC ATTGCCCTCT GGAAGTTCCA 50
 GACTCCCAAG TATGAGGTCA CTGTCATCGG TAAGCTCGAC TCGCCCCGAT 100
 ATGTTTTGGT GCTGTAGCTA ACACGATCTG AAGATGCCCC CGGTACACCGT 150
 GACTTCATCA AGAACATGAT CACTGGTACC TCCCAGGCTG ACTGCGCTAT 200
 25 CCTCATCATT GCCTCCGGTA CTGGTGAGTT CGAGGCTGGT ATCTCCAAGG 250
 ATGGCCAGAC CCGTGAGCAC GCTCTGCTGG CTTTCACCCT CGGTGTCAAG 300
 CAGCTCATCG TCGCCCTCAA CAAGATGGAC ACCTGCAAGT GGTCCGAGGA 350
 TCGTTACAAC GAAATTGTCA AGGAAACCTC CAACTTCATC AAGAAGGTCG 400
 GCTACAACCC CAAGGCCGTT CCCTTCGTCC CCATCTCTGG CTTCAACGGT 450
 30 GACAACATGC TTGAGCCCTC CTCCAACCTG CCCTGGTACA AGGGATGGGA 500
 GAAGGAGACC AAGGCCGGCA AGGTCACTGG TAAGACCCTC ATCGAGGCCA 550
 TCGACGCCAT TGAGCCCCCT GTCCGTCCCT CCAACAAGCC CCTCCGTCTT 600
 CCCCTCCAGG ATGTCTACAA GATCTCTGGT ATCGGAACGG TCCCTGTCGG 650
 CCGTGTCGAG ACCGGTATCA TCAAGCCCGG CATGGTTCGTC ACCTTCGCCC 700
 35 CCGCCAACGT CACCACTGAA GTCAAGTCCG TCGAGATGCA CCACCAGCAG 750
 CTCCAGGAGG GTGTCCCCGG TGACAACGTC GGTTCACACG TCAAGAACGT 800
 TTCCGTCAAG GAAGTCCGCC GTGGTAACGT CTGCGGTGAC TCCAAGAACG 850
 ATCCCCCTCA GGGTGCTGCC TCCTTCAACG CCCAGGTCAT CGTCCTCAAC 900
 CACCCCGGTC AGGTCGGCGC TGGTTACGCC CCCGTCCTCG ACTGCCACAC 950
 40 TGCCACATT GCTTGCAAGT TCTCTGAGCT GCTTGAGAAG ATTGACCGCC 1000
 GTACCGGCAA GTCTGTTGAG AACAAACCCA AGTTCATCAA GTCCGGTGAT 1050
 GCCGCCATCG TGAAGATGGT TCCTTCCAAG CCCATGTGTG TCGAGTCCTT 1100
 CAC 1103

45

2) INFORMATION FOR SEQ ID NO: 404

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1149 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus fumigatus*
 (B) STRAIN: WSA-172

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404

	AAGCTCAAGT	CCGAGCGTGA	GCGTGGTATC	ACCATCGACA	TTGCCCTCTG	50
	GAAGTTCCAG	ACTCCCAAGT	ATGAGGTCAC	TGTCATCGGT	AAGCTCGACT	100
5	CGCCCCGATA	TGTTTTGGTG	CTGTAGCTAA	CACGATCTGA	AGATGCCCCC	150
	GGTCACCGTG	ACTTCATCAA	GAACATGATC	ACTGGTACCT	CCCAGGCTGA	200
	CTGCGCTATC	CTCATCATTG	CCTCCGGTAC	TGGTGAGTTC	GAGGCTGGTA	250
	TCTCCAAGGA	TGGCCAGACC	CGTGAGCACG	CTCTGCTGGC	TTTCACCCTC	300
	GGTGTCAAGC	AGCTCATCGT	CGCCCTCAAC	AAGATGGACA	CCTGCAAGTG	350
10	GTCCGAGGAT	CGTTACAACG	AAATTGTCAA	GGAAACCTCC	AACTTCATCA	400
	AGAAGGTCGG	CTACAACCCC	AAGGCCGTTT	CCTTCGTCCC	CATCTCTGGC	450
	TTCAACGGTG	ACAACATGCT	TGAGCCCTCC	TCCAAGTGCC	CCTGGTACAA	500
	GGGATGGGAG	AAGGAGACCA	AGGCCGGCAA	GGTCACTGGT	AAGACCCTCA	550
	TCGAGGCCAT	CGACGCCATT	GAGCCCCCTG	TCCGTCCCTC	CAACAAGCCC	600
15	CTCCGTCTTC	CCCTCCAGGA	TGTCTACAAG	ATCTCTGGTA	TCGGAACGGT	650
	CCCTGTCGGC	CGTGTGAGGA	CCGGTATCAT	CAAGCCCCGGC	ATGGTCTGTC	700
	CCTTCGCCCC	CGCCAACGTC	ACCACTGAAG	TCAAGTCCGT	CGAGATGCAC	750
	CACCAAGCAGC	TCCAGGAGGG	TGTCCCCGGT	GACAACGTCG	GTTTCAACGT	800
	CAAGAACGTT	TCCGTCAAGG	AAGTCCGCGG	TGGTAACGTC	TGCGGTGACT	850
20	CCAAGAACGA	TCCCCCTCAG	GGTGCTGCCT	CCTTCAACGC	CCAGGTCATC	900
	GTCCTCAACC	ACCCCGGTCA	GGTCGGCGCT	GGTTACGCCC	CCGTCCTCGA	950
	CTGCCACACT	GCCCCATTG	CTTGCAAGTT	CTCTGAGCTG	CTTGAGAAGA	1000
	TTGACCGCCG	TACCGGCAAG	TCTGTTGAGA	ACAACCCCAA	GTTTCATCAAG	1050
	TCCGGTGATG	CCGCCATCGT	GAAGATGGTT	CCTTCCAAGC	CCATGTGTGT	1100
25	CGAGTCCTTC	ACTGACTACC	CCCCTCTGGG	TCGTTTCGCC	GTCCGTGAC	1149

2) INFORMATION FOR SEQ ID NO: 405

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1151 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

40

- (A) ORGANISM: *Aspergillus niger*
 (B) STRAIN: ATCC 9508

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405

45	CAAGCTCAAG	TCCGAGCGTG	AGCGTGGTAT	CACCATCGAC	ATTGCCCTCT	50
	GGAAGTTCCA	GACTGGCAAG	TATGAGGTCA	CCGTCATTGG	TATGTACTCA	100
	CAGAGTTCTC	TTTTTCATCA	AGCAATATAC	TAACGTCCAT	CATAGACGCC	150
	CCCGGTCACC	GTGACTTCAT	CAAGAACATG	ATCACTGGTA	CCTCCCAGGC	200
	TGACTGCGCT	ATCCTCATCA	TTGCCTCCGG	TACTGGTGAG	TTGAGGCTG	250
50	GTATCTCCAA	GGATGGCCAG	ACTCGTGAGC	ACGCTCTGCT	TGCTTTCACC	300
	CTCGGTGTCC	GCCAGTTCAT	CGTTGCCCTC	AACAAGATGG	ACACCTGCAA	350
	GTGGTCCGAG	GACCGTTACA	ACGAAATCGT	TAAGGAGACC	TCCAAGTTCA	400
	TCAAGAAGGT	CGGATACAAC	CCCAAGGGTG	TTCCTTTCGT	CCCCATCTCC	450
	GGTTTCAACG	GTGACAACAT	GCTCGAGCCC	TCCCCCAACT	GCCCCTGGTA	500
55	CAAGGGTTGG	GAGAAGGAGA	CCAAGGCCGG	CAAGGTCACC	GGTAAGACCC	550
	TCCTTGAGGC	CATCGACGCC	ATCGAGCCCC	CCGTCCGTCC	CTCCAACAAG	600
	CCCCTCCGTC	TTCCCCTCCA	GGATGTCTAC	AAGATCTCCG	GTATTGGAAC	650
	TGTTCCCGTC	GGTCGTGTCG	AGACCGGTAT	CATTGCCCTC	GGTATGGTCG	700
	TGACCTTCGC	TCCCGCCAAC	GTCACCACTG	AAGTCAAGTC	CGTTGAGATG	750
60	CACCACCAGC	AGCTCAAGGA	AGGTGTCCCC	GGTGACAACG	TTGGTTTCAA	800

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CGTCAAGAAC GTTTCCGTCA AGGAGGTTTCG CCGTGGTAAC GTTGCCGGTG      850
ACTCCAAGAA CGACCCCCCT CTTGGCTGTG AGAGCTTCAC CGCCCAGGTC      900
ATCGTCCTCA ACCACCCCGG TCAGGTCGGC GCTGGTTACG CTCCCGTCCT      950
GGACTGCCAC ACTGCTCACA TTGCTTGCAA GTTCGCTGAG CTCCTTGAGA     1000
5 AGATTGACCG CCGTACCGGA AAGTCTGTTG AATCTTCCCC CAAGTTCATC     1050
AAGTCCGGTG ACGCTGCCAT CGTCAAGATG ATTCCTCCA AGCCCATGTG     1100
TGTTGAGGCT TCACTGACT ACCCCCCTCT TGGTCGTTTC GCCGTCCGCG     1150
A                                                                1151

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10

2) INFORMATION FOR SEQ ID NO: 406

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 1093 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Blastoschizomyces capitatus*
 (B) STRAIN: ATCC 10663

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406

```

GCTTAAAGCT GAACGTGAAC GTGGTATCAC CATTGATATC GCTCTCTGGA      50
AGTTCGAAAC TCCTAAGTAC TACGTTACTG TTATTGATGC TCCAGGTCAC     100
30 CGTGATTTC TCAAGAACAT GATTACTGGT ACTTCCCAAG CCGATTGCGC     150
CATTCTTATC ATTGCTGCCG GTGTCGGTGA ATTCGAAGCT GGTATCTCCA     200
AGGAAGGTCA AACCAGAGAA CACGCTCTTC TCGCTTTCAC CCTTGGTGTC     250
AGACAACCTA TCATTGCCAT CAACAAGATG GACTCTGTCA AGTGGGACCA     300
AAAGAGATAC GAAGAAATCG TCAAGGAGGC TTCCAACCTC GTCAAGAAGG     350
35 TTGGTTACAA CCCCAGTCT GTTCCATTCTG TTCCTATCTC TGGTTGGAAC     400
GGTGACAACA TGTTGGAACC TACCACCAAC GCCCATGGT ACAAGGGATG     450
GACCAAGGAA ACCAAGGCTG GTGCCACTAA GGGTATGACT CTTATTGAAG     500
CCATTGACGC CATTGAACCA CCAGTAAGAC CATCCGACAA GCCACTCCGT     550
CTCCCACTCC AAGATGTTTA CAAGATTGGT GGTATCGGAA CTGTGCCAGT     600
40 CGGCCGTGTC GAAACCGGTA TCATCAAGGC CGGTATGGTC GTTACCTTTG     650
CTCCACCAAT GGTCACAACT GAAGTTAAGT CCGTTGAAAT GCACCACGAA     700
CAACTTGCTC AAGGTAACCC AGGTGACAAC GTTGGTTTCA ACGTCAAGAA     750
CGTTTCCGTT AAGGAAATCA GACGTGGTAA CGTCTGTGGT GACTCCAAGA     800
ACGATCCACC AAAGGGCTGC GAATCTTTCA ACGCTCAAGT TATCGTCTTG     850
45 AACCACCCTG GTCAAATCTC TGCTGGTTAC TCTCCAGTTC TCGATTGCCA     900
CACTGCCCAC ATTGCCTGCA GATTCGACGA ACTCCTTGAA AAGATCGACC     950
GTCGTTCTGG TAAGAAGATT GAAGACTCTC CAAAGTTTGT CAAGTCTGGT     1000
GATGCCGCTA TCGTCAAGAT GATCCCAACC AAGCCAATGT GCGTTGAAAC     1050
CTTCACTGAA TACCCACCAC TTGGTCGTTT CGCCGTCCGT GAT              1093
50

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2) INFORMATION FOR SEQ ID NO: 407

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 1101 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida albicans*

(B) STRAIN: ATCC 10231D

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407

```

10 CTTGGACAAA TTGAAGGCTG AAAGAGAAAG AGGTATCACC ATTGATATCG      50
   CTTTGTGGAA ATTCGAAACT CCAAATATACC ACGTTACCGT CATTGATGCT      100
   CCAGGTCACA GAGATTTTCAT CAAGAATATG ATCACTGGTA CTTCTCAAGC      150
   TGATTGTGCT ATTTTGATTA TTGCTGGTGG TACTGGTGAA TTCGAAGCCG      200
   GTATTTCTAA GGATGGTCAA ACCAGAGAAC ACGCTTTGTT GGCTTACACT      250
   TTGGGTGTCA AACAAATTGAT TGTGCTGTC AACAAAGATGG ACTCTGTCAA      300
15  ATGGGACAAA AACAGATTTG AAGAAATCAT CAAGGAAACC TCCAACCTCG      350
   TCAAGAAGGT TGGTTACAAC CCAAAGACTG TTCCATTYGT TCCAATCTCT      400
   GGTTTGAATG GTGACAACAT GATTGAACCA TCCACCAACT GTCCATGGTA      450
   CAAGGGTTGG GAAAAGGAAA CCAAATCCGG TAAAGTTACT GGTAAGACCT      500
   TGTTAGAAGC TATTGACGCT ATTGAACCAC CAACCAGACC AACCGACAAA      550
20  CCATTGAGAT TGCCATTGCA AGATGTTTAC AAGATCGGTG GTATTGGTAC      600
   TGTGCCAGTC GGTAGAGTTG AAACCTGGTAT CATCAAAGCC GGTATGGTTG      650
   TTACTTTTCG CCCAGCTGGT GTTACCACTG AAGTCAAATC CGTTGAAATG      700
   CATCACGAAC AATTGGCTGA AGGTGTTCCA GGTGACAATG TTGGTTTCAA      750
   CGTTAAGAAC GTTTCCGTTA AAGAAATTAG AAGAGGTAAC GTTTGTGGTG      800
25  ACTCCAAGAA CGATCCACCA AAGGGTTGTG ACTCTTTCAA TGCCCAAGTC      850
   ATTGTTTTGA ACCATCCAGG TCAAATCTCT GCTGGTTACT CTCCAGTCTT      900
   GGATTGTCAC ACTGCCACA TTGCTTGTA ATTGACACT TTGGTTGAAA      950
   AGATTGACAG AAGAACTGGT AAGAAATTGG AAGAAAATCC AAAATTCGTC      1000
   AAATCCGGTG ATGCTGCTAT CGTCAAGATG GTCCCAACCA AACCAATGTG      1050
30  TGTGAAGCT TTCACTGACT ACCCACCATT AGGTAGATTC GCTGTCAGAG      1100
   A

```

35 2) INFORMATION FOR SEQ ID NO: 408

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1089 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida albicans*

(B) STRAIN: ATCC 18804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408

```

50 GAAGGCTGAA AGAGAAAGAG GTATCACCAT TGATATCGCT TTGTGGAAAT      50
   TCGAAACTCC AAAATACCAC GTTACCGTCA TTGATGCTCC AGGTCACAGA      100
   GATTTTCATCA AGAATATGAT CACTGGTACT TCTCAAGCTG ATTGTGCTAT      150
   TTTGATTATT GCTGGTGGTA CTGGTGAATT CGAAGCCGGT ATTTCTAAGG      200
55  ATGGTCAAAC CAGAGAACAC GCTTTGTTGG CTTACACTTT GGTGTGTCAAA      250
   CAATTGATTG TTGCTGTCAA CAAGATGGAC TCTGTCAAAT GGGACAAAAA      300
   CAGATTTGAA GAAATCATCA AGGAAACCTC CAACTTCGTC AAGAAGGTTG      350
   GTTACAACCC AAAGACTGTT CCATTCGTTT CAACTCTCTG TTGGAATGGT      400
   GACAACATGA TTGAACCATC CACCAACTGT CCATGGTACA AGGGTTGGGA      450
60  AAAGGAAACC AAATCCGGTA AAGTTACTGG TAAGACCTTG TTAGAAGCTA      500

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TTGACGCTAT TGAACCACCA ACCAGACCAA CCGACAAACC ATTGAGATTG 550
CCATTGCAAG ATGTTTACAA GATCGGTGGT ATTGGTACTG TGCCAGTCGG 600
TAGAGTTGAA ACTGGTATCA TCAAAGCCGG TATGGTTGTT ACTTTCGCCC 650
CAGCTGGTGT TACCACTGAA GTCAAATCCG TTGAAATGCA TCACGAACAA 700
5 TTGGCTGAAG GTGTTCCAGG TGACAATGTT GGTTTCAACG TTAAGAACGT 750
TTCCGTTAAA GAAATTAGAA GAGGTAACGT TTGTGGTGAC TCCAAGAACG 800
ATCCACCAAA GGGTTGTGAC TCTTTCAATG CCAAGTCAT TGTTTTGAAC 850
CATCCAGGTC AAATCTCTGC TGGTTACTCT CCAGTCTTGG ATTGTCACAC 900
TGCCACATT GCTTGTAAT TCGACACTTT GGTTGAAAAG ATTGACAGAA 950
10 GAACTGGTAA GAAATTGGAA GAAAATCCAA AATTCGTCAA ATCCGGTGAT 1000
GCTGCTATCG TCAAGATGGT CCAACCAAA CCAATGTGTG TTGAAGCTTT 1050
CACTGACTAC CCACCATTAG GTAGATTTCG TGTCAGAGA 1089

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15

2) INFORMATION FOR SEQ ID NO: 409

(i) SEQUENCE CHARACTERISTICS:

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20 (A) LENGTH: 1101 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Candida albicans
    (B) STRAIN: ATCC 56884

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409

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CTTGGACAAA TTGAAGGCTG AAAGAGAAAAG AGGTATCACC ATTGATATCG 50
CTTTGTGGAA ATTCGAAACT CCAAAATACC ACGTTACCGT CATTGATGCT 100
CCAGGTCACA GAGATTTTCAAT CAAGAATATG ATCACTGGTA CTTCTCAAGC 150
35 TGATTGTGCT ATTTTGATTA TTGCTGGTGG TACTGGTGAA TTCGAAGCCG 200
GTATTTCTAA GGATGGTCAA ACCAGAGAAC ACGCTTTGTT GGCTTACACT 250
TTGGGTGTCA AACAATTGAT TGTTGCTGTC AACAAGATGG ACTCTGTCAA 300
ATGGGACAAA AACAGATTTG AAGAAATCAT CAAGGAAACC TCCAACCTCG 350
TCAAGAAGGT TGGTTACAAC CCAAAGACTG TTCCATTCGT TCCAATCTCT 400
40 GGTGGAATG GTGACAACAT GATTGAACCA TCCACCAACT GTCCATGGTA 450
CAAGGGTTGG GAAAAGGAAA CCAATCCGG TAAAGTTACT GGTAAGACCT 500
TGTTAGAAGC TATTGACGCT ATTGAACCAC CAACCAGACC AACCGACAAA 550
CCATTGAGAT TGCCATTGCA AGATGTTTAC AAGATCGGTG GTATTGGTAC 600
TGTGCCAGTC GGTAGAGTTG AAATGGTAT CATCAAAGCC GGTATGGTTG 650
45 TTACTTTCGC CCCAGCTGGT GTTACCACTG AAGTCAAATC CGTTGAAATG 700
CATCACGAAC AATTGGCTGA AGGTGTTCCA GGTGACAATG TTGGTTTCAA 750
CGTTAAGAAG GTTCCGTTA AAGAAATTAG AAGAGGTAAC GTTTGTGGTG 800
ACTCCAAGAA CGATCCACCA AAGGGTTGTG ACTCTTTCAA TGCCCAAGTC 850
ATTGTTTTGA ACCATCCAGG TCAAATCTCT GCTGGTTACT CTCCAGTCTT 900
50 GGATTGTCAC ACTGCCACA TTGCTTGTA ATTGACACT TTGGTTGAAA 950
AGATTGACAG AAGAACTGGT AAGAAATTGG AAGAAAATCC AAAATTTCGT 1000
AAATCCGGTG ATGCTGCTAT CGTCAAGATG GTCCCAACCA AACCAATGTG 1050
TGTTGAAGCT TTCCTGACT ACCCACCATT AGGTAGATTC GCTGTCAGAG 1100
A 1101

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55

2) INFORMATION FOR SEQ ID NO: 410

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1102 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida albicans*
 (B) STRAIN: ATCC 60193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410

```

15 CTTGGACAAA TTGAAGGCTG AAAGAGAAAG AGGTATCACC ATTGATATCG      50
   CTTTGTGGAA ATTCGAAACT CCAAAATACC ACGTTACCGT CATTGATGCT      100
   CCAGGTCACA GAGATTTTCAT CAAGAATATG ATCACTGGTA CTTCTCAAGC      150
   TGATTGTGCT ATTTTGATTA TTGCTGGTGG TACTGGTGAA TTCGAAGCCG      200
   GTATTTCTAA GGATGGTCAA ACCAGAGAAC ACGCTTTGTT GGCTTACACT      250
   TTGGGTGTCA AACAATTGAT TGTGCTGTGC AACAAGATGG ACTCTGTCAA      300
20 ATGGGACAAA AACAGATTG AAGAAATCAT CAAGGAAACC TCCAACCTCG      350
   TCAAGAAGGT TGGTTACAAC CCAAAGACTG TTCCATTCGT TCCAATCTCT      400
   GTTTGGGAATG GTGACAACAT GATTGAACCA TCCACCAACT GTCCATGGTA      450
   CAAGGGTTGG GAAAAGGAAA CCAATCCGG TAAAGTTACT GGTAAGACCT      500
   TGTTAGAAGC TATTGACGCT ATTGAACCAC CAACCAGACC AACCGACAAA      550
25 CCATTGAGAT TGCCATTGCA AGATGTTTAC AAGATCGGTG GTATTGGTAC      600
   TGTGCCAGTC GGTAGAGTTG AAACCTGGTAT CATCAAAGCC GGTATGGTTG      650
   TTACTTTTCG CCCAGCTGGT GTTACCACTG AAGTCAAATC CGTTGAAATG      700
   CATCACGAAC AATTGGCTGA AGGTGTTCCA GGTGACAATG TTGGTTTCAA      750
   CGTTAAGAAC GTTTCCGTTA AAGAAATTAG AAGAGGTAAC GTTTGTGGTG      800
30 ACTCCAAGAA CGATCCACCA AAGGGTTGTG ACTCTTTCAA TGCCCAAGTC      850
   ATTGTTTTGA ACCATCCAGG TCAAATCTCT GCTGGTTACT CTCCAGTCTT      900
   GGATTGTGAC ACTGCCCACA TTGCTTGTA AATTCGACACT TTGGTTGAAA      950
   AGATTGACAG AAGAACTGGT AAGAAATTGG AAGAAAATCC AAAATTTCGTC     1000
   AAATCCGGTG ATGCTGCTAT CGTCAAGATG GTCCCAACCA AACCAATGTG     1050
35 TGTGAAGCT TTCACTGACT ACCCACCATT AGGTAGATTC GCTGTCAGAG     1100
   AT

```

2) INFORMATION FOR SEQ ID NO: 411

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1102 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida albicans*
 (B) STRAIN: ATCC 90028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411

```

55 CTTGGACAAA TTGAAGGCTG AAAGAGAAAG AGGTATCACC ATTGATATCG      50
   CTTTGTGGAA ATTCGAAACT CCAAAATACC ACGTTACCGT CATTGATGCT      100
   CCAGGTCACA GAGATTTTCAT CAAGAATATG ATCACTGGTA CTTCTCAAGC      150
   TGATTGTGCT ATTTTGATTA TTGCTGGTGG TACTGGTGAA TTCGAAGCCG      200
60 GTATTTCTAA GGATGGTCAA ACCAGAGAAC ACGCTTTGTT GGCTTACACT      250

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	TTGGGTGTCA	AACAATTGAT	TGTTGCTGTC	AACAAGATGG	ACTCTGTCAA	300
	ATGGGACAAA	AACAGATTTG	AAGAAATCAT	CAAGGAAACC	TCCAACCTCG	350
	TCAAGAAGGT	TGGTTACAAC	CCAAAGACTG	TTCCATTTCG	TCCAATCTCT	400
	GGTTGGAATG	GTGACAACAT	GATTGAACCA	TCCACCAACT	GTCCATGGTA	450
5	CAAGGGTTGG	GAAAAGGAAA	CCAAATCCGG	TAAAGTTACT	GGTAAGACCT	500
	TGTTAGAAGC	TATTGACGCT	ATTGAACAC	CAACCAGACC	AACCGACAAA	550
	CCATTGAGAT	TGCCATTGCA	AGATGTTTAC	AAGATCGGTG	GTATTGGTAC	600
	TGTGCCAGTC	GGTAGAGTTG	AAACTGGTAT	CATCAAAGCC	GGTATGGTTG	650
	TTACTTTTCG	CCCAGCTGGT	GTTACCACTG	AAGTCAAATC	CGTTGAAATG	700
10	CATCACGAAC	AATTGGCTGA	AGGTGTTCCA	GGTGACAATG	TTGGTTTCAA	750
	CGTTAAGAAC	GTTTCCGTTA	AAGAAATTAG	AAGAGGTAAC	GTTTGTGGTG	800
	ACTCCAAGAA	CGATCCACCA	AAGGGTTGTG	ACTCTTTCAA	TGCCCAAGTC	850
	ATTGTTTGA	ACCATCCAGG	TCAAATCTCT	GCTGGTTACT	CTCCAGTCTT	900
	GGATTGTTCAC	ACTGCCCCACA	TTGCTTGTA	ATTCGACACT	TTGGTTGAAA	950
15	AGATTGACAG	AAGAACTGGT	AAGAAATTGG	AAGAAAATCC	AAAATTCGTC	1000
	AAATCCGGTG	ATGCTGCTAT	CGTCAAGATG	GTCCCAACCA	AACCAATGTG	1050
	TGTTGAAGCT	TTCACTGACT	ACCCACCATT	AGGTAGATTC	GCTGTCAGAG	1100
	AT					1102

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2) INFORMATION FOR SEQ ID NO: 412

	(i) SEQUENCE CHARACTERISTICS:
25	(A) LENGTH: 1101 bases
	(B) TYPE: Nucleic acid
	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear
30	(ii) MOLECULE TYPE: Genomic DNA
	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: <i>Candida dubliniensis</i>
	(B) STRAIN: NCPF 3108
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412

	CTTGATAAAA	TTGAAGGCTG	AAAGAGAAAG	AGGTATCACC	ATTGATATCG	50
	CTTTGTGGAA	ATTCGAAACT	CCAAAATACC	ACGTTACCGT	CATTGATGCT	100
40	CCAGGTCACA	GAGATTTTCAT	CAAGAACATG	ATCACTGGTA	CTTCTCAAGC	150
	TGATTGTGCT	ATTTTGATTA	TTGCTGGTGG	TACTGGTGAA	TTCGAAGCCG	200
	GTATTTCTAA	GGATGGTCAA	ACCAGAGAAC	ACGCTTTGTT	GGCTTACACT	250
	TTGGGTGTCA	AACAATTGAT	TGTTGCTGTC	AACAAGATGG	ACTCTGTCAA	300
	ATGGGACAAA	AACAGATTTG	AAGAAATCAT	CAAGGAAACC	TCTAACTTCG	350
45	TCAAGAAGGT	TGGTTACAAC	CCAAAGACTG	TTCCATTTCG	TCCAATCTCT	400
	GGTTGGAATG	GTGACAACAT	GATTGAAGCT	TCCACCAACT	GTCCATGGTA	450
	CAAGGGTTGG	GAAAAGGAAA	CCAAATCCGG	TAAGGTTACT	GGTAAGACCT	500
	TGTTAGAAGC	TATTGATGCT	ATTGAACCA	CAACCAGACC	AACCGACAAA	550
	CCATTGAGAT	TGCCATTGCA	AGATGTTTAC	AAGATCGGTG	GTATTGGTAC	600
50	TGTGCCAGTC	GGTAGAGTTG	AAACTGGTGT	CATTAAAGCC	GGTATGGTTG	650
	TCACTTTTTC	CCCAGCTGGT	GTTACCACTG	AAGTCAAATC	CGTTGAAATG	700
	CATCACGAAC	AATTGGCTGA	AGGTGTTCCA	GGTGACAATG	TTGGTTTCAA	750
	CGTTAAGAAT	GTTTCTGTCA	AAGAAATTAG	AAGAGGTAAC	GTTTGTGGTG	800
	ACTCCAAGAA	CGATCCACCA	AAGGGTTGTG	ACTCTTTCAA	TGCCCAAGTC	850
55	ATTGCTTTGA	ACCATCCAGG	TCAAATCTCT	GCTGGTTACT	CTCCAGTCTT	900
	GGATTGTTCAC	ACTGCCCCACA	TTGCTTGTA	ATTCGACACT	TTGGTTGAAA	950
	AGATTGACAG	AAGAACTGGT	AAGAAATTGG	AAGAAAATCC	AAAATTCGTC	1000
	AAATCCGGTG	ACGCTGCTAT	YGTCAGATG	GTCCCAACCA	AACCAATGTG	1050
	TGTTGAAGCT	TTCACTGACT	ACCCACCATT	AGGTAGATTC	GCTGTCAGAG	1100
60	A					1101

2) INFORMATION FOR SEQ ID NO: 413

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1098 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida catenulata*
 (B) STRAIN: ATCC 10565

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413

20	GGACAAGCTT	AAGGCTGAGC	GTGAGAGAGG	TATCACCATT	GACATTGCCT	50
	TGTGGAAGTT	CGAGACTCCC	AAGTACCACG	TCACTGTCAT	TGACGCCCCC	100
	GGTCACAGAG	ATTTCATCAA	GAACATGATC	ACTGGTACCT	CGCAGGCTGA	150
	CTGTGCTATC	TTGATCATTG	CTTCCGGTGT	CGGTGAGTTC	GAGGCTGGTA	200
	TCTCCAAGGA	CGGTCAGACC	CGTGAGCACG	CCTTGTTGGC	CTACACCTTG	250
25	GGTGTCAAGC	AGTTGATCGT	TGCCATCAAC	AAGATGGACT	CCGTCAAGTG	300
	GGACAAGAAC	AGATTCGAGG	AGATTGTCAA	GGAGACCACC	AACTTCGTCA	350
	AGAAGGTTGG	TTACAACCCC	AAGGCTGTCC	CCTTCGTCCC	CATCTCTGGC	400
	TGGAACGGTG	ACAACATGAT	TGAGGCCTCC	ACCAACTGCC	CCTGGTACAA	450
	GGGCTGGGAG	AAGGAGACCA	AGGCCGGTAA	GTCTACCGGT	AAGACCTTGT	500
30	TGGAGGCCAT	TGACGCCATT	GAGCCCCCTA	CCAGACCCAC	CGACAAGCCC	550
	TTGAGATTGC	CCTTGCAGGA	TGTCTACAAG	ATCGGTGGTA	TTGGTACGGT	600
	GCCCGTCGGC	CGTGTGAGG	CCGGTGTTCAT	CAAGCCCGGT	ATGGTCGTCA	650
	CCTTCGCCCC	CGCTGGTGTC	ACCACTGAAG	TCAAGTCCGT	CGAGATGCAC	700
	CACGAGCAGT	TGTCCGAGGG	TGTCCCCGGT	GACAACGTTG	GTTTCAACGT	750
35	CAAGAACGTC	TCTGTTAAGG	AGATCAGACG	TGGTAACGTC	TGCGGTGACT	800
	CCAAGAACGA	CCCCCCCATG	GGTTGCTCTT	CTTTCAACGC	CCAGGTTATC	850
	GTGTTGAACC	ACCCCGGTCA	GATCTCTGCC	GGTTACTCTC	CCGTCTTGGA	900
	CTGCCACACC	GCCCACATTG	CTTGCAAGTT	CGCCGAGTTG	ATCGAGAAGA	950
	TTGACAGACG	TACCGGTAAG	TCCATGGAGG	CTAACCCCAA	GTTTCGTCAAG	1000
40	TCTGGTGACG	CCGCCATCGT	CAAGATGGAG	CCCACTAAGC	CCATGTGTGT	1050
	TGAGGCCTTC	ACTGACTTCC	CTCCTTTGGG	TAGATTCGCC	GTCAGAGA	1098

2) INFORMATION FOR SEQ ID NO: 414

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1102 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida dubliniensis*
 (B) STRAIN: NCPF 3949

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414

CTTGGATAAA TTGAAGGCTG AAAGAGAAAAG AGGTATCACC ATTGATATCG 50
 CTTTGTGGAA ATTCGAAACT CCAAAATACC ACGTTACCGT CATTGATGCT 100
 CCAGGTCACA GAGATTTTCAT CAAGAACATG ATCACTGGTA CTTCTCAAGC 150
 TGATTGTGCT ATTTTGATTA TTGCTGGTGG TACTGGTGAA TTCGAAGCCG 200
 5 GTATTTCTAA GGATGGTCAA ACCAGAGAAC ACGCTTTGTT GGCTTACACT 250
 TTGGGTGTCA AACAATTGAT TGTTGCTGTC AACAAGATGG ACTCTGTCAA 300
 ATGGGACAAA AACAGATTCTG AAGAAATCAT CAAGGAAACC TCTAACTTCG 350
 TCAAGAAGGT TGGTTACAAC CCAAAGACTG TTCCATTCTGT TCCAATCTCT 400
 GGTTGGAATG GTGACAACAT GATTGAAGCT TCCACCAACT GTCCATGGTA 450
 10 CAAGGGTTGG GAAAAGGAAA CCAAATCCGG TAAGGTTACT GGTAAGACCT 500
 TGTTAGAAGC TATTGATGCT ATTGAACCAC CAACCAGACC AACCGACAAA 550
 CCATTGAGAT TGCCATTGCA AGATGTTTAC AAGATCGGTG GTATTGGTAC 600
 TGTGCCAGTC GGTAGAGTTG AAAGTGGTGT CATTAAAGCC GGTATGGTTG 650
 TCACTTTTGC CCCAGCTGGT GTTACCACTG AAGTCAAATC CGTTGAAATG 700
 15 CATCACGAAC AATTGGTTGA AGGTGTTCCA GGTGACAATG TTGGTTTCAA 750
 CGTTAAGAAT GTTTCTGTCA AAGAAATTAG AAGAGGTAAC GTTTGTGGTG 800
 ACTCCAAGAA CGATCCACCA AAGGGTTGTG ACTCTTTCAA TGCCCAAGTC 850
 ATTGTCTTGA ACCATCCAGG TCAAATCTCT GCTGGTTAYT CTCCAGTCTT 900
 GGATTGTCAC ACTGCCCACA TTGCTTGTA AATTCGACACT TTGGTTGAAA 950
 20 AGATTGACAG AAGAACTGGT AAGAAATTGG AAGAAAATCC AAAATTCGTC 1000
 AAATCCGGTG ACGCTGCTAT YGTCAAGATG GTCCCAACCA AACCAATGTG 1050
 TGTTGAAGCT TTCCTGACT ACCCACCATT AGGTAGATTC GCTGTCAGAG 1100
 AT 1102

25

2) INFORMATION FOR SEQ ID NO: 415

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 1102 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida dubliniensis*
 (B) STRAIN: CBS 7987

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415

CTTGGATAAA TTGAAGGCTG AAAGAGAAAAG AGGTATCACC ATTGATATCG 50
 CTTTGTGGAA ATTCGAAACT CCAAAATACC ACGTTACCGT CATTGATGCT 100
 45 CCAGGTCACA GAGATTTTCAT CAAGAACATG ATCACTGGTA CTTCTCAAGC 150
 TGATTGTGCT ATTTTGATTA TTGCTGGTGG TACTGGTGAA TTCGAAGCCG 200
 GTATTTCTAA GGATGGTCAA ACCAGAGAAC ACGCTTTGTT GGCTTACACT 250
 TTGGGTGTCA AACAATTGAT TGTTGCTGTC AACAAGATGG ACTCTGTCAA 300
 ATGGGACAAA AACAGATTCTG AAGAAATCAT CAAGGAAACC TCTAACTTCG 350
 50 TCAAGAAGGT TGGTTACAAC CCAAAGACTG TTCCATTCTGT TCCAATCTCT 400
 GGTTGGAATG GTGACAACAT GATTGAAGCT TCCACCAACT GTCCATGGTA 450
 CAAGGGTTGG GAAAAGGAAA CCAAATCCGG TAAGGTTACT GGTAAGACCT 500
 TGTTAGAAGC TATTGATGCT ATTGAACCAC CAACCAGACC AACCGACAAA 550
 CCATTGAGAT TGCCATTGCA AGATGTTTAC AAGATCGGTG GTATTGGTAC 600
 55 TGTGCCAGTC GGTAGAGTTG AAAGTGGTGT CATTAAAGCC GGTATGGTTG 650
 TCACTTTTGC CCCAGCTGGT GTTACCACTG AAGTCAAATC CGTTGAAATG 700
 CATCACGAAC AATTGGTTGA AGGTGTTCCA GGTGACAATG TTGGTTTCAA 750
 CGTTAAGAAT GTTTCTGTCA AAGAAATTAG AAGAGGTAAC GTTTGTGGTG 800
 ACTCCAAGAA CGATCCACCA AAGGGTTGTG ACTCTTTCAA TGCCCAAGTC 850
 60 ATTGTCTTGA ACCATCCAGG TCAAATCTCT GCTGGTTAYT CTCCAGTCTT 900

5 GGATTGTCAC ACTGCCCACA TTGCTTGTAAT ATTCGACACT TTGGTTGAAA 950
 AGATTGACAG AAGAAGTGGT AAGAAATTGG AAGAAAATCC AAAATTTCGTC 1000
 AAATCCGGTG ACGCTGCTAT YGTCAAGATG GTCCCAACCA AACCAATGTG 1050
 TGTGAAGCT TTTACTGACT ACCCACCATT AGGTAGATTG GCTGTCAGAG 1100
 AT 1102

2) INFORMATION FOR SEQ ID NO: 416

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1094 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida famata*
 (B) STRAIN: ATCC 62894

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416

25 AATTGAAGGC TGAAAGAGAA AGAGGTATCA CCATTGATAT CGCTTTATGG 50
 AAATTCGAAA CTCCAAAATA CCACGTTACC GTTATTGATG CTCCAGGTCA 100
 CAGAGATTTT ATCAAGAACA TGATTACTGG TACTTCTCAA GCTGATTGTG 150
 CTATTTTTRAT TATTGCTGGT GGTGTCGGTG AATTCGAAGC CGGTATCTCT 200
 AAGGATGGTC AAACCAGAGA ACACGCTTTA TTGGCTTACA CCTTAGGTGT 250
 30 TAGACAATTG ATTGTTGCCG TCAACAAGAT GGACTCTGTT AAATGGGACA 300
 AGGCTAGATT CGAAGAAATC ATCAAGGAAA CCTCTAACTT CGTCAAGAAG 350
 GTTGGTTACA ACCCTAAGAC TGTTCCCTTC GTYCCAATTT CTGGATGGAA 400
 CGGTGACAA ACATGTTGAAG CCTCCACCAA CTGTCCATGG TACAAGGGTT 450
 GGGAAAAGGA AACCAAGGCT GGTAAATCTA CTGGTAAGAC TTTGTTAGAA 500
 35 GCCATTGATG CCATTGAACC ACCAACCAGA CCAACCAGAA AGCCATTGAG 550
 ATTACCATTA CAAGATGTCT ACAAGATCGG TGGTATTGGT ACTGTGCCAG 600
 TCGGTAGAGT TGAAACCGGT GTTATCAAGG GTGGTATGGT TGTACCTTT 650
 GCCCCAGCCG GTGTCACTAC CGAAGTCAAA TCCGTTGAAA TGCACCACGA 700
 ACAATTAGCT GAAGGTGTTT CAGGTGACAA TGTTGGTTTC AACGTCAAGA 750
 40 ACGTTTCCGT TAAGGAAATC AGAAGAGGTA ACGTTTGTGG TGACTCCAAG 800
 AACGACCCAC CAAAGGGTGC TGAATCTTTC ACCGCTCAAG TTATTGTCTT 850
 GAACCACCCA GGTCAATCTT CTGCTGGTTA CTCTCCAGTC TTAGATTGTC 900
 ACACCGCCCA CATTGCTTGT AAATTTCGATG CTTTACTCGA AAAGATTGAC 950
 AGAAGATCCG GTAAGAAATT AGAAGACGAA CCAAAATTCG TCAAGTCCGG 1000
 45 TGATGCTGCT ATCGTCAAGA TGGTCCCAAC CAAACCAATG TGTGTTGAAG 1050
 CTTTCACTGA ATACCCACCA TTAGGTAGAT TCGCTGTTAG AGAT 1094

2) INFORMATION FOR SEQ ID NO: 417

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1101 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida glabrata*
 (B) STRAIN: ATCC 66032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417

```

5  TTTGGACAAG TTGAAGGCTG AAAGAGAAAG AGGTATCACT ATCGATATCG 50
   CTTTGTGGAA GTTCGAAACT CCAAAGTACC ACGTYACCGT TATCGATGCT 100
   CCAGGTCACA GAGATTTTCAT CAAGAACATG ATTACTGGTA CTTCTCAAGC 150
   TGACTGTGCT ATCTTGATTA TTGCTGGTGG TGTCGGTGAA TTCGAAGCYG 200
10  GTATCTCCAA GGATGGTCAA ACCAGAGAAC ACGCTCTATT GGCTTTCACC 250
   CTAGGTGTTA GACAATTGAT TGTGCTGTC AACAAGATGG ACTCTGTCAA 300
   GTGGGATGAA TCCAGATTCG CTGAAATCGT TAAGGAAACC TCCAACTTCA 350
   TCAAGAAGGT CGGTTACAAC CCAAAGACTG TTCCATTCGT CCCAATCTCT 400
   GGTTGGAACG GTGACAACAT GATTGAAGCC ACCACCAACG CTTCTTGCTA 450
15  CAAGGGTTGG GAAAAGGAAA CCAAGGCTGG TGTCGTCAAG GGTAAGACCT 500
   TGTTGGAAGC CATTGACGCT ATCGAACCAC CAACCAGACC AACTGACAAG 550
   CCATTGAGAT TGCCATTGCA AGATGTCTAC AAGATCGGTG GTATCGGTAC 600
   GGTGCCAGTC GGTAGAGTCG AAACCGGTGT CATCAAGCCA GGTATGGTTG 650
   TTACCTTCGC CCCAGCTGGT GTTACCACTG AAGTCAAGTC CGTTGAAATG 700
20  CACCACGAAC AATTGACTGA AGGTTTGCCA GGTGACAACG TTGGTTTCAA 750
   CGTTAAGAAC GTTTCCTGTTA AGGAAATCAG AAGAGGTAAT GTCTGTGGTG 800
   ACTCCAAGAA CGACCCACCA AAGGCTGCTG CTTCTTTCAA CGCTACCGTC 850
   ATTGTCTTGA ACCACCCAGG TCAAATCTCT GCTGGTTACT CTCCAGTTTT 900
   GGACTGTCAC ACCGCCCCA TTGCTTGTA GTTTGAAGAA TTGTTGGAAA 950
25  AGAACGACAG AAGATCCGGT AAGAAGTTGG AAGACTCTCC AAAGTTCTTG 1000
   AAGTCCGGTG ACGCTGCTTT GGTAAAGTTC GTTCCATCCA AGCCAATGTG 1050
   TGTCGAAGCT TTCTCCGACT ACCCACCATT GGGTAGATTC GCTGTCAGAG 1100
   A
  
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30

2) INFORMATION FOR SEQ ID NO: 418

(i) SEQUENCE CHARACTERISTICS:

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35  (A) LENGTH: 1080 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear
  
```

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

```

   (A) ORGANISM: Candida guilliermondii
   (B) STRAIN: ATCC 6260
  
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45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418

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   AGAGAAAGAG GTATCACCAT TGACATTGCT TTGTGGAAAT TCGAGACTCC 50
   AAAGTACCAC GTTACYGTCA TTGATGCCCC AGGTCACAGA GATTTTCATCA 100
50  AGAACATGAT CACTGGTACT TCTCAAGCTG ACTGTGCTAT TTTGATTATT 150
   GCTGGTGGTA CCGGTGAATT CGAAGCTGGT ATCTCTAAGG ATGGTCAAAC 200
   CAGAGAGCAC GCTTTGTTGG CTTACACCTT GGGTGTTAGA CAATTGATTG 250
   TTGCTGTCAA CAAGATGGAC TCCGTCAART GGGACAAGAA CAGATTYAG 300
   GAAATCATCA AGGAAACCTC TAACTTCGTC AAGAAGGTTG GTTACAACCC 350
55  TAAAGACTGTG CCATTCGTTT CTATCTCTGG ATGGAAYGGT GACAACATGA 400
   TTGAGGCTTC TACCAACTGT CCTTGGTACA AGGGATGGGA GAAGGAGACC 450
   AAGGCTGGTA AGTCCACCGG TAAGACTTTG TTGGAGGCCA TTGACGCCAT 500
   TGAGCCACCT CAAAGACCAA CCGACAAGCC ATTGAGATTG CCATTGCAAG 550
   ATGTYTACAA GATTGGTGGT ATTGGAACGG TGCCAGTCGG TAGAGTTGAA 600
60  ACCGGTATCA TYAAGGCCGG TATGGTTGTT ACCTTTGCCC CAGCTGGTGT 650
  
```

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YACCACTGAA GTCAAGTCCG TGGAAATGCA CCACGAACAA TTGGTTGAAG 700
GTGTTCCAGG TGACAATGTT GGTTCACACG TTAAGAACGT TTCCGTTAAG 750
GAAATTAGAA GAGGTAACGT TTGTGGTGAC TCCAAGAACG ACCCACCAAA 800
GGGTTGTGAC TCTTTCACCG CTCAAGTTAT TGTGTTGAAC CACCCTGGTC 850
5 AAATCTCTGC TGGTACTCT CCAGTTTTGG ACTGTCACAC CGCCACATT 900
GCTTGTAAT TCGACACCTT GTTGAGAAG ATTGACAGAA GAACCGGTAA 950
GAAGATGGAG GACAACCCA AGTTTGTCAA GTCCGGTGAC GCTTCTATCG 1000
TCAAGATGGT GCCATCCAAG CCAATGTGTG TTGAGGCTTT CACCGACTAC 1050
CCACCATTGG GAAGATTGCG CGTCAGAGAC 1080
10

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2) INFORMATION FOR SEQ ID NO: 419

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15 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 751 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
20
(ii) MOLECULE TYPE: Genomic DNA
(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Candida haemulonii
25    (B) STRAIN: ATCC 22991
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419

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TCTGTCAAGT GGGACAAGGC CAGATACGAG GAAATCGTCA AGGAGACCTC 50
30 TAACCTTCGTC AAGAAGGTTG GTTACAACCC TAAGACTGTT CCATTTCGTCC 100
CAATCTCTGG TTGGAACGGT GACAACATGA TTGAGGCTTC TACCAACTGT 150
GACTGGTACA AGGTTGGGA GAAGGAGACC AAGTCTGGTA AGTCCACCGG 200
TAAGACCTTG TTGGAGGCCA TTGACGCCAT TGAGCCACCA ACCAGACCAA 250
CCGACAAGCC ATTGAGATTG CCATTGCAGG ATGTCTACAA GATTGGTGGT 300
35 ATCGGAACTG TGCCAGTCGG CAGAGTTGAG ACCGGTGTTA TCAAGGCCGG 350
TATGGTTGTC ACCTTCGCCC CAGCTGGTGT CACCACTGAA GTCAAGTCTG 400
TCGAGATGCA CCACGAGCAG TTGCCAGAGG GTGTCCCAGG TGACAACGTT 450
GGTTTCAACG TCAAGAACGT TTCCGTTAAG GAAATCAGAA GAGGTAACGT 500
CTGTGGTGAC TCCAAGCAGG ACCACCAAA GGGCTGTGAC TCTTTCACCG 550
40 CTCAGGTAT TGTGTTGAAC CACCCAGGTC AGATCTCTTC TGGTTACTCT 600
CCAGTTTTGG ACTGTCACAC TGCCACATT GCTTGTAAGT TCGACACCTT 650
GGTTGAGAAG ATCGACAGAA GAACCGGTAA GAAGTTGGAA GATGAGCCAA 700
AGTTCATCAA GTCCGGTGAC GCTGCTATCG TCAAGATGGT CCAACCAAG 750
C 751
45

```

2) INFORMATION FOR SEQ ID NO: 420

```

50 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 1102 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
55
(ii) MOLECULE TYPE: Genomic DNA
(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Candida inconspicua
60    (B) STRAIN: ATCC 16783

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420

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5   TCTTGACAAG TTAAAGGCTG AAAGAGAAAG AGGTATCACT ATTGATATTG      50
    CTTTATGGAA ATTCGAAACT CCAAAGTATC ACGTTACCGT CATTGATGCT      100
    CCAGGTCACA GAGATTTTCAT TAAGAACATG ATTACTGGTA CTTCTCAAGC      150
    AGATTGTGCT ATTTTGATTA TTGCTGGTGG TGTCGGTGAA TTCGAAGCTG      200
    GTATTTCCAA GGATGGTCAA ACTAGAGAAC ACGCTTTATT AGCATTCCACC      250
    TTAGGTGTTA AGCAATTGAT TGTGCTATC AACAAGATGG ATTCTGTAA      300
10  GTGGGATGAA AAGAGATTG AAGAAATTGT CAAGGAAACC CAAAACTTCA      350
    TCAAGAAGGT TGGTTACAAC CCAAAGACTG TTCCATTCGT TCCAATTTCT      400
    GGTGGAATG GTGACAACAT GATTGAACCA TCTTCTAACT GTCCATGGTA      450
    CAAGGGTTGG ACTAAGGAAA CCAAGGCAGG TGTTGTCAAG GGTAAGACCT      500
    TATTAGAAGC TATTGATGCT ATTGAACCAC CTGTGAGACC AACTGATAAG      550
15  CCATTAAGAT TACCATTACA AGATGTTTAC AAGATTGGTG GTATTGGTAC      600
    TGTGCCAGTC GGTAGAGTTG AAACCGGTAT TATTAAGCCA GGTATGGTTG      650
    TTGTTTTTCG ACCATCTGGT GTTACCACTG AAGTCAAGTC CGTTGAAATG      700
    CACCATGAAC AATTAGAAGA AGGTGTCCCA GGTGACAATG TTGGTTTCAA      750
    CGTCAAGAAC GTCTCTGTGA AGGATATCAA GAGAGGTAAC GTTGTGGTG      800
20  ACTCCAAGAA TGACCCACCA CAAGGTTGTG CTTCTTCAA TGCTCAAGTC      850
    ATTGTCTTGA ACCACCCTGG TCAAATTTCT GCTGGTTACT CTCCAGTTTT      900
    AGATTGTCAC ACTGCCCCA TTGCATGTAA ATTGCATGAA TTAATTGAAA      950
    AGATTGACAG AAGAACTGGT AAGTCCGTTG AAGACCATCC AAAGTCTGTT      1000
    AAGTCTGGTG ATGCAGCTAT CGTTAAGATG GTTCCAACCA AGCCAATGTG      1050
25  TGTGAAGCT TTTACTGAAT ACCCACCATT AGGTAGATTC GCAGTCAGAG      1100
    AT                                     1102

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30 2) INFORMATION FOR SEQ ID NO: 421

(i) SEQUENCE CHARACTERISTICS:

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    (A) LENGTH: 1099 bases
    (B) TYPE: Nucleic acid
35  (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Candida kefyr
    (B) STRAIN: ATCC 28838

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421

```

45  TGGACAAGTT AAAGGCTGAA AGAGAAAGAG GTATCACCAT CGATATCGCT      50
    TTGTGGAAGT TCGAAACTCC AAAGTACCAA GTTACCGTTA TCGATGCTCC      100
    AGGTCACAGA GATTTTCATCA AGAACATGAT TACTGGTACT TCTCAAGCTG      150
    ACTGTGCTAT CTTGATTATT GCTGGTGGTG TCGGTGAATT CGAAGCCGGT      200
50  ATCTCCAAGG ATGGTCAAAC CAGAGAACAC GCTTTGTTGG CTTACACCTT      250
    GGGTGTTAGA CAATTGATTG TTGCTATCAA CAAGATGGAC TCTGTTAAGT      300
    GGGATGAATC TCGTTACCAA GAAATTGTTA AGGAAACCTC CAACTTCATC      350
    AAGAAGGTCG GTTACAACCC AAAGAATGTT CCATTCGTCC CAATCTCTGG      400
    TTGGAACGGT GACAACATGA TTGAAGCCAC CACCAACGCT CCATGGTACA      450
55  AGGGTTGGGA AAAGGAAACC AAGGCTGGTA CCGTCAAGGG TAAGACCTTG      500
    TTGGAAGCTA TTGACGCTAT CGAACCACCA ACCAGACCAA CTGACAAGCC      550
    ATTGAGATTG CCATTGCAAG ATGTCTACAA GATCGGTGGT ATTGGTACTG      600
    TGCCAGTCGG TAGAGTCGAA ACCGGTGTCA TCAAGCCAGG TATGGTTGTT      650
    ACCTTCGCCC CAGCCGGTGT CACTACCGAA GTTAAGTCCG TCGAAATGCA      700
60  CCACGAACAA TTGAAGAAG GTCTACCAGG TGACAACGTC GGTTTCAACG      750

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	TCAAGAACGT	TTCCGTTAAG	GAAATCAGAA	GAGGTAACGT	CTGTGGTGAC	800
	TCCAAGAACG	ATCCACCAAA	GGCTGCTGCT	TCTTTCAACG	CCACTGTTAT	850
	CGTCTTGAAC	CACCCAGGTC	AAATCTCTGC	TGGTTACTCT	CCAGTTTGG	900
	ATTGTCACAC	TGCTCACATT	GCTTGTAAGT	TCGACGAATT	GTTGGAAAAG	950
5	AACGACAGAA	GATCCGGTAA	GAAGTTGGAA	GACTCTCCAA	AGTTCTTGAA	1000
	GTCTGGTGAC	GCTGCTTTGG	TTAAGTTCGT	TCCATCTAAG	CCAATGTGTG	1050
	TTGAAGCATT	CTCTGACTAC	CCACCATTGG	GTAGATTTCG	TGTCAGAGA	1099

10

2) INFORMATION FOR SEQ ID NO: 422

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 1095 bases
15	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Candida krusei</i>
	(B)	STRAIN: ATCC 34135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422

	AAGTTAAAGG	CAGAAAGAGA	AAGAGGTATC	ACTATTGATA	TTGCTTTATG	50
	GAAGTTYGAA	ACTCCAAART	ACCACGTTAC	CGTTATTGAT	GCTCCAGGTC	100
	ACAGAGATTT	CATCAAGAAC	ATGATTACCG	GTACTTCTCA	AGCTGATTGT	150
30	GCTATTTTGA	TTATTGCTGG	TGGTGTCTGGT	GAATTCGAAG	CTGGTATCTC	200
	CAAGGATGGT	CAAAC TAGAG	AACACGCTCT	ATTGGCTTTC	ACCTTAGGTG	250
	TTAGACAATT	GATTGTTGCT	ATCAACAAGA	TGGATTCCGT	TAARTGGGAT	300
	GAAAACAGAT	TTGAAGAAAT	TGTCAAGGAA	ACCCAAAAC	TCATCAAGAA	350
	GGTTGGTTAC	AACCCAAAGA	CTGTTCCATT	CGTTCCAATY	TCTGGTTGGA	400
35	ATGGTGACAA	CATGATTGAA	GCATCCACCA	ACTGTCCATG	GTACAAGGGT	450
	TGGACTAAGG	AAACCAAGGC	AGGTGTTGTT	AAGGGTAAGA	CCTTATTAGA	500
	AGCAATCGAT	GCTATTGAAC	CACCTGTCAG	ACCAACCGAA	AAGCCATTAA	550
	GATTACCATT	ACAAGATGTT	TACAAGATTG	GTGGTATTGG	TACTGTGCCA	600
	GTCCG TAGAG	TCGAAACCGG	TGTCATTAAG	CCAGGTATGG	TTGTCAC TTT	650
40	TGCTCCAGCA	GGTGTCACCA	CCGAAGTCAA	GTCCGTTGAA	ATGCACCATG	700
	AACAATTAGA	ACAAGGTGTT	CCAGGTGATA	ACGTTGGTTT	CAACGTTAAG	750
	AACGTTTCTG	TCAAGGATAT	CAAGAGAGGT	AACGTTTGTG	GTGACTCCAA	800
	GAACGACCCA	CCAATGGGTG	CAGCTTCCTT	CAATGCTCAA	GTCATTGTCT	850
	TGAACCACCC	TGGTCAAATT	TCCGCTGGTT	ACTCTCCAGT	CTTGGATTGT	900
45	CACACTGCCC	ACATTGCATG	TAAGTTCGAC	GAATTAATCG	AAAAGATTGA	950
	CAGAAGAACT	GGTAAGTCTG	TTGAAGACCA	TCCAAAGTCY	GTCAAGTCTG	1000
	GTGATGCAGC	TATCGTCAAG	ATGGTCCCAA	CCAAGCCAAT	GTGTGTTGAA	1050
	GCTTTCACTG	AATAYCCACC	ATTAGGTAGA	TTCGCAGTCA	GAGAT	1095

50

2) INFORMATION FOR SEQ ID NO: 423

(i) SEQUENCE CHARACTERISTICS:

55	(A)	LENGTH: 1104 bases
	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida lambica*
 (B) STRAIN: ATCC 24750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423

```

5      CTTGGACAAG CTTAAGGCTG AAAGAGAAAG AGGTATCACC ATTGATATCG      50
      CTTTATGGAA GTTCGAAACT CCAAAGTACC ACGTTACCGT CATTGACGCT      100
10     CCAGGTCACA GAGATTTTCA CAAGAACATG ATTACTGGTA CCTCTCAAGC      150
      AGATTGTGCT ATTTTTRATYA TTGCTGGTGG TGTCGGTGAA TTCGAAGCTG      200
      GTATCTCTAA GGATGGTCAA ACCAGAGAAC ACGCTCTTCT TGCATTCACT      250
      CTTGGTGTTA GACAATTGAT TGTTGCTATC AACAAGATGG ACTCTGTCAA      300
      GTGGGACGAA TCCAGATTCG ATGAAATTTG TAAGGAAACC GCWAACTTCA      350
15     TCAAGAAGGT TGGTTACAAC CCAAAGACTG TTCCATTCTG CCCAATCTCT      400
      GGTGGAACG GTGACAACAT GATTGAACCA TCTGCTAACT GTCCATGGTA      450
      CAAGGGATGG ACTAAGGAAA CCAAGGCTTC CGGTGTCGTC AAGGGTAAGA      500
      CCCTTCTTGA AGCAATTGAT GCTATTGAGC CACCTGTCAG ACCAACTGAC      550
      AAGGCTTTGA GATTGCCATT RCAAGATGTC TACAAGATTG GTGGTATTGG      600
20     TACTGTGCCA GTCGGTAGAG TTGAAACCGG TATCATCAAG CCAGGTATGA      650
      TTGTCGTTTT CGCTCCAACC GGTGTTACTA CTGAAGTTAA GTCCGTTGAA      700
      ATGCACCATG AACAATTAGA AGAAGGTGTC CCAGGTGACA ATGTTGGTTT      750
      CAACGTCAAG AACGTCTCTG TTAAGGATAT TAAGAGAGGT AACGTCTGTG      800
      GTGACTCCAA GAACGACCCA CCAATGGGTT GTGCTTCCTT CAATGCTCAA      850
25     GTCATTGTTC TTAACCACCC AGGTCAAATT TCTGCTGGTT ACTCACCAGT      900
      TCTTGACTGT CACACTGCCC ACATTGCATG TAAGTTCGAY GAATTACTCG      950
      AAAAGATTGA CAGAAGAACC GGTAAAGGCTA CTGAAGACCA TCCAAAGTCT      1000
      GTCAAGTCTG GTGATGCAGC TATCGTCAAG ATGGTTCCAA CCAAGCCAAT      1050
      GTGTGTYGAA GCTTTCCTG ACTACCCACC ATTAGGTAGA TTCGCTGTYA      1100
30     GAGA
  
```

2) INFORMATION FOR SEQ ID NO: 424

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1098 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida lusitaniae*
 (B) STRAIN: ATCC 66035

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 424

```

50     GGACAAGTTG AAGGCTGAGA GAGAAAGAGG TATCACCATC GATATCGCTT      50
      TGTGGAAGTT CGAGACTCCA AAGTACCACG TTACCGTCAT TGACGCTCCA      100
      GGTCACAGAG ATTTTCATCA GAACATGATC ACTGGTACTT CCAAGCTGA      150
      CTGTGCTATC TTGATTATCG CTGGTGGTGT CGGTGAGTTC GAAGCCGGTA      200
      TCTCTAAGGA CGGTCAAACC AGAGAGCACG CTTTGTTGGC TTACACCTTG      250
55     GGTGTCAAGC AGTTGATTGT TGCTGTCAAC AAGATGGACT CCGTCAAGTG      300
      GGACCAATCT AGATTGAGG AAATCATCAA GGAAACCTCT AACTTCGTCA      350
      AGAAGGTTGG TTACAACCCT AAGACTGTTT CATTTCGTCCC AATCTCTGGT      400
      TGGAACGGTG ACAACATGAT TGAGCCATCY ACCAACTGCC CATGGTACAA      450
      GGGTTGGGAG AAGGAGACCA AGTCYGGTAA GTCCACCGGT AAGACCTTGT      500
60     TGGAGGCCAT TGACGCCATT GAGCCACCTT CGAGACCAAC CGACAAGCCA      550
  
```

	TTGAGATTGC	CATTGCAAGA	TGTCTACAAG	ATYGGTGGTA	TTGGTACTGT	600
	GCCAGTCGGT	AGAGTTGAGA	CCGGTGTTCAT	CAAGGCCGGT	ATGGTTGTCA	650
	CCTTTGCTCC	AGCTGGTGTG	ACCACTGAAG	TCAAGTCCGT	GGAAATGCAC	700
	CACGAACAAT	TGGCTGAGGG	TGTCCCAGGT	GACAACGTTG	GTTTCAACGT	750
5	CAAGAACGTT	TCCGTCAAGG	AAATCAGAAG	AGGTAACGTC	TGTGGTGACT	800
	CCAAGAACGA	CCCACCAAAG	GCTGCTGCTT	CYTTCACCTG	TCAAGTYATY	850
	GTCTTGAACC	ACCCAGGTCA	AATCTCCTCY	GGTTACTCTC	CAGTYTTGGA	900
	CTGTCACACT	GCYCACATTG	CTTGTAAGTT	CGACACCTTG	ATTGAGAAGA	950
	TCGACAGAAG	AACYGGTAAG	AAGTTGGAAG	AAGAGCCAAA	GTTTCATCAAG	1000
10	TCYGGTGACG	CTGCTATCGT	CAAGATGGTC	CCAACCAAGC	CAATGTGYGT	1050
	YGAAGCTTTC	ACCGACTACC	CACCATTGGG	TAGATTCGCT	GTCAGAGA	1098

15 2) INFORMATION FOR SEQ ID NO: 425

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 1101 bases
	(B)	TYPE: Nucleic acid
20	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Candida norvegensis</i>
	(B)	STRAIN: ATCC 22977

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425

30	TCTTGACAAG	TTAAAGGCTG	AAAGAGAAAG	AGGTATCACT	ATTGATATTG	50
	CTTTATGGAA	ATTCGAAACT	CCAAAATACC	ACGTTACCGT	TATTGATGCT	100
	CCAGGTCACA	GAGATTTTCA	TAAGAACATG	ATTACTGGTA	CTTCCCAAGC	150
	TGATTGTGCT	ATCTTAATTA	TTGCTGGTGG	TGTCGGTGAA	TTCGAAGCTG	200
35	GTATCTCCAA	GGATGGTCAA	ACCAGAGAAC	ACGCTTTATT	AGCATTCAAC	250
	TTAGGTGTTA	AGCAATTAAT	TGTTGCTATC	AACAAGATGG	ACTCTGTAA	300
	GTGGGATGAA	AAGAGATTTG	AAGAAATTGT	CAAGGAAACC	CAAAACTTCA	350
	TCAAGAAGGT	TGGTTACAAC	CCAAAGACTG	TTCCATTTCG	TCCAATTTCT	400
	GGTTGGAATG	GTGACAACAT	GATTGAACCA	TCTACTAACT	GTCCATGGTA	450
40	CAAGGGTTGG	ACTAAGGAAA	CCAAGGCAGG	TGTTGTTAAG	GGTAAGACCT	500
	TATTAGAAGC	TATTGATGCT	ATTGAACCAC	CTGTCAGACC	AACTGACAAG	550
	CCATTAAGAT	TACCATTACA	AGATGTTTAC	AAGATTGGTG	GTATTGGTAC	600
	TGTGCCAGTC	GGTAGAGTTG	AAACCGGTGT	TATTAAGCCA	GGTATGGTTG	650
	TTGTTTTTCG	ACCATCTGGT	GTTACCACTG	AAGTCAAGTC	CGTTGAAATG	700
45	CACCATGAAC	AATTAGAACA	AGGTGTCCCA	GGTGACAATG	TTGGTTTCAA	750
	CGTCAAGAAC	GTCTCTGTTA	AGGATATTAA	GAGAGGTAAC	GTTTGTGGTG	800
	ACTCCAAGAA	CGACCCACCA	CAAGGTTGTG	CTTCCTTCAA	TGCTCAAGTC	850
	ATTGTCTTGA	ACCACCCTGG	TCAAATTTCT	GCAGGTTACT	CTCCAGTTTT	900
	AGATTGTCAC	ACTGCCCCAC	TTGCATGTAA	GTTTCGATGAA	TTAATCGAAA	950
50	AGATTGACAG	AAGAACTGGT	AAGTCCGTTG	AAGACCATCC	AAAGTCTGTT	1000
	AAGTCTGGTG	ATGCAGCTAT	CGTTAAGATG	GTTCCAACCA	AGCCAATGTG	1050
	TGTTGAAGCT	TTCACTGAAT	ACCCACCATT	AGGTAGATTC	GCAGTCAGAG	1100
	A					1101

55

2) INFORMATION FOR SEQ ID NO: 426

(i) SEQUENCE CHARACTERISTICS:

60	(A)	LENGTH: 1095 bases
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(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida parapsilosis*
 (B) STRAIN: ATCC 90018

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426

	CAAATTGAAG	GCTGAAAGAG	AAAGAGGTAT	CACCATTGAT	ATCGCTTTGT	50
	GGAAATTCGA	AACTCCAAAA	TACCATGTTA	CTGTTATTGA	TGCTCCAGGT	100
15	CACAGAGATT	TCATCAAGAA	TATGATTACT	GGTACTTCTC	AAGCTGATTG	150
	TGCTATTTTG	ATTATTGCTG	GTGGTACTGG	TGAATTCGAA	GCTGGTATCT	200
	CTAAGGATGG	TCAAACCAGA	GAACACGCTT	TGTTGGCTTA	CACCTTGGGT	250
	GTTAAGCAAT	TGATTGTTGC	CATCAACAAG	ATGGACTCAG	TCAAATGGGA	300
	CAAGAACAGA	TACGAAGAAA	TTGTCAAGGA	AACTTCCAAC	TTCGTCAAGA	350
20	AGGTTGGTTA	CAACCCTAAA	GCTGTCCCAT	TCGTCCCAAT	CTCTGGTTGG	400
	AACGGTGACA	ATATGATTGA	ACCATCAACC	AACTGTCCAT	GGTACAAGGG	450
	TTGGGAAAAG	GAAACTAAAG	CTGGTAAGGT	TACCGGTAAG	ACCTTGTTGG	500
	AAGCTATCGA	TGCTATCGAA	CCACCAACCA	GACCAACTGA	CAAGCCATTG	550
	AGATTGCCAT	TGCAAGATGT	CTACAAGATT	GGTGGTATTG	GAAGTGTGCC	600
25	AGTTGGTAGA	GTTGAAACCG	GTATCATCAA	GGCTGGTATG	GTTGTTACTT	650
	TTGCCCCAGC	TGGTGTTACC	ACTGAAGTCA	AGTCCGTTGA	AATGCACCAC	700
	GAACAATTGA	CTGAAGGTGT	CCCAGGTGAC	AATGTTGGTT	TCAACGTCAA	750
	GAACGTTTCA	GTTAAGGAAA	TCAGAAGAGG	TAACGTTTGT	GGTGACTCCA	800
	AGAACGATCC	ACCAAAGGGA	TGTGAYTCCT	TCAATGCTCA	AGTTATTGTC	850
30	TTGAACCACC	CAGGTCAAAT	CTCTGCTGGT	TACTCACCAG	TCTTGGATTG	900
	TCACACTGCC	CACATTGCTT	GTAAATTCTG	CACCTTGATT	GAAAAGATTG	950
	ACAGAAGAAC	CGGTAAGAAA	TTGGAAGATG	AACCAAAATT	CATCAAGTCC	1000
	GGTGATGCTG	CYATCGTCAA	GATGGTCCCA	ACCAAGCCAA	TGTGTGTTGA	1050
35	AGCTTTCACT	GACTACCCAC	CATTGGGAAG	ATTGCTGTGT	AGAGA	1095

2) INFORMATION FOR SEQ ID NO: 427

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 752 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida rugosa*
 (B) STRAIN: ATCC 96275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427

	CTCCGTCAAG	TGGTCTCAGT	CTCGTTTCGA	GGAGATCGTC	AAGGAGGTTT	50
55	CCAACCTTCAT	CAAGAAGGTT	GGTTACAAGC	CCGATGAGGT	TCCTTTCGTC	100
	CCCATCTCTG	GCTGGAACGG	CGACAACATG	CTTGAGCCCT	CCACCAACTG	150
	CCCCTGGTAC	AAGGGATGGA	CCAAGAAGAC	CAAGAAGGGT	GAGGTCAAGG	200
	GTAAGACTCT	TCTCGAGGCC	ATTGACGCCA	TCGAGCCCCC	CTCCCCGTCCT	250
	ACCGACAAGC	CCCTCCGCTT	GCCTCTTCAG	GATGTCTACA	AGATCGGCGG	300
60	TATCGGTACG	GTACCTGTCTG	GCCGTGTCGA	GACCGGTATC	ATCAAGCCCCG	350

```

GCATGGTCGT CACTTTTCGCC CCGCTGGTG TCACCACTGA AGTGAAGTCC 400
GTGAGATGC ACCACGAGCA GATCCCCGAG GGTCTCCCCG GTGACAACGT 450
CGGTTTCAAC GTCAAGAACG TTACCGTCAA GGATATCCGC CGTGGTAACG 500
TCTGCGGTGA CTCCAAGAAC GACCCCCCA AGGGCTGCTC TTCCTTCACT 550
5 GCCCAGGTCA TCGTTTTCAA CCACCCCGGT CAGATCTCCA ACGGTTACTC 600
CCCCGTTTTG GACTGCCACA CCGCCCACAT TGCCTGCCGC TTCGACGAGA 650
TCCAGTCCAA GATGGACCGT CGTACTGGTA AGACCCTTGA GGAGAACCCC 700
AAGTTCATCA AGGCTGGTGA CTCCGCTATC GTCAAGATGG TTCCCTCCAA 750
GC 752

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10

2) INFORMATION FOR SEQ ID NO: 428

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15 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 1093 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
20 (ii) MOLECULE TYPE: Genomic DNA
    (vi) ORIGINAL SOURCE:
    (A) ORGANISM: Candida sphaerica
25 (B) STRAIN: ATCC 2504

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428

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AGTTAAAGGC TGAAAGAGAA AGAGGTATCA CCATCGATAT CGCTTTGTGG 50
30 AAGTTCGAAA CTCCAAAGTA CCAAGTTACC GTTATCGATG CTCCAGGTCA 100
CAGAGATTTC ATCAAGAACA TGATTACTGG TACTTCTCAA GCTGACTGTG 150
CTATCTTGAT TATTGCTGGT GGTGTCGGTG AATTCTGAAGC CGGTATCTCC 200
AAGGATGGTC AAACCAGAGA ACACGCTTTG TTGGCTTTCA CCTTGGGTGT 250
TAGACAATTG ATTGTTGCTG TTAACAAGAT GGATTCCGTT AAGTGGGATG 300
35 AATCTCGTTT CCAAGAAATT GTCAAGGAAA CCTCTAACTT CATCAAGAAG 350
GTCGGTTACA ACCCAAAGAC TGTTCCATTC GTCCCAATCT CTGGTTGGAA 400
CGGTGACAAC ATGATTGAAG CCACCACCAA TGCTTCATGG TACAAGGGTT 450
GGGAAAAGGA AACCAGTCC GGTGTCGTCA AGGGTAAGAC CTGTGTTGGAA 500
GCTATTGACG CTATCGAACC ACCATCCAGA CCAACTGACA AGCCATTGAG 550
40 ATTGCCATTG CAAGATGTCT ACAAGATTGG TGGTATCGGA ACTGTGCCAG 600
TCGGTAGAGT CGAAACCGGT GTTATCAAGC CAGGTATGAT TGTTACCTTT 650
GCCCCAGCCG GCTTACTAC TGAAGTTAAG TCCGTCGAAA TGCACCACGA 700
ACAATTGGAA GAAGGTCTAC CAGGTGACAA CGTCGGTTTC AACGTCAAGA 750
ACGTTTCCGT TAAGGAAATC AGAAGAGGTA ACGTCTGTGG TGACTCCAAG 800
45 AACGATCCAC CAAAGGCTGC TGCTTCTTTC AACGCCACTG TTATCGTCTT 850
GAACCATCCA GGTCAAATCT CTGCTGGTTA CTCTCCAGTT TTGGATTGTC 900
ACACTGCTCA CATTGCTTGT AAGTTCGACG AATTGTTGGA AAAGAACGAT 950
AGAAGATCCG GTAAGAAGTT GGAAGACTCT CCAAAGTTCT TGAAGTCCGG 1000
TGATGCTGCT TTGGTTAAGT TCGTTCCATC TAAGCCAATG TGTGTTGAAG 1050
50 CCTTCTCTGA CTACCCACCT CTAGGTAGAT TCGCTGTCAG AGA 1093

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2) INFORMATION FOR SEQ ID NO: 429

```

55 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 1094 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
60 (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Candida tropicalis*
 (B) STRAIN: ATCC 13803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429

```

10  AAATTGAAGG CTGAAAGAGA AAGAGGTATC ACCATTGATA TCGCTTTGTG      50
    GAAATTCGAA ACTCCAAAAT ACCACGTTAC CGTTATTGAT GCTCCAGGTC      100
    ACAGAGATTT CATCAAGAAC ATGATTACTG GTACTTCCCA AGCTGATTGT      150
    GCTATTTTGA TTATTGCTGG TGGTACTGGT GAATTCGAAG CTGGTATTTT      200
    TAAAGATGGT CAAACCAGAG AACACGCTTT GTTGGCTTAC ACCTTGGGTG      250
15  TCAAACAATT GATTGTTGCT GTCAACAAGA TGGACTCTGT TAAATGGGAC      300
    AAAAACAGAT TTGAAGAAAT TATCAAGGAA ACTTCTAACT TCGTCAAGAA      350
    GGTTGGTTAC AACCCTAAGG CTGTTCCATT CGTTCCAATC TCTGGTTTGA      400
    ATGGTGACAA CATGATTGAA GCTTCTACCA ACTGTCCATG GTACAAGGGT      450
    TGGGAAAAAG AAACCAAGGC TGGTAAGGTT ACCGGTAAGA CTTTGTGTGA      500
20  AGCCATTGAT GCTATTGAAC CACCTTCAAG ACCAACTGAC AAGCCATTGA      550
    GATTGGCCATT GCAAGATGTT TACAAGATTG GTGGTATTGG TACTGTGCCA      600
    GTCGGTAGAG TTGAACTGGG TGTCATCAA GCGCGTATGG TTGTTACTTT      650
    CGCCCCAGCT GGTGTTACCA CTGAAGTCAA ATCCGTCGAA ATGCACCACG      700
    AACCAATTGGC TGAAGGTGTC CCAGGTGACA ATGTTGGTTT CAACGTAAAG      750
25  AACGTTTCTG TTAAAGAAAT TAGAAGAGGT AACGTTTGTG GTGACTCCAA      800
    GAACGATCCA CCAAAGGGTT GTGACTCTTT CAACGCTCAA GTTATTGTCT      850
    TGAACCACCC AGGTCAAATC TCTGCTGGTT ACTCTCCAGT CTTGGATTGT      900
    CACACTGCTC ATATTGCTTG TAAATTCGAC ACCTTGTTG AAAAGATTGA      950
    CAGAAGAACT GGTAAGAAAT TGGAAGAAAA TCCAAAATTC GTCAAATCCG      1000
30  GTGATGCTGC TATTGTCAAG ATGGTTCCAA CCAAACCAAT GTGTGTTGAA      1050
    GCTTTCAC TG ACTACCCACC ATTAGGTAGA TTCGCTGTCA GAGA          1094
  
```

35 2) INFORMATION FOR SEQ ID NO: 430

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 1095 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Candida utilis*
 (B) STRAIN: Csp 388

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430

```

50  CAAGCTTAAA GCTGAGAGAG AGAGAGGTAT CACTATCGAC ATTGCTCTCT      50
    GGAAGTTTCG GACTCCAAAG TACCACGTTA CTGTCATTGA TGCCCCAGGT      100
    CACAGAGATT TCATCAAGAA CATGATTACT GGTACCTCCC AGGCTGACTG      150
    TGCTATTCTT ATCATTGCCG GTGGTGTTGG TGAGTTCGAG GCTGGTATCT      200
55  CTAAGGATGG TCAGACCAGA GATCACGCTT TGCTCGCTTT CACCCTTGGT      250
    GTTAGACAGA TGATTGTTGC TATCAACAAG ATGGACTCTG TCAAGTGGA      300
    CGAGAAGAGA TTCGAGGAGA TCGTTAAGGA GACCTCTAAC TTCATCAAGA      350
    AGGTTGGTTA CAACCCAAAG ACTGTTCCAT TTGTCCCAAT TTCYGGTTGG      400
    AACGGTGACA ACATGATTGA GGCCTCTACC AACTGTCCAT GGTACAAGGG      450
60  TTGGGAGAAG GAGACCAAGG CTGGTGTTGT CAAGGGTAAG ACCTTGCTCG      500
  
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ATGCCATTGA CGCCATTGAG CCACCAACAA GACCAACTGA CAAGCCATTG 550
AGATTGCCAC TCCAGGATGT CTACAAGATT GGTGGTATCG GAACTGTTCC 600
AGTCGGTAGA GTCGAGACCG GTGTCATCAA GCCAGGTATG GTTGTTACCT 650
TTGCCCCATC CGGTGTCACC ACTGAGGTTA AGTCCGTCGA GATGCACCAC 700
5 GAGCAGCTTG CTGAGGGTAT CCCAGGTGAC AACGTTGGTT TCAACGTTAA 750
GAACGTCTCT GTTAAGGAGA TCAGAAGAGG TAACGTTGCC GGTGACTCCA 800
AGAACGACCC ACCACAGGGT GCTGAGTCCT TCAACGCTCA GGTCATTGTC 850
TTGAACCACC CAGGTCAGAT CTCTGCTGGT TACTCTCCAG TTTTGGACTG 900
TCACACCGCC CACATTGCTT GTAAGTTCTC TGAGCTTTTG GAGAAGATTG 950
10 ACAGAAGATC CGGTAAGTCC CTTGAGGCCT CTCCAAAGTT CGTCAAGTCT 1000
GGTGATGCCG CTATCGTCAA GATGGTTCCA TCCAAGCCAT TGTGTGTTGA 1050
GGCCTTCACT GACTACCCAC CACTCGGTAG ATTCGCTGTC AGAGA 1095

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15

2) INFORMATION FOR SEQ ID NO: 431

(i) SEQUENCE CHARACTERISTICS:

```

20 (A) LENGTH: 1085 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Candida viswanathii
    (B) STRAIN: ATCC 28269

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30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431

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GCTGAAAGAG AAAGAGGTAT CACCATCGAT ATCGCTTTGT GGAAATTCGA 50
AACTCCAAAR TACCACGTTA CCGTCATTGA YGCTCCAGGT CACAGAGATT 100
TCATCAAGAA CATGATYACT GGTACTTCTC AAGCTGATTG TGCTATYTTG 150
35 ATTATCGCTG GTGGTACTGG TGAATTCGAA GCTGGTATYT CTAAGGATGG 200
TCAAACCAGA GAACACGCTT TGTTGGCCTA CACCTTGGGT GTCAAGCAAT 250
TGATTGTTGC TGTCACAAG ATGGACTCTG TCAAATGGGA CAAGAACAGA 300
TTCGAAGAAA TCATCAAGGA AACCTCCAAC TTCGTCAAGA AGGTTGGTTA 350
CAACCCAAAG ACTGTTCCAT TCGTCCCAAT CTCTGGTTGG AACGGTGACA 400
40 ACATGATTGA AGCCTCCACC AACTGCCCCAT GGTACAAGGG TTGGGAAAAG 450
GAAACCAAGG CTGGTAAGGT TACCGGTAAG ACTTTGTTGG AAGCCATTGA 500
CGCTATCGAA CCACCAACCA GACCAACTGA CAAGCCATTG AGATTGCCAT 550
TGCAAGATGT CTACAAGATT GGTGGTATCG GAACTGTGCC AGTCGGTAGA 600
GTTGAAACTG GTGTCATCAA GGCCGGTATG GTTGTCACCT TYGCCCCAGC 650
45 TGGTGTTACC ACTGAAGTCA AGTCCGTTGA AATGCACCAC GAACAATTGG 700
CTGAAGGTGT CCCAGGTGAC AACGTTGGTT TCAACGTCAA GAACGTTTCC 750
GTCAAGGAAA TCAGAAGAGG TAACGTCTGT GGTGACTCCA AGAACGACCC 800
ACCAAAGGGT TGTGASTCTT TCAACGCTCA AGTCATTGTC TTGAACCACC 850
CAGGTCAAAT CTCTGCTGGT TACTCTCCAG TCTTGGATTG TCACACTGCC 900
50 CACATTGCTT GTAAGTTTGA CACCTTGGTT GAAAAGATTG ACAGAAGAAC 950
CGGTAAGAAG TTGGAAGAAA ACCCAAAGTT TGTCAAGTCC GGTGACGCTG 1000
CTATCGTCAA GATGGTCCCA ACCAAGCCAA TGTGTGTTGA AGCYTTCAC 1050
GACTACCCAC CATTGGGTAG ATTCGCTGTC AGAGA 1085

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55

2) INFORMATION FOR SEQ ID NO: 432

(i) SEQUENCE CHARACTERISTICS:

```

60 (A) LENGTH: 1072 bases

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(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida zeylanoides*
 (B) STRAIN: ATCC 7351

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432

	AGGTATTACC	ATTGACATTG	CCTTGTGGAA	GTTGCGAGACC	CCCAAGTACC	50
	AGGTCACCGT	CATTGACGCT	CCTGGCCACA	GAGATTTTCAT	TAAGAACATG	100
15	ATCACTGGTA	CCTCCCAGGC	TGACTGTGCC	ATCTTGATCA	TTGCTGGTGG	150
	TGTTGGTGAG	TTCGAGGCTG	GTATCTCCAA	GGATGGCCAG	ACCAGAGAGC	200
	ACGCCTTGCT	TGCCTACACC	TTGGGTGTCA	AGCAATTGAT	TGTTGCTGTC	250
	AACAAGATGG	ACTCCGTCAA	GTGGGACAAG	AACAGATTCTG	AGGAGATTGT	300
	CAAGGAGACC	TCCAACCTCG	TCAAGAAGGT	TGGCTACAAC	CCCAAGACTG	350
20	TCCCCTTCGT	TCCCATCTCC	GGTTGGAACG	GTGACAACAT	GATTGAGGCC	400
	TCCACCAACT	GCCCTTGGTA	CAAGGGTTGG	GAGAAGGAGA	CCAAGGCCGG	450
	TAAGGTCACT	GGTAAGACCT	TGTTGGAGGC	TATTGACGCC	ATTGAGCCCC	500
	CCACCAGACC	CACCGACAAG	CCCTTGAGAT	TGCCCTTGCA	GGATGTCTAC	550
	AAGATTGGTG	GTATTGGAAC	GGTGCCCGTT	GGCAGAGTTG	AGACCGGCAT	600
25	CATCAAGGCC	GGTATGGTTG	TCACCTTTGC	CCCCGCTGGT	GTCACTACTG	650
	AAGTGAAGTC	TGTCGAGATG	CACCACGAGC	AATTGGCTGA	GGGTGTCCCA	700
	GGTGACAATG	TTGGTTTCAA	CGTGAAGAAC	GTTTCCGTTA	AGGAGATCAG	750
	AAGAGGTAAC	GTTTGCGGTG	ACTCCAAGAA	CGACCCCCCC	AAGGCTGCTG	800
	CTTCTTTCAA	CGCCCAGGTT	ATCGTCTTAA	ACCACCCCGG	TCAAATCTCT	850
30	GCTGGTTACT	CTCCGGTTTT	GGATTGCCAC	ACTGCCCACA	TTGCTTGCAG	900
	ATTCGACCAG	TTGATTGAGA	AGATCGACAG	AAGAACCAGG	AAGAAGATGG	950
	AGGACGACCC	TAAGTTCATC	AAGTCCGGTG	ACGCTGCCAT	CGTCAAGATG	1000
	GTTCTTTCCA	AGCCCATGTG	TGTTGAGGCC	TTCACTGACT	ACCCTCCCTT	1050
35	GGGTCGTTTC	GCTGTCAGAG	AC			1072

2) INFORMATION FOR SEQ ID NO: 433

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 751 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Coccidioides immitis*
 50 (B) STRAIN: Silveira

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 433

	AGCACCAACT	GGTCCGAGCC	TCGTTTCAAC	GAAATCGTCA	AGGAAGTCTC	50
55	CAACTTCATC	AAGAAGGTCG	GATACAACCC	CAAGGCTGTT	CCATTCGTCC	100
	CCATCTCTGG	TTTCGAAGGT	GACAACATGA	TTCAACCCTC	CACCAACGCT	150
	CCTTGGTACA	AGGGCTGGAA	CAAGGAGACC	GCCTCTGGCA	AGCACACTGG	200
	CAAGACCCTC	CTCGACGCCA	TTGATGCCAT	CGACCCCCCA	ACCCGCCCCA	250
	CCGAGAAGCC	CCTCCGTCTC	CCACTTCAGG	ATGTGTACAA	GATCTCTGGT	300
60	ATCGGAACAG	TCCCAGTCGG	CCGTGTGCGA	ACCGGTGTTA	TCAAGCCTGG	350

```

TATGGTTGTG ACCTTCGCTC CTTCCAACGT CACCACTGAA GTCAAGTCCG 400
TCGAAATGCA CCACCAGCAG CTCACCCAGG GTAACCCTGG TGACAACGTT 450
GGCTTCAACG TCAAGAACGT CTCTGTCAAG GAAGTCCGCC GCGGTAACGT 500
CGCTGGTGAC TCCAAGAACG ACCCACCAAA GGGCTGCGAC TCCTTCAACG 550
5 CCCAGGTCAT CGTCCTCAAC CACCCTGGTC AAGTCGGTGC TGGTTATGCC 600
CCAGTCCTTG ACTGCCACAC TGCCACATT GCTTGCAAGT TCTCCGAGCT 650
CCTCGAGAAG ATCGACCGCC GTACCGGTAA ATCCGTTGAG AACCAACCCA 700
AGTTCATCAA GTCTGGTGAT GCCGCTATCG TCAAGATGGT TCCATCCAAG 750
C 751

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10

2) INFORMATION FOR SEQ ID NO: 434

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1146 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptococcus albidus*
- (B) STRAIN: ATCC 66030

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434

```

AAGCTCAAGG CCGAGCGAGA GCGAGGTATC ACCATCGACA TCGCCTTGTG 50
30 GAAGTTCGAG ACCCCCAAGT ACAATGTCAC CGTCATTGAC GCCCCCGGTC 100
ACCGAGACTT CATCAAGAAC ATGATCACCG GTACCTCGCA GGCCGACTGT 150
GCCATCCTCA TCATCGCCTC CGGTATCGGA GAGTTCGAGG CTGGTATCTC 200
CAAGGACGGT CAGACCCGAG AGCACGCCCT TTTGGCCTTC ACCCTCGGTG 250
TCCGACAGCT CATCATTGCC ATCAACAAGA TGGACACCTG CAAGGTTAGT 300
35 TCGCAGGTCC TGGTCTCTGT ACGAATCTTG CTGACCCCTT TTACAGTGGT 350
CCGAAGACCG ATACAACGAA ATCGTCAAGG AGGCTTCCGG TTTCATCAAG 400
AAGGTCGGAT ACAACCCCAA GACCGTTCCC TTCGTCCCCA TCTCCGGATG 450
GCACGGAGAC AACATGTTGG AGGAGTCCAC CAACATGCCC TGGTACAAGG 500
GATGGCACAA GGAGTCCAAG GCCGGTGTG TCAAGGGAAA GACCTTGCTC 550
40 GAGGCCATCG ACGCCATCGA GCCCCCTACC CGACCTTCCG ACAAGCCCTT 600
GCGATTGCC CTCCAGGATG TCTACAAGAT CGGTGGTATC GGTACGGTGC 650
CCGTCGGTCG AGTCGAGACC GGTGTCATCA AGGCTGGTAT GGTGTCACC 700
TTCGCCCCCTG CCAACGTCAC CACCGAAGTC AAGTCCGTCG AAATGCACCA 750
CGAACAGCTC GCTGAGGGTG TTCCCGGTGA CAACGTCGGT TTCAACGTCA 800
45 AGAACGTTT CGTCAAGGAC ATCCGACGAG GAAACGTCTG CTCCGACTCG 850
AAGAACGACC CCGCTATGGA GTCTGCTTCC TTCAACGCTC AGGTCATTGT 900
CTTGAACCA CCGGGTCAGA TCGGTGCCCG CTACTCCCCG GTTTTGGACT 950
GCCACACCG TCACATTGCC TGCAAGTTTC CTGAGCTCGT TGAGAAGATC 1000
GACCGACGAA CCGGTAAGGT CATGGAGGCC GCCCCCAAGT TCGTCAAGTC 1050
50 CGGTGACGCC GCCATCGTCA AGTTGATCCC GTCCAAGCCC ATGTGTGTGC 1100
AGTCCTACTC CGAGTACCCC CCCTTGGGTC GATTCGCCGT CCGAGA 1146

```

55 2) INFORMATION FOR SEQ ID NO: 435

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1095 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double

60

(D) . TOPOLOGY: Linear

(ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

(A) ORGANISM: *Exophiala jeanselmei*

(B) STRAIN: ATCC 64755

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 435

```

10 CAAGCTGAAG GCCGAGCGTG AGCGTGGTAT CACCATCGAT ATCGCCTTGT      50
   GGAAGTTCGA GACTCCCAAG TACTATGTCA CTGTCATCGA CGCCCCTGGT      100
   CATCGTGACT TTATCAAGAA CATGATCACT GGTACTTCCC AGGCTGACTG      150
   CGCCATTCTC ATCATTTGCCG CCGGTACTGG TGAATTCGAA GCCGGTATCT      200
15 CCAAGGATGG TCAGACTCGT GAGCACGCTC TGCTCGCCTA CACCCTGGGT      250
   GTCAAGCAGC TCATTGTGCG CATCAACAAG ATGGACACCA CCAAGTGGTC      300
   CGAGGATCGT TTCAACGAAA TCATCAAGGA GACTTCCAGC TTCATCAAGA      350
   AGGTCGGCTA CAACCCCAAG TCCGTTCCCT TCGTCCCCAT CTCCGGCTTC      400
   AACGGTGACA ACATGATCGA TGTCTCCACC AACTGCCCTT GGTACAAGGG      450
20 CTGGGAGAAG GAGACCAAGG CTGGCAAGGC CTCTGGCAAG ACTCTCCTCG      500
   AGGCCATCGA CGCCATCGAC CCCCCACTC GTCCCACCGA CAAGCCTCTC      550
   CGTCTTCCTC TCCAGGATGT CTACAAGATC TCTGGTATCG GAACGGTGCC      600
   CGTCGGTCGT GTTGAGACTG GTGTCATCAA GGCCGGTATG GTCGTTACCT      650
   TCGCTCCTGC CAACGTCACC ACTGAAGTCA AGTCCGTCGA AATGCACCAC      700
25 GAACAACTCG CCGAGGGTGT TCCAGGTGAC AACGTTGGTT TCAACGTCAA      750
   GAACGTCTCC GTCAAGGAGG TTCGTCGTGG AAACGTCTGC GGTGACTCCA      800
   AGAACGACCC ACCCAAGGGT GCTGATTCCCT TCAACGCCCA GGTCATCGTC      850
   TTGAACCACC CTGGTCAAGT CGGTGCTGGC TACGCCCCAG TGTGATTG      900
   CCACACTGCC CACATTGCTT GCAAGTTCTC TGAGCTTCTC GAGAAGATTG      950
30 ACCGCCGTAC CGGTAAATCC ATCGAAAACA ACCCAAGTT CATCAAGTCT      1000
   GGTGACGCTG CCATCGTCAA GATGGTTCCC AGCAAGCCCA TGTGTGTTGA      1050
   GGCCTTCACT GACTACCCAC CTCTTGGTCG TTTGCCGTC CGTGA          1095

```

35

2) INFORMATION FOR SEQ ID NO: 436

(i)SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1113 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii)MOLECULE TYPE: Genomic DNA

(vi)ORIGINAL SOURCE:

(A) ORGANISM: *Fusarium oxysporum*

(B) STRAIN: WSA-212

(xi)SEQUENCE DESCRIPTION: SEQ ID NO: 436

```

55 AAGCTCAAGG CCGAGCGTGA GCGTGGTATC ACCATCGATA TTGCTCTCTG      50
   GAAGTTCGAG ACTCCTCGCT ACTATGTCAC CGTCATTGGT ATGTTGTCGC      100
   TCATGCTTCA TTCTACTTCT CTTTCGTACTA ACACATCACT CAGACGCTCC      150
   CGGTCACCGT GATTTTCATCA AGAACATGAT CACTGGTACT TCCCAGGCCG      200
   ATTGCGCCAT TCTCATCATT GCCGCCGGTA CTGGTGAGTT CGAGGCTGGT      250
   ATCTCCAAGG ATGGCCAGAC CCGTGAGCAC GCTCTTCTTG CCTACACCCT      300
   TGGTGTCAAG AACCTCATCG TCGCCATCAA CAAGATGGAC ACCACCAAGT      350
   GGTCTGAGGC CCGTTACCAG GAGATCATCA AGGAGACCTC CTCTTTCATC      400
60 AAGAAGGTCG GCTACAACCC CAAGGCTGTC GCTTTCGTCC CCATCTCCGG      450

```

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TTTCAACGGT GACAACATGC TTACCCCCTC CACCAACTGC CCCTGGTACA 500
AGGGTTGGGA GCGTGAGATC AAGTCCGGCA AGCTCACTGG CAAGACCCTC 550
CTCGAGGCCA TTGACTCCAT CGAGCCCCCC AAGCGTCCCG TTGACAAGCC 600
CCTTCGTCTT CCCCTTCAGG ATGTCTACAA GATCGGTGGT ATTGGAACGG 650
5 TTCCCGTCGG CCGTATCGAG ACTGGTGTCA TCAAGCCCGG TATGGTCGTT 700
ACCTTCGCTC CTTCCAACGT CACCACTGAA GTCAAGTCCG TCGAGATGCA 750
CCACGAGCAA CTCACTGAGG GCCAGCCCGG TGACAACGTT GGTTCACACG 800
TGAAGAACGT CTCCGTCAAG GACATCCGAC GTGGTAACGT CGCTGGTGAC 850
TCCAAGAACG ACCCCCCTAT GGGTGCCGCT TCTTTCACCG CCCAGGTCAT 900
10 CGTCCTCAAC CACCCCGGTC AGGTCGGTGC TGGTTACGCT CCCGTCCTCG 950
ATTGTCACAC TGCCACATT GCCTGCAAGT TCGCCGAGAT CCAGGAGAAG 1000
ATCGACCGCC GAACCGGTAA GGCTACTGAG GCCGCCCCCA AGTTCATCAA 1050
GTCTGGTGAC TCCGCCATCG TCAAGATGGT TCCCTCCAAG CCCATGTGTG 1100
TTGAGGCTTT CAC 1113
15

```

2) INFORMATION FOR SEQ ID NO: 437

```

20 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 726 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
25 (ii) MOLECULE TYPE: Genomic DNA
    (vi) ORIGINAL SOURCE:
    (A) ORGANISM: Geotrichum spp.
30 (B) STRAIN: LEV-4

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437

```

GGTCCGAGGA CAGATTCAAC GAGATTGTCA AGGAGACTTC CAACTTCATC 50
35 AAGAAGGTTG GTTAYAACCC CAAGACTGTT GCTTTCGTCC CCATCTCTGG 100
TTGGAACGGT GACAACATGA TTGAGCCCTC CACCAACTGC CCCTGGTACA 150
AGGGATGGCA GAAGGAGACC AAGGCTGGTG TACTAAGGG TAAGACCCTC 200
CTTGAGGCCA TCGATGCCAT TGAGCCCCCT GTCAGACCTT CCGACAAGCC 250
CCTCCGTCTT CCCCTCCAGG ATGTCTACAA GATCGGTGGT ATCGGAAGCTG 300
40 TGCCCGTCGG CCGTGTCGAA ACCGGTGTCA TCAAGGCCGG TATGGTCGTC 350
ACCTTCGCCC CCGCTGGTGT CACCACTGAA GTCAAGTCCG TCGAGATGCA 400
CCACGAGCTC CTCACTGAGG GTCTCCCCGG TGACAACGTT GGTTCACACG 450
TCAAGAACGT CTCCGTTAAG GATATCAGAC GTGGTAACGT CTGCGGTGAC 500
TCCAAGAACG ATCCCCCAA GGCTTGCGCT TCTTTCACCG CCCAGGTCAT 550
45 TATCTTCAAC CACCCTGGTC AGATCTCTGC TGGATACTCT CCCGTCCTTG 600
ATTGCCACAC CGCCCATATT GCTTGCAAGT TCGACACTTT GATCGAGAAG 650
ATTGACCGTC GTACTGGTAA GAAGACTGAG GACTCCCCCA AGTTCGTCAA 700
GGCCGGTGAT GCTGCTATCG TCAAGA 726
50

```

2) INFORMATION FOR SEQ ID NO: 438

```

55 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 754 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
60 (ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Histoplasma capsulatum*
 (B) STRAIN: G186A5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438

```

5      CACCACCAAG TGGTCCGAGT CCCGTTTCAA CGAAATCATC AAGGAGGTTT      50
      CCAACTTCAT CAAGAAGGTC GGATATAACC CCAAGGCTGT TCCCTTCGTG      100
10     CCAATCTCTG GTTTCGAGGG TGACAACATG ATTGAACCCT CCCCCAACTG      150
      CACATGGTAC AAGGGCTGGA ACAAGGAGAC TGCCTCTGGC AAGTCTTCTG      200
      GTAAAAACCT TCTCGATGCC ATTGACGCCA TTGAACCCCC AACCCGTCCT      250
      ACCGATAAGC CCCTCCGTCT TCCCCTCCAG GATGTGTACA AAATCTCTGG      300
      TATTGGCACT GTTCCCCTCG GACGTGTTGA GACTGGTGTC ATCAAGCCCG      350
15     GTATGGTCGT GACTTTCGCT CCCTCCAACG TCACCACTGA AGTCAAGTCC      400
      GTCGAAATGC ACCACCAACA ACTCCAGGCT GGTTACCCTG GCGACAACGT      450
      CGGCTTCAAC GTCAAGAACG TTTCAGTCAA GGAAGTCCGC CGTGGCAACG      500
      TTGCTGGCGA CTCCAAAAAT GATCCCCCTA AGGGCTGCGA ATCCTTCAAT      550
      GCCCAGGTCA TCGTCCTTAA CCACCCCGGC CAGGTTGGCG CTGGTTATGC      600
20     CCCAGTCCTC GACTGCCACA CTGCCACAT TGCTTGCAAG TTCTCTGAGC      650
      TTATTGAGAA GATCGACCGC CGTACCGGAA AGTCTGTTGA GAACAACCCC      700
      AAGTTCATCA AGTCTGGTGA TGCTGCTATC GTCAAGATGG TTCCCTCCAA      750
      GCCC
  
```

2) INFORMATION FOR SEQ ID NO: 439

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 743 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Issatchenkia orientalis kudrjanzev*
 (B) STRAIN: ATCC 6258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439

```

      TGGGATGAAA ACAGATTTGA AGAAATTGTC AAGGAAACCC AAAACTTCAT      50
      CAAGAAGGTT GGTTACAACC CAAAGACTGT TCCATTCGTT CCAATCTCTG      100
45     GTTGGAATGG TGACAACATG ATTGAAGCAT CCACCAACTG TCCATGGTAC      150
      AAGGGTTGGA CTAAGGAAAC CAAGGCAGGT GTTGTTAAGG GTAAGACCTT      200
      ATTAGAAGCA ATCGATGCTA TTGAACCACC TGTCAGACCA ACCGAAAAGC      250
      CATTAAGATT ACCATTACAA GATGTTTACA AGATTGGTGG TATTGGTACT      300
      GTGCCAGTCG GTAGAGTCGA AACCAGTGTC ATTAAGCCAG GTATGGTTGT      350
50     CACTTTTGCT CCAGCAGGTG TCACCACCGA AGTCAARTCC GTTGAAATGC      400
      ACCATGAACA ATTAGAACAA GGTGTTCCAG GTGATAACGT TGGTTTCAAC      450
      GTTAAGAACG TCTCTGTCAA GGATATCAAG AGAGGTAACG TTTGTGGTGA      500
      CTCCAAGAAC GACCCACCAA TGGGTGCAGC TTCYTTCAAT GCTCAAGTCA      550
      TTGTCTTGAA CCACCCTGGT CAAATTTCAG CTGGTTACTC TCCAGTCTTG      600
55     GATTGTCACA CTGCCACAT TGCATGTAAG TTCGACGAAT TAATCGAAAA      650
      GATTGACAGA AGAACTGGTA AGTCTGTTGA AGACCATCCA AAGTCYGTCA      700
      AGTCTGGTGA TGCAGCTATC GTCAAGATGG TCCAACCAA GCC      743
  
```

2) INFORMATION FOR SEQ ID NO: 440

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1091 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Malassezia furfur*
 (B) STRAIN: ATCC 42132

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 440

```

CAAGCTCAAG GCTGAGCGTG AGCGTGGTAT CACCATCGAC ATTGCTCTGT      50
GGAAGTTCGA GACCCCTAAG TACCACGTTA CCGTCATTGA CGCTCCTGGT      100
CACCGTGACT TCATCAAGAA CATGATTACG GGTACCTCGC AGGCTGACTG      150
CGCTATCCTC ATCATTGCCG GTGGTACCGG TGAGTTCGAG GCTGGTATCT      200
CGAAGGACGG TCAGACCCGT GAGCACGCTC TGCTCGCTTT CACCCTGGGT      250
GTGCGTCAGC TCATTGTGGC CGTCAACAAG ATGGACACCA CCAAGTACTC      300
GGAGGACCGC TTCAACGAGA TTGTCCGCGA AGTGTCGAAC TTCATCAAGA      350
AGGTCGGTTT CAACCCCAAG ACTGTTGCCT TCGTCCCAT CTGGGGCTGG      400
CACGGTGACA ACATGATCGA GGCCACCACC AACATGCCTT GGTACAAGGG      450
CTGGGAGAAG GAGACCAAGT CGGGCAAGGT CACTGGTAAG ACTCTGCTGG      500
ACGCCATCGA CGCCATCGAG CCCCCGACCC GCCCCACTGA CAAGCCCCTG      550
CGTCTCCCTC TGCAGGATGT GTACAAGATC GGTGGTATCG GTACTGTCCC      600
TGTGCGTCTG GTTGAGACCG GTGTGATCAA GCCCGGTATG GTTGTGACCT      650
TCGCTCCCTC GAACGTCACC ACTGAAGTTA AGTCGGTTGA GATGCACCAC      700
GAGTCGCTCC CTGAGGGTCT CCCCAGGTGAC AACGTTGGTT TCAACGTGAA      750
GAACGTCTCG GTTAAGGACA TTCGCCGTGG TAACGTTGCC TCGGACTCGA      800
AGAACGACCC CGCTCAGGAG GCTGCTTCGT TCAACGCGCA GGTCATTGTC      850
ATGAACCACC CTGGTCAGAT CAGCAACGGT TACTCGCCCG TGCTTGACTG      900
CCACACTGCG CACATTGCCT GCCGCTTCAA CAACATCCTC CAGAAGATCG      950
ACCGTCGCTC GGGTAAGGTG CTTGAGGAGA ACCCCAAGTT CATCAAGTCG     1000
GGTGACGCTG CCATGGTGGA GATGATCCCC ACCAAGCCCA TGTGTGTGGA     1050
GTCGTTCAAC GAGTACCCCC CTCTGGGTCG TTTCGCTGTG C              1091

```

2) INFORMATION FOR SEQ ID NO: 441

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 749 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Malassezia pachydermatis*
 (B) STRAIN: ATCC 42756

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 441

```

ACCACCAAGT ACTCGGAGGA CCGCTTCAAC GAGATTATTC GCGAGACTTC      50
GAACCTTCATC AAGAAGGTCG GTTACAACCC GAAGACTGTT GCCTTCGTCC      100
CGATCTCGGG CTGGCACGGT GACAACATGA TTGAGGCGAC CACCAACATG      150

```

	CCGTGGTACA	AGGGCTGGGA	GAAGGAGACC	AAGTCGGGCA	AGGCCACTGG	200
	TAAGACCCTT	CTGGACGCTA	TTGACGCCAT	TGAGCCGCCG	ACGCGCCCGA	250
	CCGACAAGCC	TCTCCGTCTT	CCTCTCCAGG	ATGTGTACAA	GATCGGTGGT	300
	ATCGGTACYG	TCCCAGTCCG	CCGTGTTGAG	ACCGGTGTTA	TCAAGCCCGG	350
5	TATGGTTGTG	ACCTTCGCTC	CGTCGAACGT	CACSACTGAA	GTTAAGTCGG	400
	TCGAGATGCA	CCACGAGCAG	ATCCCTGAGG	GTCTTCCGGG	TGACAACGTT	450
	GGTTTCAACG	TGAAGAACGT	GTCGGTCAAG	GACATTCGCC	GTGGTAACGT	500
	CGCCTCGGAC	TCGAAGAACG	ACCCGGCTCA	GGAGGCTGCC	TCGTTCAATG	550
	CTCAGGTCAT	TGTGATGAAC	CACCCTGGTC	AGATCAGCAA	CGGTTACTCG	600
10	CCRGTTGCTCG	ACTGCCACAC	TGCTCACATT	GCCTGCCGCT	TCAACAACAT	650
	CCTCCAGAAG	ATCGACCGTC	GTTCCGGTAA	GGTTCTYGAA	GAGAACCCCA	700
	AGTTCATCAA	GTCGGGTGAC	GCTGCCATGG	TTGAGATGAT	CCCGACCAA	749

15

2) INFORMATION FOR SEQ ID NO: 442

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 1150 bases
20	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

(A)	ORGANISM: <i>Malbranchea filamentosa</i>
(B)	STRAIN: ATCC 48174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 442

	ACTGAAGGCC	GAGCGTGAGC	GTGGTATCAC	CATCGATATC	GCCCTCTGGA	50
	AGTTCGAGAC	CCCCAAGTAC	CATGTCACCG	TCATTGGTAC	GTTCGACATG	100
	TTCGACCTTT	TGCCTAGTGT	CCCCTTCTAA	CCACAGTTTA	TAGACGCCCC	150
35	TGGCCATCGT	GATTTTCGTCA	AGAACATGAT	CACTGGTACT	TCCCAGGCTG	200
	ATTGCGCTAT	CCTCATCATT	GCTTCCGGCA	CTGGTGAATT	CGAGGCTGGT	250
	ATCTCCAAGG	ATGGCCAGAC	CCGTGAGCAC	GCTCTGCTTT	CCTTCACCCCT	300
	CGGTGTTAGG	CAGCTCATTG	TCGCCCTCAA	CAAGATGGAC	ACTGTCAACT	350
	TCGCTGAGGC	CCGTTACAAC	GAGATTGTCA	AGGAAGTCTC	CAACTTCATC	400
40	AAGAAGGTCG	GCTACAACCC	CAAGGCCGTT	CCTTTCGTCC	CCATCTCCCG	450
	TTTCGAGGGT	GACAACATGA	TCGAGGCCTC	CACCCGCATT	CCTTGGTACA	500
	AGGGCTGGAA	CAAGGAGACC	GCCAGTGGCA	AGAGCACCGG	CAAGACCCTY	550
	CTCGAGGCCA	TTGATGCCAT	CGAACCCCGG	GTCCGTCCCA	CCGACAAGCC	600
	CCTYCGTCTC	CCTCTTCAGG	ATGTGTACAA	GATCTCCGGT	ATTGGCACTG	650
45	TTCTGTTCGG	TCGTGTTGAG	ACTGGTGTCA	TCAAGCCTGG	TATGGTCGTT	700
	ACTTTCGCCC	CCGCCAACGT	CACCACTGAA	GTCAAGTCCG	TCGAGATGCA	750
	CCACCAGCAG	CTCCAGGCCG	GTAACCCCGG	TGACAACGTC	GGCTTCAACG	800
	TCAAGAACGT	TTCCGTCAAG	GAAGTCCGCC	GTGGCAACGT	TGCCTCCGAC	850
	TCCAAGAACG	ACCCCGCCAA	GGGCTGCGAC	TCCTTCAACG	CCCAGGTCAT	900
50	CGTCCTTAAC	CACCCCGGTC	AGGTCGGTGC	TGGATACGCT	CCCGTCCTCG	950
	ATTGCCACAC	TGCCCACATT	GCTTGCAAGT	TCTCTGAGCT	TCTTGAGAAG	1000
	ATCGATCGCC	GTACCGGTAA	ATCCGTTGAG	GACCACCCCA	AGTTCATCAA	1050
	GTCTGGTGAT	GCCGCTATCG	TCAAGATGGT	TCCCTCCAAG	CCTATGTGCG	1100
55	TTGAGGCTTT	CACTGACTAC	CCTCCCCTTG	GTCGTTTCGC	CGTCCGTGAC	1150

2) INFORMATION FOR SEQ ID NO: 443

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1099 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Metschnikowia pulcherrima*
 (B) STRAIN: DSM 70336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 443

15	GGACAAGTTG	AAGGCTGAGA	GAGAGAGAGG	TATCACCATC	GACATTGCCT	50
	TGTGGAAGTT	CGAGACTCCT	AAGTACCACG	TCACCGTYAT	TGACGCCCCA	100
	GGTCACAGAG	ATTTTCATCA	GAACATGATC	ACTGGTACTT	CCCAGGCTGA	150
	CTGTGCTATC	TTGATTATCG	CYGGTGGTGT	TGGTGAGTTC	GAGGCTGGTA	200
	TCTCCAAGGA	TGGCCAGACC	AGAGAGCACG	CTTTGTTGGC	YTACACCTTG	250
	GGTGTTAGAC	ARTTGATTGT	TGCCGTCAAC	AAGATGGACT	CTGTCAAGTG	300
20	GGACAAGAAC	AGATTGAGG	AGATCATCAA	GGAGACCTCT	AACTTCGTCA	350
	AGAAGGTTGG	TTACAACCCT	AAGACYGTGC	CATTCGTGCC	AATYTCTGGT	400
	TGGAACGGTG	ACAACATGAT	TGAGGCYTCC	ACTAACTGCC	CATGGTACAA	450
	GGGTTGGGAG	AAGGAGACCA	AGGCCGGTAA	GTCTWCCGGT	AAGACCTTGT	500
	TGGAGGCCAT	TGACGCCATT	GAGCCACCAA	CCAGACCTAC	CGACAAGGCC	550
25	TTGAGATTGC	CTTTGCAGGA	TGTCTACAAG	ATCGGTGGTA	TCGGAACGGT	600
	GCCAGTCGGC	CGTGTCGAGA	CCGGTGTCTA	TAAGGCCGGT	ATGGTTGTYA	650
	CCTTYGCCCC	AGCTGGTGTG	ACCACTGAGG	TCAAGTCCGT	CGAGATGCAC	700
	CACGAGCAGT	TGGTCGAGGG	TCTTCCAGGT	GACAAYGTTG	GTTTCAACGT	750
	CAAGAACGTC	TCCGTTAAGG	AGATCAGAAG	AGGTAACGTC	TGTGGTGAAT	800
30	CCAAGCAGGA	CCCACCAAAG	GGTGCCGCTT	CTTTCACCGC	YCAGGTTATT	850
	GTGTTGAACC	ACCCTGGTCA	GATCTCCTCT	GGTTACTCTC	CAGTGTGGGA	900
	CTGYCACACC	GCCCACATTG	CCTGTAARTT	CGACACCTTG	TTGGAGAAGA	950
	TTGACAGAAG	AACTGGTAAG	TCCTTGGAGT	CYGAGCCTAA	GTTTCGTCAAG	1000
	TCYGGTGACG	CCGCCATTGT	CAAGATGGTG	CCAACCAAGC	CAATGTGTGT	1050
35	TGAGGCTTTC	ACCGACTACC	CACCTTTGGG	TAGATTCGCC	GTCAGAGAC	1099

2) INFORMATION FOR SEQ ID NO: 444

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1153 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Paecilomyces lilacinus*
 (B) STRAIN: ATCC 42570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 444

55	CAAGCTCAAG	GCCGAGCGTG	AGCGTGGTAT	CACCATCGAC	ATTGCCCTCT	50
	GGAAGTTCGA	GACTCCCAAG	TACTATGTCA	CCGTCATTGG	TACGTCGACT	100
	CGCGCGAGAC	TGGTCGCAAT	TTCCACGTCG	CTAACGTGCT	TGAACAGACG	150
	CTCCCGGCCA	CCGTGACTTC	ATCAAGAACA	TGATCACTGG	TACCTCCAG	200
	GCTGACTGCG	CTATCCTCAT	TATCGCTGCC	GGCACTGGTG	AGTTCGAGGC	250
60	TGGTATCTCC	AAGGATGGCC	AGACCCGTGA	GCACGCTCTG	CTCGCCTACA	300

CCCTCGGTGT TAAGCAGCTC ATCGTCGCTA TCAACAAGAT GGACACCACC 350
 AAGTGGTCTG AGGCCCGTTT CCAGGAGATC ATCAAGGAGA CCTCCAACCTT 400
 CATCAAGAAG GTCGGCTACA ACCCCAAGAC CGTCGCTTTC GTCCCCATCT 450
 CTGGTTTCCA CGGCGACAAC ATGCTTTCCC CCTCCACCAA CTGCCCCCTGG 500
 5 TACAAGGGCT GGGAGAAGGA GACCAAGGCT GGCAAGTCCA CCGGCAAGAC 550
 CCTCCTTGAG GCCATCGACT CCATCGAGCC CCCCAGCGC CCCAGCGACA 600
 AGCCCCCTCCG CTTTCCCCTT CAGGATGTGT ACAAGATCGG CGGTATCGGC 650
 ACAGTCCCTG TCGGCCGTAT CGAGACTGGT GTCATCAAGC CCGGCATGGT 700
 CGTGACCTTC GCTCCTTCCA ACGTCACCAC CGAAGTCAAG TCCGTTGAGA 750
 10 TGCACCACGA GCAGCTCTCC GAGGGTGTCC CCGGTGACAA CGTCGGCTTC 800
 AACGTCAAGA ACGTCTCCGT CAAGGAGATC CGTCGTGGCA ACGTCGCCCG 850
 TGACTCCAAG AACGACCCCC CTCTGGGTGC CGCTTCTTTC GATGCCCCAGG 900
 TCATCGTCCT CAACCACCCC GGCCAGGTGC GTGCTGGCTA CGCCCCCGTC 950
 CTCGACTGCC ACACCGCCCA CATTGCCTGC AAGTTCGCCG AGATCAAGGA 1000
 15 GAAGATCGAC CGCCGTACCG GCAAGTCTGT CGAGTCCGCC CCAAGTTCA 1050
 TCAAGTCTGG CGACTCTGCC ATCGTCAAGA TGATTCCCTC CAAGCCCATG 1100
 TGCGTTGAGG CTTTCACCGA CTACCCTCCT CTGGGCCGCT TCGCCGTCCG 1150
 TGA 1153

20

2) INFORMATION FOR SEQ ID NO: 445

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 763 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Paracoccidioides brasiliensis*
 (B) STRAIN: ATCC 32071

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 445

TACCACTAAG TGGTCCGAGA CCCGATTCAA TGAAATTATC AAGGAAGTCA 50
 CCAATTTTCAT TAAGAAGGTC GGATATAACC CCAAGACTGT TCCTTTTCGTT 100
 40 CCCATTTCTG GTTTCGAGGG TGACAACATG ATCGAGCCCT CTGCCAACTG 150
 CCCATGGTAC AAGGGCTGGT CCAAGGAGAC TGCTCAGGGC AAGTACTCTG 200
 GCAAGACCCT TCTTGAGGCC ATCGACGCCA TTGAGCCCCC CACCCGTCTT 250
 ACCGATAAAC CTCTCCGTCT TCCCCTCCAG GATGTCTACA AGATCTCCGG 300
 TATTGGCACT GTTCCTGTCT GACGTGTTGA GACTGGAGTC ATCAAGCCCG 350
 45 GTATGGTTCGT GACCTTCGCT CCCGCCAACG TCACCACTGA AGTCAAGTCC 400
 GTCGAAATGC ACCACCAGCA GCTTACCGCC GGTAACCCCG GTGACAACGT 450
 CGGCTTCAAC GTCAAGAATG TTTCCGTCAA AGAAGTCCGC CGTGGTAACG 500
 TTGCCGGTGA CTCTAAGAAT GATCCCCCAA AGGGCTGCGA TTCCTTCAAT 550
 GCCCAGGTCA TCGTCCTCAA CCACCTGGT CAGGTTGGCG CTGGTTATGC 600
 50 CCCAGTCCTC GACTGCCATA CTGCCCACAT TGCCTGCAAA TTCGCTGAGC 650
 TCCTTGAGAA GATTGATCGA CGAACC GGAA AGTCTGTTGA GAACAACCCC 700
 AAGTTCATCA AGTCCGGTGA TGCTGCTATC GTCAAGATGA TTCCTTCCAA 750
 GCCCATGTGC GTC 763

55

2) INFORMATION FOR SEQ ID NO: 446

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 1346 bases

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Penicillium marneffe*
 (B) STRAIN: ATCC 64101

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446

	AAGCTCAAGG	CTGAGCGTGA	GCGTGGTATC	ACCATCGATA	TTGCTCTCTG	50
	GAAGTTCCAG	ACTGCCAAGT	ACGAGGTTAC	CGTCATTGAC	GCCCCCGGTC	100
15	ACCGTGATTT	CATCAAGAAC	ATGATCACTG	GTACCTCCCA	GGCCGATTGC	150
	GCTATTCTCA	TCATTGCCTC	TGGTACTGGT	GAATTCGAGG	CTGGTATCTC	200
	CAAGGATGGC	CAGACTCGTG	AGCACGCTCT	TTTGGCTTTC	ACCCTCGGTG	250
	TCCGTCAGCT	CATTGTTGCC	CTCAACAAGA	TGGACACTTG	CAAGTGGTCT	300
	CAGGGTGAGT	ACTCGTACCT	GCGTTTGGCC	TTGAATATCT	TACTAATGCA	350
20	CCATAGATCG	TTACAACGAA	ATTGTCAAGG	AGACTTCCAA	CTTCATCAAG	400
	AAGGTCGGAT	ACAACCCCAA	GAACGTTTCT	TTCGTTCTTA	TCTCCGGTTT	450
	CAACGGTGAC	AACATGCTTG	AGCCCTCCCC	CAACTGCCCC	TGGTACAAGG	500
	GTTGGGAGAA	GGAGACCAAG	GCCGGTAAGG	TCACTGGTAA	GACCCCTCCTC	550
	GAGGCCATCG	ACGCCATTGA	GCCCCCTACC	CGTCCC GCCA	ACAAGGTTAG	600
25	TCCCTCCTCG	ACTACTCAAA	CCCTCCTCAT	AAGTTCAGAT	TACTGACTCG	650
	TTCACAGCCC	CTCCGTCTTC	CCCTCCAGRA	TGTCTACAAG	ATCGGTGGTA	700
	TTGGAACGGT	TCCCGTCCGT	CGTGTGAGA	CTGGTACCAT	CGTTCCTGGT	750
	ATGGTTGTCA	CCTTGTAAGT	CACTCTCCTC	GCTTATCCTA	CCTGAAATCA	800
	TCATGTGCTA	ACTTGACACT	CAGCGCTCCC	GCCAACGTCA	CCACTGAAGT	850
30	CAAGAGTGTT	GAAATGCACC	ACCAGCAGCT	CACTGCCGGT	CAGCCCCGGTG	900
	ACAACGTTGG	TTTCAACGTG	AAGAACGTCT	CCGTCAAGGA	AATCCGTCGT	950
	GGTAACGTTG	CTGGTGACAG	CAAGAACGAC	CCCCCTGCCG	GTGCTGCCTC	1000
	CTTCAACGCC	CAGGTCATCG	TCCTCAACCA	CCCCGGTCAG	GTCGGTGCTG	1050
	GTTACGCCCC	AGTCCTCGAT	TGCCACACTG	CCCACATTGC	TTGCAAGTTC	1100
35	GCTGAGCTCC	TCGAGAAGAT	TGACCGTCGT	ACCGGAAAGT	CTGTTGAGGA	1150
	CCACCCCAAG	TTCATCAAGT	CCGGTGACGC	TGCCATCGTC	AAGATGATTC	1200
	CTTCCAAGCC	CATGTGTGTT	GAGGCTTTCA	CCGAGTACCC	TCCTCTCGGT	1250
	CGTTTCGCCG	FTCGCGAGTA	AGTTTTATCT	CCGTTGTCTA	TTTTCCATCC	1300
40	TTCCCTTCTC	CTCCGTCTTC	CATATATACT	TTTTCAGTTA	TATGTG	1346

2) INFORMATION FOR SEQ ID NO: 447

45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1094 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pichia anomala*
 (B) STRAIN: ATCC 18205

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 447

	AAGTTAAAAG	CTGAACGTGA	AAGAGGTATC	ACTATTGATA	TTGCTTTATG	50
60	GAAATTCGAA	ACTCCAAAAT	ACCATGTTAC	CGTTATTGAT	GCTCCAGGTC	100

	ACAGAGATTT	CATCAAAAAT	ATGATTACTG	GTACTTCCCA	AGCTGATTGT	150
	GCTATYTTAA	TTATTGCCGG	TGGTATTGGT	GAATTCGAAG	CTGGTATCTC	200
	AAAAGATGGT	CAAACCAGAG	AACACGCTTT	NTTAGCTTAC	ACCTTAGGTG	250
	TTAAACAATT	GATTGTTGCT	ATCAACAAGA	TGGATTCCGT	TAAATGGGAT	300
5	GAATCTCGTT	TCGAAGAAAT	TGTCAAGGAA	ACYTCAAAC	TTATCAAGAA	350
	AGTTGGTTAC	AACCCAAAAA	CTGTTCCATT	CGTTCCAATC	TCAGGTTGGA	400
	ATGGTGATAA	CATGATTGAA	CCATCAWCTA	ACTGTCCATG	GTACAAAGGT	450
	TGGAAAAAAG	AAACCAAAGC	TGGTGAAGCT	AAAGGTAAAA	CTTTATTAGA	500
	AGCCATTGAT	GCTATTGACC	CACCATCAAG	ACCAACTGAT	AAACCATTAC	550
10	GTTTACCATT	ACAAGATGTT	TACAARATTG	GTGGTATTGG	TACTGTGCCA	600
	GTCGGTAGAG	TTGAAACCGG	TGTTATCAAA	CCAGGTATGG	TTGTTACCTT	650
	TGCCCCAGCT	GGTGTTACCA	CTGAAGTCAA	ATCTGTTGAA	ATGCATCATG	700
	AACAATTGAC	TGAAGGTTTA	CCAGGTGACA	ATGTTGGTTT	CAACGTTAAG	750
	AATGTTTCTG	TTAAAGAAAT	CCGTCGTGGT	AACGTCTGTG	GTGACTCTAA	800
15	AAACGATCCA	CCAAAAGCTG	CTGAATCATT	CAATGCTCAA	GTTATTGTCT	850
	TAAACCATCC	AGGTCAAATC	TCTGCTGGTT	ACTCTCCAGT	TTTAGATTGT	900
	CACACTGCTC	ACATTGCTTG	TAAATTTGAC	ACTTTAATTG	AAAAAATTGA	950
	CAGACGTACT	GGTAAGAAAT	TAGAAGAAGC	TCCAAAATTC	ATCAAATCAG	1000
	GTGATGCTGC	TATTGTTAAA	TTTGTTCAT	CAAAACCATT	ATCAGTTGAA	1050
20	GCTTTCACTG	ACTACCCACC	ATTAGGTCGT	TTCGCTGTCA	GAGA	1094

2) INFORMATION FOR SEQ ID NO: 448

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1100 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pichia anomala*
 (B) STRAIN: ATCC 2149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 448

40	CTTAGATAAG	TTAAAAGCTG	AACGTGAAAG	AGGTATCACT	ATTGATATTG	50
	CTTTATGGAA	ATTCGAAACT	CCAAAATACC	ATGTTACCGT	TATTGATGCT	100
	CCAGGTCACA	GAGATTTTCAT	CAAAAATATG	ATTACTGGTA	CTTCCCAAGC	150
	TGATTGTGCT	ATMTTAATTA	TTGCCGGTGG	TATTGGTGAA	TTCGAAGCTG	200
	GTATCTCAAA	AGATGGTCAA	ACCAGAGAAC	ACGCTTTRTT	AGCTTACACC	250
45	TTAGGTGTTA	AACAATTGAT	TGTTGCTATC	AACAAGATGG	ATTCCGTTAA	300
	ATGGGATGAA	TCTCGTTTCG	AAGAAATTGT	CAAGGAAACY	TCAAACCTTA	350
	TCAAGAAAGT	TGGTACAACC	CAAAAACGTG	TCCATTCGTT	CCAATCTCAG	400
	GTTGGAATGG	TGATAACATG	ATTGAACCAT	CAACTAACTG	TCCATGGTAC	450
	AAAGGTTGGA	AAAAAGAAAC	CAAAGCTGGT	GAAGCTAAAG	GTAAAACCTT	500
50	ATTAGAAGCC	ATTGATGCTA	TTGATCCACC	ATCAAGACCA	ACTGATAAAC	550
	CATTACGTTT	ACCATTACAA	GATGTTTACA	ARATTGGTGG	TATTGGTACT	600
	GTGCCAGTCG	GTAGAGTTGA	AACCGGTGTT	ATCAAACCAG	GTATGGTTGT	650
	TACCTTTGCC	CCAGCTGGTG	TTACCACTGA	AGTCAAATCT	GTTGAAATGC	700
	ATCATGAACA	ATTGACTGAA	GGTTTACCAG	GTGACAATGT	TGGTTTCAAC	750
55	GTTAAGAATG	TTTCTGTAA	AGAAATCCGT	CGTGGTAACG	TCTGTGGTGA	800
	CTCTAAAAAC	GATCCACCAA	AAGCTGCTGA	ATCATTCAAT	GCTCAAGTTA	850
	TTGTCTTAAA	CCATCCAGGT	CAAATCTCTG	CTGGTTACTC	TCCAGTTTAA	900
	GATTGTCACA	CTGCTCACAT	TGCTTGTAAG	TTTGACACTT	TAATTGAAAA	950
	AATTGACAGA	CGTACTGGTA	AGAAATTAGA	AGAAGCTCCA	AAATTCATCA	1000
60	AATCAGGTGA	TGCTGCTATT	GTAAATTTG	TTCCATCAAA	ACCATTATCA	1050

GTTGAAGCTT TCACTGACTA CCCACCATTA GGTCGTTTCG CTGTCAGAGA 1100

5 2) INFORMATION FOR SEQ ID NO: 449

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 1201 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pseudallescheria boydii*
(B) STRAIN: ATCC 44331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 449

20 CAAGCTCAAG GCCGAGCGTG AGCGTGGTAT CACCATCGAT ATCGCCCTCT 50
GGAAGTTCGA GACCCCAAG TACCAGGTCA CCGTCATTGG TATGTCTTTG 100
TGCTTTTGT GCTTTTGTG CCTGTGCCTC GCACAATTCC AGCCCTCGAT 150
AATTATGAAC CTCGTACTAA TATGTCGTTT TCCCACTACC CACAGACGCC 200
25 CCCGGCCATC GTGATTTTCAT CAAGAACATG ATTACTGGTA CCTCCCAGGC 250
TGATTGCGCC ATTCTCATCA TTGCCTCCGG TACTGGTGAG TTCGAGGCTG 300
GCATCTCCAA GGATGGCCAG ACCCGTGAGC ACGCTCTTCT CGCCTTCACC 350
CTCGGTGTCA AGAACCTCAT TGTTGCCATC AACAAGATGG ACACCAACAA 400
CTGGTCCGAG GACCGATACA AGGAGATCAT CAAGGAGACC TCCAACCTCA 450
30 TCAAGAAGGT CGGCTACAAC CCAAGGCCG TTCCTTTTCGT CCCCATCTCC 500
GGTTTCCACG GAGACAACAT GCTTACCCCT TCCACCAACT GCCCCTGGTA 550
CAAGGGTTGG GTCCGTGAGG TCAAGGGTAA CACCCTTACC GGCAAGACCC 600
TTCTCGAGGC CATCGACTYC ATCGAGCCCC CCAAGCGTCC CACCGAGAAG 650
CCCCTCCGTC TTCCCTTCA GGACGTCTAC AAGATCGGTG GTATTGGCAC 700
35 TGTGCCCCGTC GGCCGTATCG AGACCGGTAT CCTCAAGCCC GGTATGGTCG 750
TCACCTTCGC TCCCTCCAAC GTCACCACTG AAGTCAAGTC CGTCGAGATG 800
CACCACGAGC AGCTTACCGA GGGTGTCCCC GGTGACAACG TTGGTTTCAA 850
CGTGAAGAAC GTCTCCGTCA AGGATATCCG CCGTGGCAAC GTCTGCGGTG 900
ACTCCAAGAA CGACCCCTCC GCTGCTGCCG CCTCTTTCCA GGCCCAGGTC 950
40 ATTTGCTCTCA ACCACCCCGG CCAGATCGGT GCTGGTTACG CTCCCGTTCT 1000
TGACTGCCAC ACTGCCCAACA TTGCTTGCAA GTTCGCCGAG CTCCTTGAGA 1050
AGATCGACCG CCGTACCGGT AAGTCGGTCG AGAACAACCC CAAGTTCGTC 1100
AAGTCTGGTG ATGCCGCCAT CGTCAAGATG GTTCCCTCCA AGCCCATGTG 1150
TGTTGAGTCC TTCACCGAGT ACCCCCTCT CGGTCGTTTC GCCGTCCGTG 1200
45 A 1201

2) INFORMATION FOR SEQ ID NO: 450

50 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1095 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

60 (A) ORGANISM: *Rhizopus oryzae*

(B) STRAIN: ATCC 56015

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 450

5	CAAGCTTAAG	GCTGAACGTG	AACGTGGTAT	CACCATCGAT	ATTGCTCTCT	50
	GGAAGTTCGA	AACCCCCAAG	TACCAAATTA	CCGTTATTGA	TGCTCCCGGT	100
	CACCGTGATT	TCATCAAGAA	CATGATTACC	GGTACTTCTC	AAGCCGATTG	150
	TGCTATTCTT	ATCATTGCTG	GTGGTACTGG	TGAATTCGAA	GCTGGTATCT	200
	CCAAGGATGG	TCAAACCCGT	GAACACGCCC	TTTTGGCTTT	CACTCTCGGT	250
	GTCCGTCAAT	TGATTGTTGC	TGTCAACAAG	ATGGATACCA	CCAAGTGGTC	300
10	CGAAGCTCGT	TTCAACGAAA	TYGTCAAGGA	AGTTTCTTCC	TTCATCAAGA	350
	AGATTGGTTA	CAACCCCCAAG	TCTGTTCCTT	TCGTCCCCAT	CTCTGGTTGG	400
	CACGGTGACA	ACATGTTGGA	AGAATCTACC	AACATGCCCT	GGTACAAGGG	450
	ATGGAACAAG	GAAACCAAGG	CTGGTGCCAA	GTCTGGTAAG	ACCCTCTTGG	500
15	ATGCCATTGA	CAACATTGAC	CCTCCTACCC	GTCCTGTTGA	CAAGCCTCTC	550
	CGTCTTCCTC	TTCAAGATGT	TTACAAGATT	GGTGGTATCG	GTAAGTGTCC	600
	CGTCGGTCGT	GTCGAAACTG	TGCTGTCACC	GGCTGGTATG	GTTGTACCT	650
	TCGCTCCTGC	TCGTGTCACC	ACTGAAGTTA	AGTCCGTCGA	AATGCACCAC	700
	GAAACCCTCA	CTGAAGGTCT	CCCCGGTGAC	AACGTCGGTT	TCAACGTCAA	750
20	GAACGTCTCC	GTCAAGGATA	TCCGTCGTGG	TAACGTCTGT	TCTGACTCCA	800
	AGAACGACCC	CGCCAAGGAA	GCCGGTTTCT	TCACCGCTCA	AGTCATTATC	850
	TTGAACCACC	CTGGTCAAAT	TGGTGCTGGT	TACGCTCCYG	TTTTGGATTG	900
	TCACACTGCT	CACATTGCCT	GTAAGTTCGC	TGAATTGATC	GAAAAGATTG	950
	ACAGACGTTT	CGGTAAGTCC	TTGGAAGCTA	CTCCCAAGTT	CGTCAAGTCT	1000
25	GGTGACTCTG	CCATCGTCAA	GATGATCCCC	TCCAAGCCCA	TGTGTGTTGA	1050
	AGCTTACACT	GACTACCCTC	CTCTCGGTCT	TTTCGCTGTT	CGTGA	1095

30 2) INFORMATION FOR SEQ ID NO: 451

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 1092 bases
	(B)	TYPE: Nucleic acid
35	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Rhodotorula minuta</i>
	(B)	STRAIN: ATCC 10658

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 451

45	GCTGAAGGCC	GAGCGAGAGC	GTGGTATCAC	CATCGATATC	GCTCTATGGA	50
	AGTTCGAGAC	CCCCAAGTAC	AACGTCACCG	TCATTGACGC	TCCAGGACAT	100
	CGTGATTTC	TCAAGAGTGA	GTAAACCATA	ACATCAAACA	GTGTTGCAAA	150
	CATCAGCTAA	TGCATGTTAT	GCGTCCAGAC	ATGATTACTG	GTAATTCCCA	200
50	GGCCGATTGC	GCTATTCTCA	TCATCGCCAC	CGGTGTTGGT	GAGTTCGAGG	250
	CTGGTATCTC	CAAGGATGGC	CAGACCCGAG	AGCACGCCCT	TCTCGCCTTC	300
	ACCCTCGGTG	TCAGACAGCT	CATCGTTGCC	TTGAACAAGA	TGGACTCGGT	350
	CAAGGTAGGC	TAACCTCACA	ACGTCGGCTT	CCCATCATTC	ATTCACTTAC	400
	CTGTCTTGTC	TTCCACCCTC	CAGTTCTCCG	AGTCCCGATA	CGATGAAATC	450
55	GTCAAGGAGA	CATCCGGTTT	CATCAAGAAG	GTCCGATTCT	ACCCCAAGGG	500
	TGTTCCCTTC	GTCCCATCT	CAGGATGGCA	CGGAGACAAC	ATGATCGAGG	550
	AGTCCACCAA	CATGCCTTGG	TACAAGGGAT	GGAAGAAGAC	CACCAAGACC	600
	GGCGAGTACA	AGGGAAAGAC	CCTGCTCGAG	GCCATCGACT	CCATCGAGCC	650
	CCCCACCCGT	CCTACCGACA	AGCCTCTCCG	ACTTCCCTC	CAGGATGTCT	700
60	ACAAGATTGG	TGGTATCGGA	ACAGTGCCAG	TCGGACGAGT	CGAGACTGGT	750

	ACCATCAAGG	CTGGTATGGT	CGTCACCTTC	GCTCCTTCAG	CTGTCACCAC	800
	CGAAGTCAAG	TCTGTTGAGA	TGCACCACGA	GCAGCTCGAG	GCTGGTCTTC	850
	CAGGTGACAA	CGTCGGATTTC	AACATCAAGA	ACGTTTCAGT	CAAGGATATC	900
	CGAAGAGGAA	ACGTCTGCGG	TGACTCCAAG	AACGATCCCC	CCAAGGAGGC	950
5	TGCTTCCTTC	ACCGCCCAGG	TCATTGTCCT	CAACCACCCC	GGTCAAATCG	1000
	GTAACGGATA	CTCTCCAGTT	CTCGATTGCC	ACACTGGTGA	GTCATTCTTC	1050
	CATATTAGTT	TGAACTCTTT	TGAACAATAC	TAACGTGAAT	CATTATACTT	1100
	TTCAGCCCAC	ATTGCATGCA	AGTTCGACAC	CCTCCTAGAG	AAGATTGACC	1150
	GACGATCCGG	AAAGTCCATC	GAAGATACCC	CCAAGTTCGT	CAAGTCTGGT	1200
10	GACGCCGCCA	TCGTCAAGAT	GGTCCCCACC	AAGCCAATGT	GCGTTGAGGC	1250
	TTTCACCGAC	TACCCACCTC	TTGGACGATT	CGCCGTCCGT	GA	1292

15 2) INFORMATION FOR SEQ ID NO: 452

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 1289 bases
	(B)	TYPE: Nucleic acid
20	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Sporobolomyces salmonicolor</i>
	(B)	STRAIN: ATCC 32311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 452

30	AAGCTCAAGG	CCGAGCGTGA	GCGTGGTATC	ACCATCGATA	TCGCTCTCTG	50
	GAAGTTCGAG	ACCCCCAAGG	TGCGTTCTCA	CCCCGGCTGA	GGAGCACGCA	100
	CGCCGAGGGCT	CACGCTGCGC	CTCTTACAGT	ACATGATCAC	CGTCATCGAC	150
	GCCCCGGGTG	ACCGTGACTT	CATCAAGAAC	ATGATCACCG	GTACCTCGCA	200
35	GGCCGACTGC	GCCATCCTCA	TCATCGCCGC	CGGTACCGGT	GAGTTCGAGG	250
	CTGGTATCTC	GAAGGACGGC	CAGACCCGCG	AGCACGCCCT	CCTCGCCTTC	300
	ACCCTCGGTG	TCCGTCAGCT	CATCGTCGCC	ATCAACAAGA	TGGACACGAC	350
	CAAGTACTCG	GAGGCCCGTT	TCGAGGAGAT	CATCAAGGAG	ACCTCCAACT	400
	TCATCAAGAA	GGTCGGCTTC	AACCCCAAGA	ACGTCCCCCT	CGTCCCCATC	450
40	TCGGGATGGC	ACGGTGACAA	CATGATTGAG	GAGACCGCCA	ACATGCCCTG	500
	GTACAAGGGA	TGGAAGAAGG	AGACCAAGGC	CGGTGAGGTC	AAGGGCAAGA	550
	CCCTCCTCGA	CGCCATCGAC	GCGATCGAGC	CCCCTTCGCG	CCCTACCGAC	600
	AAGCCCCCTC	GTCTTCCCCT	CCAGGTTTCG	TTCCCTGCTC	GCGGTTTACG	650
	CTGCTACTTC	GAGCTGACCC	GCGAGCTCTG	CCCGAACAGG	ATGTCTACAA	700
45	GATCGGTGGT	ATCGGCACAG	TCCCCGTCGG	CCGTGTCGAG	ACCGGCACGA	750
	TCAAGGCCGG	TATGGTCGTC	GTCTTCGCCC	CGGCCAACGT	CACCACTGAG	800
	GTCAAGTCGG	TCGAGATGCA	CCACGAGCAG	CTCGAGGCTG	GTCTCCCGGG	850
	AGACAACGTC	GGCTTCAAGT	GCGTCTCATC	ATGTTTTTGC	TTGCTCGGC	900
	CATTTTTTCA	GTCTTGACCC	CGTTTTGCCC	CTCGACAGCG	TCAAGAACGT	950
50	TTCCGTTAAG	GACATCCGTC	GCGGTAACGT	CTGCGGTGAC	TCGAAGAACG	1000
	ACCCCCCCAA	GGAGGCCGCT	TCCTTCAAGG	CCCAGGTCAT	CGTCATGAAC	1050
	CACCCCGGTC	AGATCGGCAA	CGGTTACGCT	CCCCTTCTCG	ACTGCCACAC	1100
	CGCCCCACAT	GCCTGCAAGT	TCGACACCCT	CCTCGAGAAG	ATCGACCGTC	1150
	GCTCGGGCAA	GTCGATTGAG	GACCTCCCCA	AGTTCGTCAA	GTCGGGTGAC	1200
55	GCCGCCATCG	TCAAGATGGT	TCCCTCCAAG	CCGATGTGTG	TCGAGTCGTT	1250
	CGCCGAGTAC	CCCCCTCTCG	GACGTTTCGC	CGTCCGTGA		1289

60 2) INFORMATION FOR SEQ ID NO: 453

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1070 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Sporothrix schenckii*
 (B) STRAIN: WSA-148

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 453

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15 GTGAGCGCGG TATCACCATC GATATTGCTC TGTGGAAGTT CGAGACCCCC 50
   AAGTACTACG TCACCGTCAT TGACGCCCCC GGTTCATCGCG ATTTTCATCAA 100
   GAACATGATC ACTGGTACCT CGCAGGCCGA CTGCGCCATT CTCATCATTG 150
   CCGCTGGTAC TGGTGAGTTC GAGGCTGGTA TCTCCAAGGA TGGCCAGACT 200
20 CGTGAGCACG CTCTGCTCGC CTACACCCTG GGTGTGCGGC AGCTGATCGT 250
   CGCCATCAAC AAGATGGACA CGGCCAAGTG GGCTGAGGCT CGTTACCAGG 300
   AGATCATCAA GGAGACCTCC AACTTCATCA AGAAGGTCGG CTACAACCCC 350
   AAGACTGTTG CCTTCGTCCC CATCTCGGGC TTCCACGGCG ACAACATGCT 400
   TACTCCCTCG ACCAACTGCC CCTGGTACAA GGGCTGGGAG AAGGAGGGCA 450
25 AGAGCGGCAA GGTTACCGGT AAGACTCTGC TGGACGCCAT TGACGCCGTC 500
   GAGCCCCCCA AGCGCCCCAC GGACAAGCCC CTGCGTCTGC CCCTCCAGGA 550
   TGTCTACAAG ATCGGCGGTA TCGGCACTGT CCCTGTCGGC CGTATCGAGA 600
   CTGGTGTCTT GAAGCCCGGC ATGGTTCGTC CCTTTGCCCC GTCCAACGTC 650
   ACCACTGAAG TCAAGTCCGT CGAGATGCAC CACGAGCAGC TTGTTGAGGG 700
30 TGTTCCCGGC GACAACGTCG GCTTCAACGT CAAGAACGTC TCCGTCAAGG 750
   AGATCCGTCG TGGCAACGTT GCCGGTGACT CCAAGAACGA CCCCCCTCG 800
   GGCGCCGCCA CCTTCAACGC CCAGTTCATT GTCCTGAACC ACCCCGGCCA 850
   GGTTCGGCAAC AGCTACGCCC CGGTTCTGGA CTGCCACACC GCCCACATTG 900
   CCTGCAAGTT CACCGAGATC CTTGAGAAGA TCGACCGCCG TACCGGCAAG 950
35 TCGGTTGAGA ACAACCCCAA GTTCATCAAG TCGGGTGACG CCGCCATTGT 1000
   CAAGCTGACG CCCTCGAAGC CCATGTGCGT TGAGGCCTTC ACTGACTACC 1050
   CCCCTCTGGG CCGTTTCGCC 1070

```

2) INFORMATION FOR SEQ ID NO: 454

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1092 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Stephanoascus ciferrii*
 (B) STRAIN: ATCC 52550

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 454

```

60 CTTAAGTCTG AGCGTGAGAG AGGTATCACC ATCGATATTG CTCTCTGGAA 50
   ATTCGAGACT CCTAAGTACA ACGTTACCGT CATTGATGCT CCAGGTCACA 100
   GAGATTTTCAT CAAGAACATG ATTACTGGTA CTTCCCAGGC CGATCTTGCC 150
   ATCCTTATCA TTGCTGGTGG TGTGCGGTGAG TTCGAGGCTG GTATCTCCAA 200

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GGACGGTCAG ACCAGAGAGC ACGCTCTTCT TTCTTTCACC CTTGGTGTCA 250
GAAACATGAT TGTGCTGTC AACAGATGG ACTCCGTCAG GTGGTCTGAG 300
GATCGTTTCA ACGAAATTGT CAAGGAGACC TCCAACCTCG TCAAGAAGGT 350
TGGTTACAAC CCTAAGAATA TTGCTTTCGT TCCTATCTCC GGTGGAACG 400
5 GTGACAATAT GATTGAGCCA TCCACCAACT GCCCATGGTA CAAGGGTTGG 450
GAGCGTGAGA CCAAGAACGG TACTGCCAAG GGTAAGACCA TCTTGGAGGC 500
CATTGACTCT ATGGAGCCAC CTTCCAGACC AGTTGACAAG CCTCTCCGTC 550
TTCCTCTTCA GGACGTTTAC AAGATTGGTG GTATTGGTAC GGTGCCAGTT 600
GGTCGTGTTG AGACTGGTGT TATCAAGCCA GGTATGGTTG TTACCTTTGC 650
10 CCCAGCTGGT GTCACCACTG AAGTCAAGTC TGTCGAGATG CACCACGAAC 700
AGATCCCAGA AGGTACCCCA GGTGACAACG TTGGTTTCAA CGTCAAGAAC 750
GTCTCCGTCA AGGAAATCAG ACGTGGAAC GTTACTGGTG ACTCCAAGAA 800
CGACCCACCA AAGGGCTGCG ACTCTTTCAA CGCTCAGGTC ATCATCTTCA 850
ACCACCCTGG TCAGATCTCT GCTGGTTACG CTCCAGTTTT GGACTGCCAC 900
15 ACTGCTCACA TTGCTTGCAA GTTTGAGGAG CTCATTGAGA AGATTGACAG 950
ACGTTCCGGT AAGAAGGTCG AAGACTCTCC TAAGTTCGTC AAGGCCGGTG 1000
ATGCCGCCAT TGTCAAGATG GTTCCATCCA AGCCAATGTG TGTGAAACC 1050
TTCCTGAGT ACCCACCTCT TGGTCGTTTC GCCGTCCGTG AC 1092

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20

2) INFORMATION FOR SEQ ID NO: 455

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(i) SEQUENCE CHARACTERISTICS:
25 (A) LENGTH: 1149 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Trichophyton mentagrophytes
    (B) STRAIN: WSA-225
35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 455

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GCCGAGCGTG AGCGTGGTAT CACCATCGAT ATCGCCCTCT GGAAGTTCGA 50
GACCCCCAAG TACAATGTCA CCGTCATTGG TATGTTTTCT CTTTACCTTT 100
40 CCCCTCCATC GTCTTGCTGT GCCATACTA ACGAGAGTAG ACGCCCCCGG 150
TCACCGTGAC TTCATCAAGA ACATGATCAC TGGTACCTCC CAGGCCGACT 200
GTGCTATTCT CATCATTGCT GCCGGTACTG GTGAGTTCGA GGCTGGTATC 250
TCCAAGGATG GCCAGACCCG TGAGCACGCT CTGCTCGCCT TCACCCTTGG 300
TGTCAAGCAG CTCATCGTTG CCATCAACAA GATGGACACC ACCAACTGGT 350
45 CCGAGGACCG TTTCAAGGAA ATCATCAAGG AAGTCACCAA CTTTATCAAG 400
AAGGTTGGCT ACGACCCCAA GGGTGTTCCT TTCGTTCCAA TCTCTGGTTT 450
CAACGGTGAC AACATGATTG AGGCCTCCAC CAACTGCCCA TGGTACAAGG 500
GATGGAACAA GGAGACTAAG GCCGGTGGTG CCAAGACTGG CAAGACCCTC 550
CTCGAGGCCA TCGATGCCAT CGACATGCCA ACCCGTCCTA CCGACAAGCC 600
50 CCTCCGTCTC CCACTCCAGG ATGTCTACAA GATCTCTGGT ATCGGAACTG 650
TACCAGTCGG TCGTGTTGAG ACCGGTATCA TCAAGCCCGG TATGGTCGTC 700
ACCTTCGCCC CTGCCAACGT CACCACTGAA GTCAAGTCCG TCGAAATGCA 750
CCACCAGCAG CTTCAGCAGG GTGTCCCCGG TGACAACGTC GGCTTCAACG 800
TCAAGAACGT TTCCGTCAAG GAAGTCCGCC GTGGTAACGT TGCCGGTGAC 850
55 TCCAAGAACG ACCCACCATC CGGCTGTGCC TCCTTCAACG CCCAGGTCAT 900
CGTCTCAAC CACCCCGGCC AGATCGGTGC TGGTTACGCC CCAGTCCTCG 950
ACTGCCACAC TGCTCACATT GCTTGCAAGT TCGTGAGCT CCTCGAGAAG 1000
ATTGACCGCC GTACCGGTAA ATCCGTCGAA GCCAACCCCA AGTTCGTCAA 1050
GTCTGGTGAT GCCGCTATCG CCAAGATGGT TCCCTCCAAG CCTATGTGCG 1100
60 TTGAGGCTTT CACTGACTAC CCCCCACTTG GTCGTTTCGC CGTCCGTGA 1149

```


2) INFORMATION FOR SEQ ID NO: 456

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1101 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichosporon cutaneum*
 (B) STRAIN: ATCC 62965

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 456

20	TCTTGACAAG	CTTAAAGCTG	AACGTGAACG	TGGTATCACC	ATTGATATCG	50
	CTCTCTGGAA	GTTTCGAACT	CCTAAGTACT	ACGTTACTGT	TATTGATGCT	100
	CCAGGTCACC	GTGATTTTCAT	CAAGAACATG	ATTACTGGTA	CTTCCCAAGC	150
	CGACTGCGCC	ATTCTTATCA	TTGCTGCCGG	TGTCGGTGAA	TTCGAAGCTG	200
	GTATCTCCAA	GGAAGGTCAA	ACCAGAGAAC	ACGCTCTTCT	CGCTTTCACC	250
25	CTTGGTGTCA	GACAACTTAT	CATTGCCATC	AACAAGATGG	ACTCTGTCAA	300
	GTGGGACCAA	AAGAGATACG	AAGAAATCGT	CAAGGAGGCT	TCCAACTTCG	350
	TCAAGAAGGT	TGGTTACAAC	CCCAAGTCTG	TTCCATTCGT	TCCTATCTCT	400
	GGTTGGAACG	GTGACAACAT	GTTGGAACCT	ACCACCAACG	CCCCATGGTA	450
	CAAGGGATGG	ACCAAGGAAA	CCAAGGCTGG	TGCCACTAAG	GGTATGACTC	500
30	TTATTGAAGC	CATTGACGCC	ATTGAACCAC	CAGTAAGACC	ATCCGACAAG	550
	CCACTCCGTC	TCCCCTCCA	AGATGTTTAC	AAGATTGGTG	GTATCGGAAC	600
	TGTGCCAGTC	GGCCGTGTCT	AAACCCGGTAT	CATCAAGGCC	GGTATGGTCT	650
	TCACCTTTGC	TCCACCAATG	GTCACCACTG	AAGTTAAGTC	CGTTGAAATG	700
	CACCACGAAC	AAGTTGCTCA	AGGTAACCCA	GGTGACAACG	TTGGTTTCAA	750
35	CGTCAAGAAC	GTTTCCGTTA	AGGAAATCAG	ACGTGGTAAC	GTCTGTGGTG	800
	ACTCCAAGAA	CGATCCACCA	AAGGGCTGCG	AATCTTTCAA	CGCTCAAGTT	850
	ATCGTCTTGA	ACCACCCTGG	TCAAATCTCT	GCTGGTTACT	CTCCAGTTCT	900
	CGATTGCCAC	ACTGCCCCAC	TTGCCTGCAG	ATTGACGAA	CTCCTTGAAA	950
	AGATCGACCG	TCGTTCCGGT	AAGAAGATTG	AAGACTCTCC	AAAGTTTGTC	1000
40	AAGTCTGGTG	ATGCCGCTAT	CGTCAAGATG	ATCCCAACCA	AGCCAATGTG	1050
	CGTTGAAACC	TTCCTGAAT	ACCCACCACT	TGGTCGTTTC	GCCGTCCGTG	1100
	A					1101

2) INFORMATION FOR SEQ ID NO: 457

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1085 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Wangiella dermatitidis*
 (B) STRAIN: WSA-229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 457

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5   GTTGAAGGCC GAGCGTGAGC GTGGTATCAC CATCGATATC GCCCTCTGGA      50
    AGTTCGAGAC CCCCAAGTAC TATGTCACCG TCATCGACGC CCCGGGTCAT      100
    CGTGACTTTA TCAAGAACAT GATCACTGGT ACCTCGCAGG CCGACTGCGC      150
    CATCTTGATC ATTGCCGCCG GTACCGGTGA ATTCTGAAGCC GGTATCTCCA      200
    AGGATGGTCA GACCCGTGAG CACGCTCTGC TCGCCTACAC CTTGGGTGTC      250
    AAGCAGCTCA TCGTCGCCAT CAACAAGATG GACACCACCA AGTGGTCCGA      300
    GGAGCGTTTC AACGAAATCA TCAAGGAGAC TTCCAACCTC ATCAAGAAGG      350
    TCGGCTACAA CCCCAAGGCC GTTCCTTTTC TCCCCATCTC CGGCTTCAAC      400
10  GGTGACAACA TGATTGAGGT CTCCACCAAC TGCCCGTGGT ACAAGGGATG      450
    GGAGAAGGAG TCCAAGGCTG GCAAGGCCAC CGGCAAGACC CTCCTCGAGG      500
    CCATTGACGC CATCGACCCA CCCACCCGTC CCACCGACAA GCCTCTCCGT      550
    CTCCCTCTCC AGGATGTCTA CAAGATCTCT GGTATCGGAA CGGTTCCTGT      600
    CGGTCGTGTA GAGACCGGTA CCATCAAGGC CGGTATGGTC GTCACCTTCG      650
15  CTCCCGCCAA CGTCACCACT GAAGTCAAGT CCGTCGAAAT GCACCACGAG      700
    CAGCTCGCCG AGGGTCTGCC AGGTGACAAC GTTGGCTTCA ACGTCAAGAA      750
    CGTCTCCGTC AAGGAGGTTT GTCGTGGTAA CGTTGCCGGT GACTCCAAGA      800
    ACGACCCGCC CAAGGGTGCC GAGTCCTTCA ACGCCAGGT CATGTCTCTC      850
    AACCACCCTG GTCAGATCGG TGCCGGCTAC GCTCCAGTCT TGGATTGCCA      900
20  CACTGCCCAC ATTGCTTGCA AGTTCGCCGA GTTGCTCGAG AAGATCGACC      950
    GTCGTACCGG AAAGTCCATC GAGAACAACC CCAAGTTCAT CAAGTCTGGT     1000
    GATGCTGCCA TCGTCAAGAT GATTCCACAG AAGCCCATGT GTGTCGAGGC     1050
    TTTACCGGAC TATCCTCCTC TGGGTCGTTT CGCTG                      1085

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2) INFORMATION FOR SEQ ID NO: 458

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    (i) SEQUENCE CHARACTERISTICS:
30  (A)   LENGTH: 492 bases
    (B)   TYPE: Nucleic acid
    (C)   STRANDEDNESS: Double
    (D)   TOPOLOGY: Linear

    (ii) MOLECULE TYPE: Genomic DNA

    (vi) ORIGINAL SOURCE:
    (A)   ORGANISM: Aspergillus fumigatus
    (B)   STRAIN: DAL-95
40  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 458

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    TGTCTTCATC CGGAATTGAT TGTGAGTCGT TCCACATGCT CACCTAGTTT      50
    TCGCTCGATC TTTTCACTAA CGCAAACCAT GTAGAACAAC ATTGCCAAGG      100
45  CCCACGGTGG TTA CTCCGTC TTA CTGGTG TTGGTGAGCG TACTCGTGAG      150
    GGTAACGATC TGTACCACGA AATGCAGGAG ACTGGTGTCA TTCAGCTCGA      200
    GGGTGAATCC AAGGTCGCAC TGGTGTTCGG ACAGATGAAC GAGCCCCCCC      250
    GTGCCCGTGC CCGTGTGCC CTTACCGGTC TGACCATTCG CGAGTACTTC      300
    CGTGACGAGG AGGGTCAGGA CGTGCTGCTC TTCATTGACA ACATTTTCCG      350
50  TTTACCCAG GCCGGTTCTG AGGTGTCTGC CCTTCTCGGT CGTATCCCCT      400
    CTGCCGTCGG TTACCAGCCC ACCCTGGCCG TCGACATGGG TGGTATGCAG      450
    GAGCGTATCA CCACCACCAA GAAGGGTTCT ATTACCTCCG TC                      492

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55

2) INFORMATION FOR SEQ ID NO: 459

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    (i) SEQUENCE CHARACTERISTICS:
    (A)   LENGTH: 1154 bases
60  (B)   TYPE: Nucleic acid

```

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Blastoschizomyces capitatus*
(B) STRAIN: ATCC 10663

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 459

```

10      GTCCGTGGTC AAGAAGTTAT TGACACTGGT GCCCAATTA CCATTCCTGT      50
      TGGTCGTGGT ACTCTTGGTA GAATTATCAA CGTCATTGGT GAACCAATTG      100
      ACGAACGTGG TCCTATCAAG GCTTCTAAGT ATGCTCCTAT CCATACTGAA      150
15      CCACCAACCT TTGCTGAACA ATCTACTTCT GCTGAAGTTC TTGAAACTGG      200
      TATCAAGGTT GTCGATCTTC TTGCTCCTTA CGCCCGTGGT GGTAAGATTG      250
      GTCTTTTCGG TGGTGCTGGT GTCGGTAAGA CTGTCTTCAT TCAAGAAGTT      300
      ATTAACAACA TTGCCAAGGC TCACGGTGGT TTCTCTGTCT TCACTGGTGT      350
      CGGTGAAAGA ACCCGTGAAG GTAACGATCT TTACCGTGAA ATGAAGGAAA      400
20      CTGGTGTCAT CAACCTCGAA GGTGACTCCA AGGTCGCTCT CGTTTTCGGT      450
      CAAATGAACG AACCTCCAGG TGCCCGTGCC CGTGTCGCTT TGACTGGTCT      500
      TACCATTGCC GAATACTTCC GTGATGAAGA AGGACAAGAT GTCTTGCTTT      550
      TCGTTGACAA CATTTTCAGA TTCACCCAAG CCGGTTCTGA AGTCTCTGCT      600
      CTTTTGGGTC GTATTCCATC TGCCGTCGGT TACCAACCTA CCCTTGCTAC      650
25      CGATATGGGT GCCCTCCAAG AACGTATTAC CACCACCAA AAGGGTTCCG      700
      TCACATCTGT CCAAGCCGTC TATGTCCCAG CAGACGATTT GACTGATCCT      750
      GCCCCAGCCA CCACCTTCGC TCACTTGGAC GCCACCACTG TCTTGCTCTG      800
      TTCCATTTCC GAATTGGGTA TCTACCCAGC TGTCGATCCT CTCGATTCCA      850
      AGTCTCGTCT TTTGGATCCT GAAGTTATTG GACACGAACA CTACGAAGTT      900
30      GCCACTCAAG TTCAACAAAC CCTCCAAGCT TACAAGTCTC TCCAAGATAT      950
      CATTGCCATT TTGGGTATGG ATGAATTGTC TGAAGCTGAT AAGCTTACTG      1000
      TCGAACGTGC CCGTAAGATC CAAAGATTCC TTTCCCAACC ATTCGCTGTT      1050
      GCCGAAGTTT TCACTGGTAT CGAAGGTCGT CTCGTTCCAT TGAAGGAAAC      1100
      CGTCAGATCT TTCAAGGAAA TCCTTGAAGG TAAGTACGAT CACCTTCCAG      1150
35      AAGC

```

2) INFORMATION FOR SEQ ID NO: 460

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1295 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida albicans*
(B) STRAIN: ATCC 18804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 460

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55      CCAATTCGAC GAAGGAAACT TGCCAGCTAT TTTGAATGCT TTGACTTTGA      50
      AGAACGGTGA CCAAGACTTG GTCTTGGAAG TTGCTCAACA TTTGGGTGAA      100
      AACACCGTCA GAGCTATTGC TATGGATGGT ACTGAAGGTT TAGTCAGAGG      150
      TACCGAAGTC AACGATACCG GTGCCCAAT CTCCGTCCCA GTCGGTAGAG      200
      GTACTTTAGG TAGAATCATC AATGTTGTTG GTGAACCAAT TGATGACAGA      250
60      GGTCCAATTG AATGTAAGGA AAAGAAACCA ATTCACGCTG AACCACCATC      300

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	ATTCGTTGAA	CAATCCACTG	CTGCCGARAT	TTTGGAAC	GGTATCAAGG	350
	TTGTGCGACTT	GTTGGCCCCA	TACGCCAGAG	GTGGTAARAT	TGGTTTATTC	400
	GGTGGTGCTG	GTGTCGGTAA	GACCGTCTTT	ATCCAAGAAT	TGATTAACAA	450
	CATTGCCAAA	GCCCATGGTG	GTTTCTCTGT	CTTTACCGGT	GTYGGTGAAA	500
5	GAACCAGAGA	AGGTAACGAT	TTGTACCGTG	AAATGAAAGA	AACCGGTGTC	550
	ATCAACTTGG	AAGGTGACTC	CAAGGTCGCT	TTGGTCTTCG	GTCAAATGAA	600
	CGAACCACCA	GGTGCTAGAG	CTAGAGTTGC	TTTGACTGGT	TTGACCATTG	650
	CTGAATACTT	CAGAGATGAA	GAAGGTCAAG	ATGTCTTGTT	GTTTCATTGAT	700
	AACATTTTCA	GATTCACCCA	AGCTGGTTCC	GAAGTGCTCG	CTTTGTTAGG	750
10	TCGTATTCCA	TCTGCTGTCC	GTTATCAACC	AACCTTAGCC	ACTGATATGG	800
	GTCTTTTGCA	AGAACGTATT	ACCACCACCA	AGAAAGGTTC	CGTCACCTCT	850
	GTCCAAGCTG	TCTATGTCCC	AGCTGATGAT	TTGACCGATC	CTGCTCCAGC	900
	CATACATTTC	GCCCATTGGG	ATGCCACTAC	TGTCTTGTCT	AGAGGTATTT	950
	CTGAATTGGG	TATCTACCCA	GCTGTGATC	CATTGGATTTC	CAAAATCCAGA	1000
15	TTATTGGACG	CTTCTGTTGT	TGGTCAAGAA	CATTACGATG	TCGCTACTGG	1050
	TGTTCAACAA	ACTTTACAAG	CTTACAAATC	CTTACAAGAT	ATCATTGCTA	1100
	TTTTGGGTAT	GGATGAATTG	TCTGAAGCTG	ATAAATTGAC	TGTCGAAAGA	1150
	GCCCGTAAGA	TCCAAAGATT	CTTGTCTCAA	CCATTGCTG	TTGCTGAAGT	1200
	TTTCACTGGT	ATCCCAGGTA	GATTAGTCAG	ATTGCAAGAC	ACTGTCAAAT	1250
20	CATTCAAGGA	TGTTTTGGAA	GGTAAATACG	ATAACTTGCC	AGAAA	1295

2) INFORMATION FOR SEQ ID NO: 461

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1277 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida dubliniensis*
 (B) STRAIN: NCPF 3949

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 461

40	TAACTTGCCA	GCTATTTTGA	ATGCTTTGAC	TTTGAAGAAC	GGTGACCAAG	50
	ATTTAGTTTT	GGAAGTTGCT	CAACATTTGG	GTGAAAACAC	CGTCAGAGCT	100
	ATTGCTATGG	ATGGTACTGA	AGGTTTAGTC	AGAGGTACTG	AAGTCAACGA	150
	TACCGGTGCC	CCAATCTCCG	TTCCAGTCGG	TAGAGGTACC	TTAGGTAGAA	200
	TCATCAATGT	TGTTGGTGAA	CCAATTGATG	ACAGAGGTCC	AATTGAATGT	250
45	AAGGAAAAGA	AACCAATTCA	TGCAGAACCA	CCATCCTTCG	TTGAGCAATC	300
	CACTGCTGCG	GAAATTTTGG	AAACCGGTAT	CAAGGTGTC	GACTTATTGG	350
	CCCCATACGC	CAGAGGTGGT	AAGATTGGTT	TGTTGCGTGG	TGCTGGTGTC	400
	GGTAAGACCG	TCTTTATCCA	AGAATTGATT	AACAACATTG	CTAAAGCCCA	450
	TGGTGGTTTC	TCCGTCTTTA	CCGGTGTCCG	TGAAAGAACC	AGAGAAGGTA	500
50	ACGATTTGTA	CCGTGAAATG	AAAGAAACCG	GTGTCATCAA	CTTAGAAGGT	550
	GACTCCAAGG	TCGCTTTGGT	CTTTGGACAA	ATGAACGAAC	CACCAGGTGC	600
	TAGAGCTAGA	GTTGCTTTGA	CTGGTTTGAC	TATTGCTGAA	TACTTCAGAG	650
	ATGAAGAAGG	TCAAGATGTC	TTGTTGTTCA	TCGATAACAT	TTTCAGATTG	700
	ACCCAAGCTG	GTTCCGAAGT	GTCTGCTTTG	TTAGGTCGTA	TTCCATCTGC	750
55	CGTCGGTTAT	CAACCAACCT	TAGCTACTGA	TATGGGTCTT	TTGCAAGAAC	800
	GTATTACCAC	CACCAAGAAA	GGTTCCGTCA	CCTCTGTCCA	AGCTGTCTAT	850
	GTCCCAGCTG	ATGATTTGAC	CGATCCTGCT	CCAGCCACCA	CATTCGCCCCA	900
	TTTGGATGCC	ACTACTGTCT	TGTCTAGAGG	TATTTCTGAA	TTGGGTATTT	950
	ACCCAGCTGT	CGATCCATTG	GATTCCAAAT	CCAGATTATT	GGACGCTGCC	1000
60	GTTGTTGGTC	AAGAACATTA	TGATGTCGCT	ACTGGTGTTT	AACAAACTTT	1050

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GCAAGCTTAC AAATCCTTAC AAGATATCAT TGCTATTTTG GGTATGGATG 1100
AATTGCTCTGA AGCTGATAAA TTGACTGTCTG AAAGAGCCCCG TAAGATTCAA 1150
AGATTCTTGT CTCAACCAT TCGCCGTGCTG GAAATTTTCA CTGGTATTCC 1200
AGGTAGATTA GTCAGATTGC AAGACACTGT CAAATCATTC AAGGATGTTT 1250
5 TGGAAGGTAA ATACGATCAC TTGCCAG 1277

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2) INFORMATION FOR SEQ ID NO: 462

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1278 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida famata*
 (B) STRAIN: ATCC 62894

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 462

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25 G T A A C T T G C C   A G C T A T T T T G   A A C G C T T T T G A   C C T T G A A G A A   C G G T G A A A A C   50
   G A C T T A G T T T   T A G A A G T T G C   C C A A C A T T T G   G G T G A A A A C A   C C G T C A G A G C   100
   T A T T G C T A T G   G A T G G T A C T G   A A G G T T T A G T   T A G A G G T A C T   C C A G T T A C C G   150
   A T T C T G G T G C   T C C A A T T T C T   G T C C C A G T C G   G T A G A G G T A C   T T T A G G T A G A   200
   A T C T T G A A C G   T T A T T G G T G A   A C C A A T T G A T   G A A C A A G G T C   C A G T T G A T G C   250
30 C A A G G A A A C C   A G A C C A A T T C   A C C A A G A C C C   A C C A G C A T T C   G T T G A T C A A T   300
   C C A C C A A G G C   T G A A G T T T T G   G A A A C T G G T A   T C A A G G T T G T   C G A T T T A T T A   350
   G C C C C T T A C G   C T A G A G G T G G   T A A G A T T G G T   T T A T T C G G T G   G T G C C G G T G T   400
   C G G T A A G A C C   G T C T T T A T C C   A A G A A T T G A T   T A A C A A C A T T   G C C A A G G C C C   450
   A T G G T G G T T T   C T C T G T T T T C   A C T G G T G T C G   G T G A A A G A A C   C A G A G A A G G T   500
35 A A C G A T T T A T   A T A G A G A A A T   G A A G G A A A C T   G G T G T C A T T A   A C T T G G A A G G   550
   T G A C T C C A A G   G T C G C C T T G G   T T T T C G G T C A   A A T G A A C G A A   C C A C C A G G T G   600
   C T A G A G C T A G   A G T T G C T T T A   A C C G G T T T A A   C C A T T G C C G A   A T A C T T C A G A   650
   G A C G A A G A A G   G T C A A G A T G T   G T T A T T G T T C   G T C G A T A A C A   T T T T T A G A T T   700
   C A C C C A A G C C   G G T T C C G A A G   T G T C T G C T T T   G T T A G G T C G T   A T T C C A T C G G   750
40 C T G T C G G T T A   T C A A C C A A C C   T T A G C C A C T G   A T A T G G G T C T   T T T A C A A G A A   800
   A G A A T T A C C A   C C A C C A C C A A   G G G T T C C G T T   A C T T C T G T C C   A A G C T G T C T A   850
   C G T C C C A G C C   G A T G A T T T A A   C C G A T C C T G C   T C C A G C T A C C   A C T T T C G C C C   900
   A C T T G G A T G C   T A C C A C T G T G   T T G T C T C G T G   G T A T C T C T G A   A T T G G G T A T T   950
   T A C C C A G C T G   T C G A T C C A T T   G G A T T C C A A A   T C C A G A T T G T   T A G A T G C T G A   1000
45 T A T C G T T G G T   A A A G A A C A C T   A C G A A G T T G C   C A C T G G T G T C   C A A C A A A C C T   1050
   T A C A A G C T T A   C A A A T C T T T A   C A A G A T A T C A   T T G C T A T T T T   A G G T A T G G A T   1100
   G A A T T G T C T G   A A G C C G A T A A   A T T G A C T G T C   G A A A G A G C C A   G A A A G A T C C A   1150
   A A G A T T C T T G   T C T C A A C C A T   T C G C C G T T G C   C G A A G T T T T C   A C C G G T A T C C   1200
   C A G G T A G A T T   A G T T A G A T T G   C A A G A C A C T G   T T A A A T C T T T   C A A G G A A G T C   1250
50 T T A G A A G G T A   A A T A T G A T C A   C T T A C C A G   1278

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2) INFORMATION FOR SEQ ID NO: 463

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1154 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Candida glabrata*
 (B) STRAIN: ATCC 66032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 463

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10 TCTGGTCAGA GGCAGAAAGG TCGTCGACAC AGGTGCCCCA ATCTCCGTCC      50
   CTGTCGGCAG AGAGACCCTG GGCAGAATCA TCAACGTTAT CCGTGAACCT      100
   ATCGACGAGC GTGGCCCAAT CAACTCAAAG TTGAGAAAGC CTATCCACGC      150
   CGACCCTCCT TCCTTCGCAG AACAGTCCAC CGCCGCCGAA GTCTTGGAAG      200
   CAGGTATCAA GGTCGTCGAC TTGCTGGCCC CTTACGCCAG AGGTGGTAAG      250
15 ATCGGTCTGT TCGGTGGTGC CGGTGTCTGT AAGACCGTGT TCATCCAAGA      300
   ACTGATCAAC AACATCGCAA AGGCTCACGG TGGTTTCTCC GTGTTACAG      350
   GTGTCGGTGA AAGAACCAGA GAAGGTAACG ATTTGTACAG AGAAATGAAG      400
   GAAACCGGTG TCATCAACTT GGAAGGTGAC TCTAAGGTCG CCTTGGTCTT      450
   CGGCCAAATG AACGAACCAC CAGGAGCCAG AGCCAGAGTC GCCTTGACCG      500
20 GTTTGACCAT CGCAGAATAC TTCAGAGATG AAGAAGGTCA AGATGTCCTG      550
   CTGTTCTGTCG ACAACATTTT CAGATTCACC CAAGCCGGTT CAGAAGTCTC      600
   CGCTTTGCTA GGTCTGTATC CATCCGCCGT CGGTTATCAA CCAACCTTGG      650
   CCACCGATAT GGTCTGTGTT CAAGAAAGAA TTACCACCAC AAAGAAGGGT      700
   TCCGTCACCT CCGTCCAAGC CGTCTACGTG CCTGCAGATG ATTTAACAGA      750
25 TCCTGCCCTT GCCACTACTT TCGCGCACTT GGACGCCACC ACCGTCTTGT      800
   CCAGAAGTAT CTCAGAATTG GGTATCTACC CAGCTGTCGA CCCATTGGAC      850
   TCCAAGTCTA GATTGCTAGA CGCTGCCGTT GTCGGTGAAG AGCATTACAA      900
   CGTCGCCACA AAGGTCCAAG AAACCTTTACA AACTTACAAG TCTCTGCAAG      950
   ATATCATCGC CATTTTGGGT ATGGATGAAT TGTCCGAACA AGATAAGCTA     1000
30 ACTGTCGAAA GAGCAAGAAA GATCCAAAGA TTCTTGTCCT AACCATTTCG      1050
   TGTCGCTGAA GTTTTCACCG GTATCGAAGG TAAGCTGGTC AGATTGAAGG      1100
   ACACCATCTC CTCTTTCAAG GCTGTCTTGG AAGGTAAGTA CGATGATCTT      1150
   CCAAG
  
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35

2) INFORMATION FOR SEQ ID NO: 464

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 1293 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Candida guilliermondii*
 (B) STRAIN: ATCC 6260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 464

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   CCACTACGAG GACGGTAACC TTCCTGCTAT TTTCAACGCC TTGACTCTTA      50
   AGAACGGTGA CCAAACTTG GTTTTGGAAG TTGCCAGCA TTTGGGTGAA      100
55 AACACCGTCA GAACATTGC TATGGATGGT ACTGAAGGTT TGGTTAGAGG      150
   TGCCAGCGTC ACTGACACTG GTGCTCCTAT CTCTGTGCCT GTTGGTCGTG      200
   GTACTTTGGG TCGTATCATC AACGTTATTG GTGAGCCAAT TGACGAGCGT      250
   GGACCAATCG AGTCCAAGCA AAAGAAGCCC ATTCACGCTG AACCACCATC      300
   GTTCGTCGAA CAATCCACTT CTGCCGAGGT TTTGGAAACC GGTATCAAGG      350
60 TTGTCGACTT GTTGGCTCCA TACGCCAGAG GTGGTAAGAT TGGATTGTTC      400
  
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GGTGGTGCCG GTGTCGGTAA GACTGTGTTT ATCCAAGAGT TGATTAACAA 450
CATTGCCAAG GCTCACGGTG GTTCTCCGT GTTCACCGGT GTCGGTGAAA 500
GAACCAGAGA AGGTAACGAT TTGTACCGTG AAATGAAGGA AACTGGTGTC 550
ATCAACTTGG AAGGTGAATC CAAGGTGGCC TTGGTGTTCTG GTCAAATGAA 600
5 CGAACCTCCA GGAGCTAGAG CCAGAGTTGC CCTTACCGGT TTGACCATCG 650
CTGAATACTT CAGAGATGAG GAGGGTCAAG ATGTGTTGTT GTTCGTCGAC 700
AACATTTTCA GATTCACCTCA AGCTGGTTCT GAAGTGTCCG CTTTGTGTTGG 750
TCGTATTCCCT TCGGCTGTCTG GTTACCAACC TACTTTGGCC ACCGATATGG 800
10 GTCCAAGCTG TCTATGTGCC AGCCGATGAT TTGACCGATC CTGCTCCTGC 900
TACTACTTTT GCTCACTTGG ATGCTACCAC TGTGTTGTCT AGAGGTATCT 950
CCGAGTTGGG TATTTACCCA GCTGTGATC CTTTGGATTC CAAGTCGAGA 1000
TTGTTGGATG CCTCTGTTGT CGGTGAGGAG CACTACTCGG TTGCTTCTAA 1050
CGTTCAACAA ACCTTGCAAG CTTACAAGTC TTTGCAAGAT ATCATTGCCA 1100
15 TTTTGGGTAT GGACGAATTG TCGGAAGCTG ACAAGTTGAC CGTCGAGAGA 1150
GCCCCGTAAGA TCGAGAGATT CTTGTCTCAA CCATTGCTG TTGCCGAAGT 1200
TTTCACTGGT ATCAGTGGTA AGTTGGTCAG ATTGGAGGAC ACTATCAGAT 1250
CTTTCAAGGA AGTCTTGGA AGTAAGTACG ATCACTTGCC AGA 1293

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20

2) INFORMATION FOR SEQ ID NO: 465

(i) SEQUENCE CHARACTERISTICS:

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25 (A) LENGTH: 1293 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

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30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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    (A) ORGANISM: Candida haemulonii
    (B) STRAIN: ATCC 22991

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 465

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CACTTTGACG ATGGTAACTT GCCAGCCATT TTCAACGCCT TGAAGTTGAA 50
GAACGGTGAC CAGGACTTGG TCTTGAGGTT CGCCCAGCAC TTGGGTGAGA 100
40 ACACCGTCAG AACCATTGCC ATGGACGGTA CCGATGGTTT GGTCAGAGGC 150
GAGGCTGTCA CTGACACTGG TGCTCCAATC TCCGTGCCTG TTGGTCGTGA 200
GACTTTGGGT CGTATCATCA ACGTTATTGG TGAGCCAATT GACGAGAGAG 250
GACCAATCAA GTCCAAGAAG AGAAACCCAA TCCACACTGA CCCACCAACC 300
TTCGTTGAGC AGTCTACTTC TGCTGAGGTT TTGGAGACTG GTATTAAGGT 350
45 TGTCGACTTG TTGGCCCCCTT ACGCCAGAGG TGGTAAGATT GGTTTGTTCG 400
GTGGTGCCGG TGTCGGTAAG ACCGTCTTTA TCCAAGAGTT GATTAACAAC 450
ATTGCCAAGG CCCACGGTGG TTTCTCTGTC TTTACCGGTG TCGGTGAGAG 500
AACCAGAGAA GGTAACGATT TGTACCGTGA AATGCAGGAG ACCGGTGTCA 550
TCAACTTCGA GGGTGACTCC AAGGTCGCCT TGGTCTTCGG TCAGATGAAC 600
50 GAGCCACCAG GAGCTAGAGC TAGAGTTGCT TTGACCGGTT TGACCATTCG 650
CGAATACTTC AGAGATGAAG AAGGTCAGGA TGTGTTGTTG TTCGTTGACA 700
ACATTTTCAG ATTCACCTCAG GCTGGTTCCG AGGTGTCCGC CTTGTTGGGT 750
CGTATTCCAT CTGCTGTCCG TTACCAGCCA ACCTTGGCCA CCGATATGGG 800
TACCTTGCAA GAAAGAATTA CCACCACCAA GAAGGGTTCC GTCACCTCTG 850
55 TCCAGGCCGT TTACGTGCCA GCTGATGATT TGACCGATCC TGCCCCAGCT 900
ACCACTTTCTG CTCACCTGGA TGCTACCACT GTGTGTGCTA GAGGTATTTT 950
CGAGTTGGGT ATCTACCCAG CTGTCGACCC ATTGGACTCC AAGTCTAGAT 1000
TGTTGGATGC CTCTGTTGTC GGTAAGGAGC ACTACGATGT TGCTACCAAC 1050
GTCCAGCAGA CCTTGACGGC CTACAAGTCC TTGCAGGATA TCATTGCCAT 1100
60 TTTGGGTATG GATGAATTGT CCGAAGCCGA CAAGTTGACT GTCGAGAGAG 1150

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CTAGAAAGAT	TCAGAGATTC	TTGTCCCAGC	CATTCGCCGT	CGCCGAGGTT	1200
TTCCTGGTA	TCGAGGGTAA	GTTGGTCAGA	TTGGAGGAGA	CCGTCAAGTC	1250
TTTCAAGGAG	GTCTTGATG	GTAAGTACGA	CCACTTGCCA	GAG	1293

5

2) INFORMATION FOR SEQ ID NO: 466

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1111 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida inconspicua*
 (B) STRAIN: ATCC 16783

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 466

AACGGTGGAT	CTAAGTTAGT	CTTAGAAGTT	GCTCAACATT	TGGGTGAAAA	50
CACTGTCAGA	ACCATTGCTA	TGGATGGTAC	TGAAGGTTTA	GTTAGAGGTC	100
AACCAGTTAA	TGATACTGGT	GCTCCAATCT	CTGTCCCAGT	CGGTAGAGGT	150
ACTTTAGGTA	GAATCTTAAA	CGTTATTGGT	GATCCAGTCG	ATGAAAGAGG	200
TCCAATTGAT	TGTAAGGAAA	GAAAACCAAT	TCATCAAGAT	CCTCCTGCTT	250
TCGTTGAACA	ATCTACTGAA	GCTGAAGTTT	TAGAAAACGG	TATTAAGGTT	300
GTTGATTTAT	TAGCTCCTTA	CGCTAGAGGT	GGTAAGATTG	GTTTATTCGG	350
TGGTGCTGGT	GTCGGTAAAA	CCGTTTTTCAT	TCAAGAATTA	ATTAACAATG	400
TTGCAAAGGC	TCATGGTGGT	TTCTCAGTTT	TCACTGGTGT	CGGTGAAAGA	450
ACCAGAGAAG	GTAATGATTT	ATACAGAGAA	ATGAAGGAAA	CTGGTGTTAT	500
TAACCTTAGAA	GGTGAATCTA	AGGTCGCCTT	AGTTTTCGGT	CAAATGAATG	550
AACCACCAGG	AGCAAGAGCA	AGAGTTGCTT	TAACCGGTTT	AACTATTGCT	600
GAATACTTCA	GAGATGAAGA	AGGTCAAGAT	GTCTTGTTAT	TCATTGATAA	650
CATTTTCAGA	TTTACTCAAG	CAGGTTCTGA	AGTTTCTGCA	TTGTTAGGTA	700
GAATTCCATC	CGCTGTCGGT	TATCAACCAA	CTTTAGCAAC	TGATATGGGT	750
CTTTTACAAG	AAAGAATTAC	AACTACTAAG	AAAGGTTCGG	TTACTTCTGT	800
CCAAGCAGTT	TATGTCCCAG	CAGATGATTT	AACTGATCCT	GCTCCAGCAA	850
CTACTTTTCG	CCACTTAGAT	GCAACTACTG	TCTTATCTAG	AGGTATTTCC	900
GAATTAGGTA	TTTACCCAGC	TGTCGATCCA	TTAGATTCTA	AATCTAGATT	950
ATTAGATGTT	GCTGTTGTTG	GTCAAGAACA	TTATGATGTT	GCAACTCAAG	1000
TTCAAGAAAC	TTTACAAGCA	TACAAATCTT	TACAAGATAT	TATTGCTATT	1050
TTAGGTATGG	ATGAATTATC	TGAACAAGAT	AAATTAACCG	TTGAAAGAGC	1100
AAGAAAGATT	C				1111

2) INFORMATION FOR SEQ ID NO: 467

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1283 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 60 (A) ORGANISM: *Candida kefyr*

	AACTTGGAAG	GTGAATCCAA	GGTCGCCTTA	GTTTTCGGTC	AAATGAACGA	600
	ACCACCAGGA	GCTAGAGCAA	GAGTTGCTTT	AACTGGTTTG	ACCATTGCAG	650
	AATATTTTCAG	AGATGAAGAA	GGTCAAGATG	TCTTGTTATT	CATTGATAAC	700
	ATTTTCAGAT	TCACCCAAGC	AGGTTCTGAA	GTCTCTGCAT	TATTAGGTAG	750
5	AATTCCATCT	GCTGTCGGTT	ATCAACCAAC	TTTAGCAACC	GATATGGGTC	800
	TTTTACAAGA	AAGAATTACC	ACCACCAAGA	AGGGTCCGT	TACTTCTGTC	850
	CAAGCTGTTT	ATGTCCCAGC	CGATGATTTA	ACCGATCCTG	CTCCAGCTAC	900
	TACTTTCGCC	CACTTGGATG	CAACCACTGT	CTTGTCYAGA	GGTATTTCCG	950
	AATTAGGTAT	CTACCCAGCT	GTCGATCCAT	TAGATTCTAA	GTCTAGATTA	1000
10	TTAGATGTTG	CAGTTGTTGG	TCAAGAACAT	TATGAAGTTG	CAACTCAAGT	1050
	CCAAGAAACT	TTACAAGCTT	ACAAGTCTTT	ACAAGATATT	ATTGCTATTT	1100
	TGGGTATGGA	TGAATTATCT	GAACAAGATA	AGTTAACYGT	TGAAAGAGCA	1150
	AGAAAGATCC	AAAGATTCTT	ATCTCAACCA	TTCTCTGTTG	CAGAAGTTTT	1200
	CACTGGTATT	CCAGGTAAGT	TAGTCAGATT	AGAAGAAACC	ATCAAGTCTT	1250
15	TCAGGGATGT	TCTTGCAGGT	AAGTACGATC	ACTTACC		1287

2) INFORMATION FOR SEQ ID NO: 469

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1283 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida lambica*
 (B) STRAIN: ATCC 24750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 469

35	TCGAACAAGG	TCAATTACCA	CCAATTCTTA	ACGCTTTGGT	CATGGAAAAC	50
	GATGGTCAAA	AGTTAGTTTT	GGAAGTTGCT	CAACATTTGG	GTGAAAACAC	100
	CGTCAGAACC	ATTGCTATGG	ACGGTACCGA	AGGTTTAGTT	AGAGGTCAAC	150
	CTGTTAACGA	CACTGGTGCT	CCAATCTCTG	TCCCAGTTGG	TAGAGGTACT	200
	CTTGGTAGAA	TCTTGAACGT	CACTGGTGAC	CCAGTYGATG	AAAGAGGTCC	250
40	TGTCGAMTGT	AAGGAGAGAA	GACCAATTCA	CCAAGACCCA	CCTGCTTTTCG	300
	TTGACCAATC	CACTGAAGCT	GAAGTTTTGG	AAACCGGTAT	TAAGGTTGTC	350
	GATTTATTAG	CACCTTACGC	TAGAGGTGGT	AAGATTGGTT	TGTTCCGGTGG	400
	TGCTGGTGTC	GGTAAGACCG	TTTTCATCCA	AGAATTGATT	AACAATGTTG	450
	CTAAGGCCCA	CGGTGGTTTC	TCCGTTTTCA	CTGGTGTCGG	TGAAAGAACC	500
45	AGAGAAGGTA	ACGATTTATA	CAGAGAAATG	AAGGAAACCG	GTGTTATTAA	550
	CCTTGAAGGT	GAATCTAAGG	TCGCCCTCGT	TTTCGGTCAA	ATGAACGAAC	600
	CACCAGGAGC	AAGAGCTAGA	GTTGCTCTTA	CTGGTTTGAC	CATTGCTGAA	650
	TACTTCAGAG	ATGAAGAAGG	TCAAGATGTC	TTGCTTTTCA	TTGACAACAT	700
	TTTCAGATTC	ACCCAAGCAG	GTTCCGAAGT	GTCTGCTTTG	TTAGGTAGAA	750
50	TTCCWTCTGC	CGTTGGTTAC	CAACCAACCT	TAGCAACCGA	TATGGGTTTG	800
	TTACAAGAAA	GAATTACCAC	CACCAAGAAG	GGTTCCTGTC	CCTCCGTCCA	850
	AGCTGTTTAC	GTCCCAGCTG	ATGATTTRAC	TGACCCTGCA	CCAGCAACCA	900
	CTTTCGCCCA	CTTGGATGCT	ACCACCGTCT	TGTCTAGAGG	TATTTCCGAA	950
	TTAGGTATTT	ACCCAGCTGT	CGATCCATTA	GATTCTAAGT	CTAGATTATT	1000
55	GGATGTCGCT	GTTGTCGGTC	AAGAACATTA	TACCGTTGCA	ACYCAAGTCC	1050
	AAGAACTTT	ACAAGCTTAC	AAGTCCTTAC	AAGATATCAT	TGCTATTTTG	1100
	GGTATGGACG	AATTATCTGA	ACAAGATAAG	CTTACTGTTG	AAAGAGCAAG	1150
	AAAGATCCAA	AGATTCTTTT	CCCAACCTTT	CTCCGTCGCA	GAAGTTTTCA	1200
	CTGGTATCCC	AGGTAAGCTT	GTCAGATTAG	AAGAAACCAT	TATTTCTTTC	1250
60	AGAGATGTCC	TCGATGGTAA	GTACGACCAC	TTA		1283

2) INFORMATION FOR SEQ ID NO: 470

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1140 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida lusitanae*
 (B) STRAIN: ATCC 66035

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 470

20	AGGTGCCTCT	GTCAC	TGACA	CTGGT	TCTCC	AATCT	CTGTC	CCTGT	TGGTC	50
	GTGAA	ACCTT	GGGTAG	AATT	ATCAAC	GTTG	TTGGT	GAGCC	AATTG	100
	AGAGG	CCCCA	TCAACT	CCAA	GAAGAG	AAAC	CCAAT	TCACA	CTGAG	150
	ATCGT	TTTGTT	GAACA	ATCCA	CTTCT	GCTGA	AGTTT	TGGAG	ACTGG	200
	AGGTT	GTCTGA	CTTGTT	TGGCC	CCTTA	CGCCA	GAGGT	TGGTA	GATTG	250
25	TTCGG	TGGTG	CCGGT	GTCTGG	TAAGAC	CGTT	TTCAT	CCAAG	AGTTG	300
	CAACAT	TGCC	AAGGCC	CACG	GTGGT	TTTCTC	TGTTTT	CACT	GGTGT	350
	AAAGA	ACCAG	AGAAG	GTAAC	GATTT	GTACC	GTGAA	ATGCA	AGAGA	400
	GTCAT	CAACT	TCGAG	GGTGA	CTCCA	AAGGTC	GCCTT	TGGTCT	TCGGT	450
	GAACG	AACCA	CCAGG	AGCCA	GAGCT	AGAGT	TGCTT	TGACC	GGTTT	500
30	TTGCC	GAGTA	CTTCAG	AGAC	GAAGAG	GGCC	AAGAT	GTCTT	GTTGT	550
	GACAAC	ATTT	TCAGAT	TCAC	CCAGG	CCGGT	TCTGA	AGTGT	CTGCT	600
	GGGTC	GTATT	CCATCC	GCTG	TCGGT	TACCA	ACCAAC	CCTTG	GCCAC	650
	TGGGT	GCTTT	GCAAG	AGAGA	ATTACC	ACCA	CCAAG	AAGG	TTCCG	700
	TCTGT	CCAAG	CCGTT	TATGT	TCCAG	CTGAT	GACTT	GACTG	ACCCT	750
35	AGCCA	ACCACC	TTGCG	CCCACT	TGGAC	GCCAC	CACTG	TGTTG	TCCAG	800
	TCTCT	GAAAT	GGGTAT	CTAC	CCAGC	TGTCG	ACCCAT	TGGA	CTCCA	850
	AGATT	GTTGG	ACGCT	TCTAT	TGTTG	GTAAG	GAGCA	CTACG	AAGTT	900
	TAACG	TTCAA	CAAAC	TTTGC	AAGCT	TACAA	GTCTT	TGCAA	GATAT	950
	CCATT	TTGGG	TATGG	ATGAA	TTGTC	TGAGG	CTGAC	AAAGT	GACCG	1000
40	AGAGC	CAGAA	AGATC	CAAAG	ATTCT	TGTCT	CAACC	ATTTCG	CTGTT	1050
	GGTTT	TCACT	GGTAT	CCCAG	GTAGA	TTGGT	CAGAT	TGGAG	GACAC	1100
	GATCC	TTCAA	GGAAG	TTTTG	GACGG	TAAGT	ACGAC	CACTT		1140

2) INFORMATION FOR SEQ ID NO: 471

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1296 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida norvegensis*
 (B) STRAIN: ATCC 22977

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 471

	TCAATTCGAA	CAAGGTCAAT	TACCACCAAT	TTTAAACGCT	TTAGTCATGG	50
	ACAACGGTGG	AACTAAGTTA	GTTTTAGAAG	TTGCTCAACA	TTTAGGTGAA	100
	AACACCGTCA	GAACCATTGC	TATGGATGGT	ACTGAAGGTT	TAGTTAGAGG	150
5	TCAACCAAGTT	AATGATACTG	GTGCTCCAAT	CTCTGTCCCA	GTCGGTAGAG	200
	GTACTTTAGG	TAGAATCTTA	AACGTTATTG	GTGATCCAGT	CGATGAAAGA	250
	GGTCCAATCG	ATTGTAAGGA	AAGAAAACCA	ATTCATCAAG	ATCCTCCTGC	300
	TTTCGTTGAA	CAATCAACTG	AAGCTGAAGT	TTTAGAAACT	GGTATTAAAG	350
	TTGTGCGATTT	ATTAGCTCCT	TACGCTAGAG	GTGGTAAGAT	TGGTTTATTC	400
10	GGTGGTGCAG	GTGTTGGTAA	AACCGTTTTT	ATTCAAGAAT	TAATTAACAA	450
	TGTTGCAAAA	GCTCATGGTG	GTTTCTCCGT	TTTCACTGGT	GTCGGTGAAA	500
	GAAC TAGAGA	AGGTAACGAT	TTATACAGAG	AAATGAAGGA	AACTGGTGTT	550
	ATTAATTTAG	AAGGTGATTC	TAAGGTCGCA	TTAGTTTTTCG	GTCAAATGAA	600
	CGAACCACCT	GGAGCAAGAG	CAAGAGTTGC	TTTAACTGGT	TTAACTATTG	650
15	CTGAATATTT	CAGAGATGAA	GAAGGTCAAG	ATGTCTTGTT	ATTCATTGAT	700
	AACATTTTCA	GATTTACTCA	AGCAGGTTCT	GAAGTTTCCG	CTTTGTTAGG	750
	TAGAATTCCA	TCCGCTGTCG	GTTATCAACC	AACTTTAGCA	ACTGATATGG	800
	GTCTTTTACA	AGAAAGAATT	ACTACTACTA	AGAAAGGTTT	TGTTACTTCC	850
	GTTCAAGCAG	TTTATGTCCC	AGCAGATGAT	TTAACTGATC	CTGCTCCAGC	900
20	AACTACTTTC	GCCCACTTAG	ATGCAACTAC	TGTCTTATCT	AGAGGTATTT	950
	CCGAATTAGG	TATTTACCCA	GCTGTCGATC	CATTAGATTG	TAAATCTAGA	1000
	TTATTAGATG	TTGCAGTTGT	TGGTCAAGAA	CATTATGATG	TTGCAACTCA	1050
	AGTTCAAGAA	ACTTTACAAG	CTTACAAATC	TTTACAAGAT	ATTATTGCTA	1100
	TTTTAGGTAT	GGATGAATTA	TCTGAACAAG	ATAAATTAAC	CGTTGAAAGA	1150
25	GCTAGAAAAA	TTCAAAGATT	CTTATCTCAA	CCTTTCTCTG	TCGCAGAAGT	1200
	TTTCACTGGT	ATCCCAGGTA	AGCTTGTTAG	ATTAGAAGAA	ACTATTTCTT	1250
	CATTCAGAGA	TGTCTTAGCA	GGTAAGTACG	ATCACTTACC	AGAAAA	1296

30

2) INFORMATION FOR SEQ ID NO: 472

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 1297 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida parapsilosis*
 (B) STRAIN: ATCC 90018

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 472

	ACACTTCGAA	GAAGGAAACT	TGCCAGCTAT	TTTGAACGCT	TTGACCTTGA	50
	AAAACGGTAA	ACAAGACTTG	GTCTTGGAAG	TTGCCCAACA	TTTGGGTGAA	100
	AACACCGTCA	GAGCAATTGC	TATGGATGGT	ACTGAAGGTT	TAGTTAGAGG	150
50	TACTTCTGTC	ACTGACACTG	GTGCCCCAAT	TTCTGTCCCA	GTTGGTAGAG	200
	GTACTTTGGG	TAGAATCATC	AATGTTACTG	GTGACCCAAT	TGATGAAAGA	250
	GGTCCAATTG	AATGTAAGAA	GAGAAACCCA	ATCCACGCTG	AACCACCTTC	300
	ATTCATTGAA	CAATCCACTG	CTGCTGAAGT	TTTGGAAACC	GGTATTAAGG	350
	TTGTGCACTT	GTTGGCTCCA	TACGCTAGAG	GTGGTAAGAT	TGGTTTGTTC	400
55	GGTGGTGCCG	GTGTCGGTAA	AACCGTGTTT	ATCCAAGAAT	TGATCAACAA	450
	CATTGCCAAG	GCACATGGTG	GTTTCTCGGT	TTTCACTGGT	GTGGTGAAA	500
	GAACCAAGAG	AGGTAACGAT	TTGTACCGTG	AAATGAAGGA	AACTGGTGTT	550
	ATCAACTTGG	AAGGTGACTC	CAAGGTCGCT	TTGGTTTTTCG	GTCAAATGAA	600
	CGAACCACCT	GGAGCTAGAG	CTAGAGTTGC	TTTGACTGGT	TTGACCATTG	650
60	CTGAATACTT	TAGAGATGAA	GAAGGTCAAG	ATGTCTTGTT	GTTTATTGAC	700

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AACATTTTCA GATTCACCCA AGCTGGTTCA GAAGTGTCTG CTTTGTGTTGG 750
TCGTATTCCA TCCGCTGTCG GTTATCAACC AACCTTGGCC ACCGATATGG 800
GTCTTTTTCGA AGAACGTATT ACCACTACCA AAAAGGGTTC AGTTACTTCA 850
GTCCAAGCCG TTTACGTGCC AGCTGATGAT TTAACCGATC CTGCTCCAGC 900
5 TACCACTTTC GCTCACTTGG ATGCCACCAC TGTGTTGTCT AGAGGTATTT 950
CGGAGTTGGG TATTTACCCA GCTGTCGATC CATTGGATTG CAAATCCAGA 1000
TTGTTGGATG CTGCCGTTGT TGGTCAAGAA CATTACGACG TTGCCACTGG 1050
TGTTCAACAA ACTTTACAAG CTTACAAGTC CTTGCAAGAT ATCATTGCTA 1100
TCTTGGGTAT GGATGAATTG TCCGAACAAG ATAAATTGAC TGTGAAAGA 1150
10 GCTCGTAAGA TTCAAAGATT CTTGTCTCAA CCATTGCTG TCGCTGAAGT 1200
TTTCACTGGT ATTCCAGGTA AATTGGTTAG ATTGTCTGAA ACTGTCAAGT 1250
CATTCAAGGA AGTCTTGGA GGTAAAGTACG ATAACCTGCC AGAAAAT 1297

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15

2) INFORMATION FOR SEQ ID NO: 473

(i) SEQUENCE CHARACTERISTICS:

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20 (A) LENGTH: 1285 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

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    (A) ORGANISM: Candida rugosa
    (B) STRAIN: ATCC 96275

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 473

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CCAGTTTGGC AACGACCTCC CTGCCATTTT GAACGCCCTC ACTCTTCAGC 50
GTGAAGACGG TAACAAGCTT GTTCTTGAGG TTGCCAGCA TCTCGGTGAG 100
AACACCGTCC GTACCATTGC TATGGACGGT ACCGAGGGTT TGGTGCGTGG 150
35 CACTGGTGTC CACGACACCG GACACCCCAT CATGACTCCC GTCGGTGACG 200
GTACCCTGGG ACGTATTCTT AACGTCACCG GTGACCCTGT AGACGAGCGT 250
GGTCCCGTCA AGACTGACAA GTTCCGCCCC ATCCACGCCG AGGCCCTGC 300
CTTCGATGAG CAGGCTACCA GTGCCGAGGT TCTTGAGACC GGTATCAAGG 350
TTGTGCACTT GCTCGCTCCT TACGCCAAGG GTGGTAAGAT TGGTTTGTTT 400
40 GGTGGTGCCG GTGTCGGCAA GACCGTCTTC ATCCAGGAGC TGATTAACAA 450
CATCGCCAAG GCCCACGGTG GTTACTCCGT GTTCACTGGT GTCGGTGAGC 500
GTACTCGTGA GGGTAACGAT TTGTACAAGG AAATGATCGA GTCCGGTGTC 550
ATCAACCTCG ATGGTGAGTC CAAGGTCGCC TTGGTGTTTCG GTCAGATGAA 600
CGAGCCCCCT GGAGCCCGTG CCCGTGTCGC CCTTACCGGT CTTACCATCG 650
45 CTGAGTATTT CCGTGATGAG GAGGGTAAGG ATGTCTTGTT GTTCGTTGAC 700
AACATTTTCC GCTTCACTCA GGCCGGTTCT GAGGTGTCCG CTTGCTTGG 750
TCGTATTCCT TCCGCTGTCG GTTACCAGCC TACCCTGGCC ACCGATATGG 800
GTGCCCTTCA GGAGCGTATC ACCACCACCA AGAAGGGTTC CGTTACATCC 850
GTCCAGGCCG TCTACGTCCC TGCCGATGAT TTGACTGATC CCGCCCTGC 900
50 CACCACCTTC GCCCATTTGG ATGCCACCAC TGTCTTGTCT CGTGCCATCT 950
CTGAGTTGGG TATCTACCCC GCTGTCGACC CTCTCGACTC CAAGTCCCGT 1000
CTTCTTGACG CCGCTGTCGT TGGTCAGGAG CACTACGATA CTGCCACCTC 1050
CGTTCAGCAG ACTTTGCAGG CTTACAAGTC TTTGCAGGAT ATCATTGCCA 1100
TTCTTGGTAT GGATGAGTTG TCCGAGTCTG ACAAGCTCAC CGTCGAGCGT 1150
55 GCTCGTAAGA TCCAGCGTTT CCTCTCCAG CTTTTCGCTG TTGCTGAGGT 1200
CTTCACTGGT ATTCAAGGCC GTCTTGTTCC TCTCAAGGAC ACTGTCCGCT 1250
CCTTCAAGGA GATTCTCGAA GGTAAGTACG ATGCT 1285

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60

2) INFORMATION FOR SEQ ID NO: 474

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1283 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida sphaerica*
 (B) STRAIN: ATCC 2504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 474

TTGAACAAGG	TCAATTGCCA	GCTATTTTGA	ACGCTTTGGA	AATCGACACT	50
CCAGAAGGAA	AGTTGGTTTT	GGAAGTCGCT	CAACATTTGG	GTGAAAACAC	100
TGTCAGAACC	ATTGCTATGG	ATGGTACTGA	AGGTTTAGTC	CGTGGTGAAA	150
ACGTTTCTGA	CACTGGTGCT	CCAATTTCCG	TCCCAGTTGG	TAGAGAAACC	200
TTGGGTAGAA	TTATCAACGT	TATTGGTGAG	CCAATTGACG	AAAGAGGTCC	250
AATCAACTCC	AAGATGAGAA	AGCCAATTCA	TGCTGATCCT	CCATTATTCTG	300
TTGAACAATC	CACTGCTGCT	GAAGTTTGG	AAACTGGTAT	CAAGGTTGTC	350
GACTTGTTGG	CCCCATACGC	CAGAGGTGGT	AAGATTGGTT	TGTTCCGGTGG	400
TGCCGGTGTC	GGTAAGACCG	TTTTTCATCCA	AGAATTGATT	AACAACATTG	450
CCAAGGCTCA	TGGTGGTTTC	TCTGTCTTCA	CTGGTGTCCG	TGAAAGAACC	500
AGAGAAGGTA	ACGATTTGTA	CCGTGAAATG	AAGGAAACTG	GTGTTATCAA	550
CTTGGAAGGT	GATTCTAAGG	TCGCGTTGGT	TTTCGGTCAA	ATGAACGAAC	600
CTCCTGGAGC	TAGAGCTAGA	GTCGCCTTGA	CTGGTTTGAC	CATCGCTGAA	650
TACTTCAGAG	ATGAAGAAGG	TCAAGATGTC	TTGTTGTTTA	TCGACAACAT	700
TTTCAGATTC	ACACAAGCCG	GTTCCGAAGT	GTCCGCTTTG	TTGGGTCGTA	750
TTCCATCCGC	TGTCGGTTAT	CAACCAACTT	TGGCCACCGA	TATGGGTTTG	800
TTGCAAGAAA	GAATTACTAC	CACCAAGAAG	GGTTCCGTCA	CTTCTGTCCA	850
AGCCGTTTAC	GTGCCAGCTG	ATGATTTGAC	TGATCCTGCT	CCAGCTACCA	900
CTTTGCGGCA	TTTGGATGCC	ACCACTGTGT	TGTCCAGAGG	TATCTCTGAA	950
TTGGGTATCT	ACCCAGCTGT	CGATCCTTTG	GATTCCAAAT	CTAGATTGTT	1000
GGATGCTGCC	GTCGTTGGTC	AAGAACATTA	CGATGTCGCT	ACTCAAGTTC	1050
AACAAACTTT	GCAAGCTTAC	AAGTCTTTGC	AAGATATCAT	TGCCATTTTG	1100
GGTATGGATG	AATTGTCCGA	ACAAGATAAG	TTGACCGTCG	AAAGAGCTAG	1150
AAAGATTCAA	AGATTCTTGT	CTCAACCTTT	CGCTGTCGCT	GAAGTCTTCA	1200
CTGGTATCCC	AGGTAGATTG	CTCAGATTAA	AGGACACCAT	CTCTTCTTTC	1250
AAGGCTGTCT	TGGACGGTAA	GTACGATCAC	TTG		1283

2) INFORMATION FOR SEQ ID NO: 475

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1290 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida tropicalis*
 (B) STRAIN: ATCC 13803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 475

	CGACGAAGGT	AACTTGCCAG	CTATTTTGAA	TGCTTTGACT	TTGAAGAACG	50
	GTGACCAAGA	CTTGGTTTTG	GAAGTTGCTC	AACATTTGGG	TGAAAACACC	100
	GTCAGGGCTA	TTGCTATGGA	TGGTACCGAA	GGTTTAGTCA	GAGGTACTGC	150
5	TGTCACTGAT	ACCGGTGCTC	CAATTTCTGT	CCCAGTTGGT	AGAGGTACCT	200
	TGGGTAGAAT	TATCAACGTT	GTTGGTGAAC	CAATTGATGA	CAGAGGTCCA	250
	ATTGAATGTA	AGGAAAGAAA	GCCAATTCAC	GCTGAACCAC	CTTCATTTCG	300
	TGAACAATCT	ACTGCTGCCG	AAATTTTGGG	AACCGGTATT	AAGGTTGTCG	350
	ATTTGTTGGC	TCCTTACGCT	AGAGGTGGTA	AGATTGGTTT	GTTCGGTGGT	400
10	GCTGGTGTCT	GTAAAACCGT	CTTCATCCAA	GAATTGATTA	ACAACATTGC	450
	CAAAGCTCAT	GGTGGTTTCT	CTGTCTTTAC	CGGTGTCGGT	GAAAGAACCA	500
	GAGAAGGTAA	CGATTTGTAC	CGTGAAATGA	AAGAACTGG	TGTCATCAAC	550
	TTGGAAGGTG	ACTCCAAGGT	CGCCTTGGTC	TTCGGTCAAA	TGAACGAACC	600
	ACCTGGTGCT	AGAGCTAGAG	TTGCTTTGAC	TGGTTTGACC	ATTGCTGAAT	650
15	ACTTCAGAGA	TGAAGAAGGT	CAAGATGTCT	TGTTGTTTAT	TGACAACATT	700
	TTCAGATTCA	CCCAAGCTGG	TTCCGAAGTG	TCTGCTTTGT	TGGGTCGTAT	750
	TCCATCTGCT	GTCGGTTATC	AACCAACCTT	GGCCACTGAT	ATGGGTCTTT	800
	TGCAAGAACG	TATTACCACC	ACCAAGAAAG	GTTCTGTAC	TTCTGTCCAA	850
	GCTGTTTATG	TCCCAGCCGA	TGATTTAACC	GATCCAGCTC	CAGCTACCAC	900
20	CTTCGCTCAC	TTGGATGCCA	CTACTGTCTT	GTCTAGAGGT	ATTTCTGAAT	950
	TGGGTATTTA	CCCAGCTGTC	GATCCATTGG	ATTCTAAATC	CAGATTATTG	1000
	GATGCTACTG	TTGTTGGTCA	AGAACATTAT	GATGTTGCCA	CTGGTGTTCA	1050
	ACAACTTTA	CAAGCTTACA	AGTCCTTGCA	AGATATCATT	GCTATTTTGG	1100
	GTATGGATGA	ATTGTCGGA	GCCGATAAAT	TGACTGTCGA	AAGAGCTCGT	1150
25	AAGATTCAAA	GATTCTTGTC	CCAACCATTG	GCTGTTGCCG	AAGTTTTCAC	1200
	TGGTATCCCA	GGTAGATTGG	TTAGATTACA	AGATACTGTT	AAATCTTTCA	1250
	AAGATGTCTT	GGAAGGTAAA	TACGATCACT	TGCCAGAAAA		1290

30

2) INFORMATION FOR SEQ ID NO: 476

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 1267 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida utilis*
- (B) STRAIN: Csp 388

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 476

	TTTGAACGCC	CTTGAGATCA	AGAACCACGA	GTCTGGAAGA	TTGGTCCTCG	50
	AGGTTGCCCA	GCACTTGGGT	GAGAACACTG	TCAGAACTAT	TGCCATGGAT	100
	GGTACCGAAG	GTCTCGTCCG	TGGTGAGTCT	GTTGTTGACA	CCGGTTCTCC	150
50	AATTACTGTC	CCAGTTGGTC	GTGAGACCTT	GGGTCGTATC	ATCAACGTTA	200
	TTGGTGAGCC	AATTGATGAG	CGTGGTCCAA	TCAACACCAA	GCACAGAAAC	250
	CCAATTCACG	CTGAGCCACC	ATCCTTCGCT	GAGCAGTCTA	CTGCTGCTGA	300
	GGTTTTGGAG	ACTGGTATCA	AGGTTGTCGA	CCTTCTCGCC	CCATACGCCA	350
	GAGGTGGTAA	GATTGGTCTC	TTTGGTGGTG	CCGGTGTCGG	TAAGACCGTT	400
55	TTCATCCAGG	AGTTGATTAA	CAACATTGCC	AAGGCCACAG	GTGGTTTCTC	450
	TGTTTTCCAC	GGTGTCGGTG	AGAGAACCAG	AGAGGGTAAC	GATTTGTACC	500
	GTGAGATGAA	GGAGACTGGT	GTCATCAATC	TCGAGGGTGA	GTCCAAGGTT	550
	GCTCTCGTCT	TCGGTCAGAT	GAACGAGCCA	CCAGGTGCCC	GTGCCCGTGT	600
	CGCTTTGACC	GGTTTGACCA	TTGCTGAGTA	CTTCAGAGAT	GAGGAGGGTC	650
60	AGGATGTCTT	GTTGTTTATT	GACAACATTT	TCAGATTCAC	CCAGGCCCGT	700

	TCCGAGGTGT	CTGCCTTGCT	TGGTCGTATT	CCATCCGCTG	TCGGTTACCA	750
	GCCAACTTTG	GCCACCGATA	TGGGTTTGTT	GCAGGAGAGA	ATTACCACCA	800
	CCCAGAAGGG	TTCCGTCACT	TCTGTCCAGG	CCGTTTACGT	CCCAGCTGAT	850
	GATTTGACTG	ATCCTGCTCC	AGCCACCACT	TTCGCCCCACT	TGGACGCCAC	900
5	CACTGTGTTG	TCCCGTGGA	TCTCTGAGTT	GGGTATTTAC	CCAGCTGTCG	950
	ACCCATTGGA	CTCCAAGTCC	AGATTGTTGG	ACGCTGCCGT	TGTTGGTGAC	1000
	GAGCACTACA	ACACCGCCAC	CGATGTCCAG	CAGACCCTTC	AGGCTTACAA	1050
	GTCTCTCCAG	GATATCATTG	CTATTTTGGG	TATGGATGAG	TTGTCTGAGG	1100
	CTGACAAAGTT	GACTGTGCGAG	AGAGCCAGAA	AGATTTCAGCG	TTTCCTTTCC	1150
10	CAGCCATTCG	CTGTCGCTGA	GGTTTTTACC	GGTATCCCAG	GTAGATTGGT	1200
	TAGACTTCAG	GACACCATCA	AGTCCTTCAG	AGAGGTTTGT	GACGGTAAGT	1250
	ACGACCACTT	GCCAGAG				1267

15

2) INFORMATION FOR SEQ ID NO: 477

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 1296 bases
20	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Candida viswanathii</i>
	(B)	STRAIN: ATCC 28269

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 477

	CCAATTCGAC	GAAGGTAGCT	TGCCAGCTAT	CTTGAACGCC	TTGACCTTGA	50
	AGAACGGTGA	CCAAGACTTG	GTCTTGGAAG	TTGCCCAACA	CTTGGGTGAA	100
	AACACTGTCA	GAGCTATTGC	TATGGATGGT	ACCGAAGGTT	TGGTCAGAGG	150
35	TACTGCTGTC	ACTGACACCG	GTGCTCCAAT	CTCCGTCCCA	GTCGGTAGAG	200
	GTACCTTGGG	TAGAATCATC	AACGTTGTTG	GTGAACCAAT	TGACGACAGA	250
	GGTCCAATTG	AATGTAAGGA	AAGAAAGCCA	ATTACGCTG	AACCACCTTC	300
	TTTCGTTGAA	CAATCCACTG	CTGCCGAAAT	TTTGGAACCC	GGTATCAAGG	350
	TTGTGCACTT	GTTGGCCCCA	TACGCCAGAG	GTGGTAAGAT	TGGTTTGTTC	400
40	GGTGGTGCCG	GTGTCGGTAA	GACTGTCTTT	ATCCAAGAGT	TGATTAACAA	450
	CATTGCCAAG	GCCCATGGTG	GTTTCTCTGT	CTTCACTGGT	GTCCGTGAAA	500
	GAACCAGAGA	AGGTAACGAT	TTGTACCGTG	AAATGAAGGA	AACCGGTGTC	550
	ATCAACTTGG	AAGGTGACTC	CAAGGTCGCC	TTGGTTTTCG	GTCAAATGAA	600
	CGAACCACCT	GGTGCTAGAG	CTAGAGTTGC	TTTGACTGGT	TTGACCATTG	650
45	CCGAATACTT	CAGAGACGAA	GAAGGTCAAG	ATGTCTTGTT	GTTTATTGAC	700
	AACATTTTCA	GATTACACCA	AGCCGGTTCC	GAAGTGTCTG	CTTTGTTGGG	750
	TCGTATTCCA	TCTGCCGTCC	GTTATCAACC	AACCTTGCC	ACCGATATGG	800
	GTCTTTTGCA	AGAACGTATT	ACCACCACCA	AGAAGGGTTC	CGTCACCTCT	850
	GTCCAAGCTG	TCTATGTCCC	AGCCGATGAT	TTGACCGATC	CTGCTCCAGC	900
50	CACCACCTTC	GCTCACTTGG	ATGCCACTAC	TGTCTTGTCT	AGAGGTATTT	950
	CCGAATTGGG	TATCTACCCA	GCTGTGATC	CATTGGACTC	CAAGTCCAGA	1000
	TTGTTGGATG	CTGCTGTTGT	TGGTCAAGAA	CATTACGATG	TTGCCACTGG	1050
	TGTCCAACAA	ACCTTGCAAG	CTTACAAGTC	TTTGCAAGAT	ATCATTGCCA	1100
	TTTTGGGTAT	GGATGAATTG	TCTGAATCCG	ATAAGTTGAC	TGTCGAAAGA	1150
55	GCTCGTAAGA	TCCAAGATT	CTTGTCGCAA	CCATTTGCTG	TTGCCGAAGT	1200
	TTTCACTGGT	ATCCCAGGTA	GATTAGTTAG	ATTGCTGGAA	ACCGTCCAAT	1250
	CTTTCAAAGA	CGTCTTGGCT	GGTAAATACG	ATCACTTGCC	AGAAAA	1296

60

2) INFORMATION FOR SEQ ID NO: 478

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1295 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida zeylanoides*
 (B) STRAIN: ATCC 7351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 478

TCAATTCGAG	CAAGGCAACC	TCCCTGCCAT	CTTGAACGCT	CTCACCTTGA	50
AGAATGGTGA	CAACGACTTG	GTTTTGGAAG	TTGCCCAGCA	CTTGGGTGAG	100
AACACCCGTCA	GAGCCATTGC	CATGGATGGT	ACCGAGGGTT	TGGTTAGAGG	150
TGCGTCCGTC	AAGGACACTG	GCGCCCCTAT	CTCGGTCCCC	GTTGGCCGCG	200
GGACTTTGGG	TCGTATCATC	AACGTCACCG	GTGACCCCAT	TGACGAGAGA	250
GGTCCCATCG	AGCTGACCCA	GAGAAACCC	ATCCACGCCG	ACCCCCCTC	300
GTTTCGTTGAG	CAGTCCACCA	ACGCTGAGGT	TTTGGAGACT	GGTATCAAGG	350
TTGTTCGATTT	GTTGGCTCCC	TACGCCAGAG	GTGGTAAGAT	TGGTTTGTTT	400
GGTGGTGCCG	GTGTCGGTAA	GACCGTCTTC	ATTCAGGAGT	TGATCAACAA	450
CATCGCCAAG	GCCACGGTG	GGTTCCTCGT	CTTCACTGGT	GTCGGTGAGA	500
GAAGTAGAGA	GGGTAACGAC	TTGTACCGTG	AGATGAAGGA	GACCGGTGTC	550
ATCAACTTGG	AGGGTGACTC	CAAGGTGGCC	TTGGTGTTTC	GTCAGATGAA	600
CGAGCCCCCT	GGAGCCAGAG	CCAGAGTCGC	CTTGACCGGG	TTGACCATTG	650
CCGAATACTT	TAGAGACGAG	GAGGGTCAGG	ATGTGTTGTT	GTTTCGTCGAC	700
AACATCTTCA	GATTCACCCA	AGCTGGTTCG	GAGGTGTCGG	CCTTGTTGGG	750
TCGTATTCCC	TCTGCCGTCG	GTTACCAGCC	CACCTTGGCA	ACTGATATGG	800
GATTGTTGCA	GGAGCGTATC	ACCACGACCA	AGAAGGGTTC	CGTCACCTCA	850
GTGCAGGCCG	TCTACGTCCC	CGCTGATGAC	TTGACTGACC	CTGCTCCCGC	900
CACCACCTTT	GCCCACTTGG	ACGCCACCAC	CGTGTGTGTC	AGAGGTATCT	950
CTGAGTTGGG	TATCTACCCC	GCCGTCGACC	CCTTGGACTC	CAAATCGAGA	1000
TTGTTGGACG	CTGCCGTGGT	CGGTCAGGAG	CACTACGATG	TTGCCTCGAA	1050
CGTCCAGCAG	ACCTTGACAG	CCTACAAGTC	CTTGCAGGAT	ATCATTGCCA	1100
TTTTGGGTAT	GGATGAGTTG	TCCGAGGCTG	ACAAGTTGAC	CGTTGAGAGA	1150
GCCAGAAAGA	TCCAGAGATT	CTTGTGCGCAG	CCCTTCGCTG	TTGCCGAGGT	1200
TTTCACTGGT	ATCAAGGGTA	GATTGGTCAG	ATTGGAGGAC	ACCGTCAGAT	1250
CTTTCAAGGA	GGTTTTGGAG	GGTAAGTACG	ACCACTTGCC	CGAGA	1295

2) INFORMATION FOR SEQ ID NO: 479

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Coccidioides immitis*
 (B) STRAIN: Silveira

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 479

```

5   TTCAGGAATT GATTGTAAGT TCTGTTATCA ACTAAAGCCG ACAGCGGTTG      50
    CTGATATGCT CTAGAACAAC ATTGCTAAGG CTCACGGTGG TTACTIONCGTG      100
    TTCACTGGTG TCGGTGAGCG TACCCGTGAG GGTAACGATT TGTACCATGA      150
    AATGCAAGAG ACCCGTGTCA TTCAACTCGA CGGAGAGTCC AAGGTCGCTC      200
    TTGTCTTCGG TCAAATGAAC GAGCCCCCTG GTGCCCGTGC CCGTGTTGCC      250
    CTTACCGGTT TGACCATTCG TGAATACTTC CGTGACGAGG AAGGCCAAGA      300
    CCGTAGGCTT CATGCTTCTA TCGCTAGGGG CGTGTGATAC AGGAGGCTAA      350
    TCGCTTTTCT AGTGCTTCTC TTTATTGACA ACATTTTCCG TTTCACTCAA      400
10  GCTGGTTCTG AAGTGTCTGC CTTGCTCGGT CGTATTCTCT CCGCTGTCGG      450
    TTACCAACCT ACTCTCGCCG TCGACATGGG TGTTATGCAG GAACGTATCA      500
    CCACCACCAC CAAGGGATCC ATTACTTCAG TGCA                        534

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15 2) INFORMATION FOR SEQ ID NO: 480

(i) SEQUENCE CHARACTERISTICS:

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20  (A) LENGTH: 494 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

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    (A) ORGANISM: Cryptococcus albidus
    (B) STRAIN: ATCC 66030

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30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 480

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    CGTCTTGATT CAAGAATTGA TCAACAACAT CGCCAAGGCC CACGGTGGTT      50
    ACTCGGTCTT CACCGGTGTC GGTGAGCGAA CTCGAGAGGG TAACGATCTG      100
    TACCACGAAG TGAGTTGCGC CGTCCGAGTG TTTCCCGGGG AATCGCAAGA      150
35  CTGATGTTGT CCCTTCTTCT CAGATGAGGG AAACCGGTGT CATCAACCTC      200
    GAGGGTGA CT CCAAGGTCGC CTTGGTCTTC GGTCAGATGA ACGAGCCCCC      250
    TGGAGCCCGA GCCCGAGTCG CCTTGACCGG TTTGACCATT GCCGAATACT      300
    TCCGAGACGA GGAGGGTCAG GATGTCTTGT TGTTCAATTGA CAACATTTTC      350
    CGATTCACCC AAGCCGGTTC CGAAGTGTCC GCCTTGTTGG GTCGTATCCC      400
40  CTCCGCCGTC GGTACCAGC CCACTCTGTC CACCGACATG GGTACCATGC      450
    AGGAGCGAAT TACCACCACC AAGAAGGGTT CCATCACTTC CGTC            494

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45 2) INFORMATION FOR SEQ ID NO: 481

(i) SEQUENCE CHARACTERISTICS:

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50  (A) LENGTH: 415 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

55 (vi) ORIGINAL SOURCE:

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    (A) ORGANISM: Fusarium oxysporum
    (B) STRAIN: WSA-212

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 481

60

5 TTCAGGAGCT TATCAACAAC ATCGCCAAGG CCCACGGTGG TTACTCCGTC 50
 TTCACTGGTG TCGGTGAGCG AACTCGTGAG GGTAACGATC TGTACCACGA 100
 AATGCAGGAG ACTTCCGTCA TTCAGCTTGA TGGCGAGTCC AAGGTCGCCC 150
 TGGTCTTCGG TCAGATGAAC GAGCCCCCTG GAGCTCGTGC CCGTGTCGCC 200
 CTTACCGGTC TTACTGTAGC TGAATACTTC AGAGATGAGG AGGGTCAGGA 250
 CGTGCTGCTC TTCATTGACA ACATTTTCCG ATTCACTCAG GCCGGTTCCG 300
 AGGTGTCTGC CTTTCTCGGT CGTATCCCCT CTGCCGTCGG TTACCAGCCC 350
 ACCCTCGCCG TCGACATGGG TGGTATGCAA GAGCGTATTA CCACCACCAC 400
 CAAGGGTTCC ATTAC 415

10

2) INFORMATION FOR SEQ ID NO: 482

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1281 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Geotrichum* spp.
 25 (B) STRAIN: Lev-4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 482

30 AGGACAACCT CCCCCTATT CTTAACGCTC TTGAGCTTAA GAGAGATAAC 50
 GGTGAGAAGC TCGTTCTCGA GGTGCCCCAG CATCTGGGTG AGAACAACGT 100
 CCGTACTATT GCTATGGACG GTACTGAGGG TCTCGTCCGT GGTGAGCCCC 150
 TTGTTGACAC CGGTGCCCCC ATTACCATTC CCGTTGGTCG TGGTACTCTT 200
 GGTAGAATTA TCAACGTCAT TGGTGAGCCC ATCGATGAGC GTGGACCCAT 250
 TGAGGCTACC AAGTACCTCC CCATCCACAC CGAGCCCCCC ACCTTCGCTG 300
 35 AGCAGTCTAC CTCCGCTGAG GTTCTTGAGA CTGGTATCAA GGTTGTGCGAT 350
 CTCCTTGCCC CCTACGCCCC TGGTGGTAAG ATTGGTCTCT TCGGTGGTGC 400
 CCGTGTCGGT AAGACCGTTT TCATTGAGGA GCTGATTAA AACATTGCCA 450
 AGGCCCATGG TGGTTTCTCC GTTTTCACCG GTGTCGGTGA GAGAACCCGT 500
 GAGGGTAACG ATTTGTACCG TGAGATGAAG GAGACCGGTG TCATCAACCT 550
 40 CGAGGGTGAG TCTAAGGTCG CTCTCGTTTT CGGTCAGATG AACGAGCCCC 600
 CTGGAGCCCC TGCCCGTGTT GCTCTTACTG GTCTTACCAT TGCTGAGTAC 650
 TTCCGTGATG AGGAGGGTCA GGATGTGTTG CTCTTCGTTG ACAACATTTT 700
 CCGTTTCACT CAGGCCGGTT CCGAGGTGTC TGCCCTTTTG GGTCGTATTC 750
 CCTCCGCTGT CGGTTACCAG CCCACCCTTG CCACTGATAT GGGTGCCCTG 800
 45 CAAGAGCGTA TTACCACCAC CCAGAAGGGT TCCGTCACCT CCGTCCAGGC 850
 CGTCTACGTC CCTGCCGATG ATTTGACCGA TCCTGCCCTT GCTACCACCT 900
 TCGCCCATTT GGATGCCACC ACCGTCTTGT CGCGTTCCAT TTCTGAGTTG 950
 GGTATCTACC CCGCTGTCGA TCCCCTTGAT TCCAAGTCTC GTCTTTTGGA 1000
 50 TATCACCGTC GTTGGCCAGG AGCACTACGA TGTTGCTACC CAGGTCCAGC 1050
 AGACCCTCCA GTCCTACAAG TCTCTTCAGG ATATCATTGC CATTTTGGGT 1100
 ATGGATGAGT TGTCTGAGGC TGATAAGCTT ACTGTGAGC GTGCCCCTAA 1150
 GATCCAGAGA TTCCTTTCCC AGCCCTTCAC TGTCGCTGAG GTTTTCACTG 1200
 GTATCGAGGG CCGTCTCGTT CCTTTGAAGG ACACGTTCG CTCTTTCAAG 1250
 55 GAGATCCTTG AGGGCAAGTA CGACCACCTC C 1281

2) INFORMATION FOR SEQ ID NO: 483

60 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 586 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Histoplasma capsulatum*
 (B) STRAIN: G185A5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 483

15	ATTCAAGAAT	TGATCGTACG	TTCCTCCGCC	CCACACACGA	TCAATGGAGA	50
	AAGAAACAAA	TTTTTTGGGA	GTGGTCATTT	TTTCTAATAA	TCGAATAGA	100
	ACAACATTGC	CAAAGCCAC	GGTGGTTACT	CCGTGTTCAC	TGGTGTCCGC	150
	GAGCGGACCC	GTGAAGGAAA	TGACTTGTAC	CACGAAATGC	AGGAAACCCG	200
	TGTTATCCAG	CTCGATGGAG	AGTCCAAGGT	CGCCCTCGTT	TTCGGTCAGA	250
	TGAACGAGCC	TCCCGGAGCC	CGTGCCCGTG	TTGCCCTCAC	TGGTCTGACC	300
20	GTGCGCGAGT	ACTTCCGTGA	CGAGGAAGGC	CAAGACGGTA	TGTATAAGTA	350
	TACACCGTAG	CAAATCAACA	CAGAGCTTCA	CTCAGCTCG	GATTTAGTGC	400
	TTCTCTTCAT	CGACAACATT	TTCCGCTTCA	CTCAGGCCGG	TTCCGAAGTG	450
	TCTGCCCTGC	TCGGCCGTAT	TCCCTCCGCC	GTCGGTTACC	AACCCACCCT	500
	CGCCGTGGAC	ATGGGTGGTA	TGCAGGAACG	TATCACCCT	ACCACCAAGG	550
25	GCTCCATCAC	CTCTGTGCAR	GCCGTCTACG	TCCCGG		586

2) INFORMATION FOR SEQ ID NO: 484

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1145 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Malassezia furfur*
 (B) STRAIN: ATCC 42132

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 484

45	GCGTGGCCAG	AAGGTCATTG	ACACTGGTGC	TCCCATCACC	ATCCCCGTCTG	50
	GTGGTGCCAC	ACTGGGTCGT	ATTCTGAACG	TCACGGGTGA	CCCTATTGAC	100
	GAGCGTGGCC	CCGTTAAGAC	TGACGTTTTT	CGCCCCATTC	ACCGTGACCC	150
	CCCTGCCTTT	GTCGAGCAGT	CGACTGATGC	CGAGATTCTC	GAGACTGGTA	200
	TCAAAGTCGT	TGACCTGATT	GCCCCTTACG	CCCGTGGTGG	TAAGATTGGT	250
50	CTGTTCGGTG	GTGCCGGTGT	CGGTAAGACC	GTGCTTATCC	AGGAGCTCAT	300
	CAACAACATC	GCCAAGGCCC	ACGGTGGTTT	CTCCGTGTTC	ACTGGTGTCTG	350
	GTGAGCGTAC	TCGTGAGGGT	AACGATTTGT	ACCACGAGAT	GATTGAAACC	400
	GGTGTCAATTA	ACCTCGAGGG	TGACTCGAAG	GTGGCTCTGG	TGTTCCGGTCA	450
	GATGAACGAG	CCCCCGGGTG	CCCGTGCGCG	TGTCGCTCTT	ACTGGTCTGA	500
55	CTGTGGCCGA	GTACTTCCGT	GACGACGAGG	GCCAGGATGT	GCTGCTGTTC	550
	ATTGACAACA	TTTTCCGTTT	CACCCAGGCC	GGTTCGGAGA	CTTCGGCTCT	600
	GCTGGGTCGT	ATCCCTTCGT	CGGTCGGTTA	CCAGCCCACT	TTGTCGACCG	650
	ATATGGGTGC	CATGCAGGAG	CGTATCACCA	CCACCAAGAA	GGGTTCGATT	700
	ACGTCGGTGC	AGGCCGTCTA	CGTGCCCGCC	GATGATGTCA	CTGACCCTGC	750
60	CCCTGCCACT	ACCTTCGCCC	ACCTTGACGC	TACCACTGTG	CTTGACCGTT	800

	CGATCGCTGA	GCTGGGTATC	TACCCCGCTG	TTGACCCGTT	GAACTCGAAC	850
	TCGCGTATGC	TTGACCCCGC	TATTGTGGGT	CAGGAGCACT	ACGACGTGGC	900
	CTCTGGCGTG	CAGAAAGCTGC	TCCAGGACTA	CAAGTCGCTT	CAAGATATCA	950
	TTGCCATTCT	GGGTATGGAT	GAGCTTTCTG	AGGAGGACAA	GCTCACTGTC	1000
5	GAGCGTGCCC	GTAAGATGCA	GCGTTTTCATG	TCGCAGCCTT	TCGCTGTCGC	1050
	CCAGGTCTTT	ACTGGTATCG	AAGGTCGTCT	TGTTGCCCTG	AAGGACACGA	1100
	TCAAGGCCTG	CAAGGAGATC	CTGTCCGGCA	AGCACGACAA	CCTCC	1145

10

2) INFORMATION FOR SEQ ID NO: 485

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 1261 bases
15	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

(A)	ORGANISM: <i>Malassezia pachydermatis</i>
(B)	STRAIN: ATCC 42756

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 485

	TCCCGCCATC	TTCAACGCCC	TGGAGGTCCA	GGACATGAAG	AACGGTGGCC	50
	GCCTTGTTCT	GGAGGTGACC	CAGCACCTTG	GTGAGAACAC	TGTTTCGTTGC	100
	ATTGCTATGG	ACGGTACCGA	GGGTCTTGTC	CGTGGTCAGA	AGGTCCTTGA	150
30	CACTGGTGCC	CCGATCACTA	TCCCTGTCTGG	TAACGGTACC	TTGGGCGGYA	200
	TCCTGAACGT	CACTGGTGAG	CCTGTGGATG	AGCGTGGTCC	GGTTAAGACT	250
	GACGTCTACT	GTCCAATCCA	CCGTGAGCCC	CCGGCGTTTCG	TTGAGCAGTC	300
	GACTGATGCT	GAGATTCTTG	AGACTGGTAT	CAAGGTGGTC	GACCTGCTCG	350
	CCCCATACGC	TCGTGGTGGT	AAGATTGGTC	TWTTCCGGTGG	TGCYGGTGTY	400
35	GGTAAGACCG	TGCTGATTCA	GGAGCTTATC	AACAACATTG	CCAAGGCCCA	450
	CGGTGGTTTC	TCGGTGTTCA	CTGGTGTCGG	TGAGCGTACT	CGTGAGGGTA	500
	ACGATCTGTA	CCATGAAATG	ATTGAGACTG	GTGTCATCAA	CGTTGACGGT	550
	GACTCGAAGG	TCGCTCTCGT	GTTCCGGTCAG	ATGAACGAGC	CCCCGGGTGC	600
	CCGTGCCCCGT	GTCCGCCCTGA	CYGGTCTGAC	CATCGCCGAG	TACTTCCGTG	650
40	ACGACGAGGG	TCAGGATGTG	CTGCTCTTCA	TTGACAACAT	TTTCCGTTTC	700
	ACTCAGGCTG	GTTCCGAGAC	TTCGGCTCTG	CTGGGTCTGTA	TCCCGTCGGC	750
	TGTCGGTTAC	CAGCCKACCC	TTGCCACGGA	TATGGGTGCC	ATGCAGGARC	800
	GTATYACCAC	CACCAAGAAG	GGTTCGATTA	CCTCGGTGCA	GGCYGTTTAC	850
	GTTCCGGCCG	ACGATGTGAC	TGACCCTGCC	CCGGCCACGA	CCTTCGCCCCA	900
45	CTTGACGCC	ACCACGGTGT	TGGACCGTTC	GATTGTCYGAG	CTGGGTATCT	950
	ACCCGGCCGT	CGACCCGCTG	AACTCGAAGT	CGCGTATGCT	TGACCCGTCA	1000
	ATTGTCGGTG	TGGAGCACTA	CAACGTTGCT	TCGGGTGTCC	AGAAGCTTCT	1050
	YCAGGACTAC	AAGTCGCTCC	AAGATATCAT	TGCCATTCTG	GGTATGGATG	1100
	AGTTGTCCGA	GGAGGACAAG	CTCACTGTCG	AGCGTGCCCG	TAAGATGCAG	1150
50	CGTTTCCTGT	CGCAGCCTTT	CGCTGTGGCC	CAGGTCTTCA	CTGGTATCGA	1200
	GGGTCGTCTT	GTGTCGCTCA	AGGACACCAT	CAACGCCTGC	AAGGAGATTCT	1250
	TGTCCGGTAA	G				1261

55

2) INFORMATION FOR SEQ ID NO: 486

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 1282 bases
60	(B)	TYPE: Nucleic acid

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Metschnikowia pulcherrima*
(B) STRAIN: DSM 70336

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 486

	AGGAGGGCAA	CTTGCCAGCT	ATCTTCAACG	CTTTGACGTT	GAAGAACGGC	50
	GACCAGAAGT	TGGTCTTGGA	GGTGGCCAG	CACTTGGGTG	AGAACACCGT	100
	CAGAACCAAT	GCCATGGACG	GTACCGAGGG	TTTGGTCAGA	GGCGCCTCTG	150
15	TCACCGACAC	YGGTGCCCT	ATCTCCGTGC	CTGTCGGCCG	TGAGACCTTG	200
	GGTCGTATTA	TCAATGTTGT	TGGTGAGCCA	ATCGACGAGA	GAGGCCCAAT	250
	CAACACCAAG	AAGAGAAACC	CTATTACAC	CGACCCACCT	TCGTTTGTCC	300
	AGCAATCCAC	TTCCGCCGAG	GTCTTGGAGA	CTGGTATCAA	GGTTGTGAC	350
	TTGTTGGCCC	CTTACGCCAG	AGGTGGTAAG	ATTGGTTTGT	TCGGTGGTGC	400
20	CGGTGTCGGT	AAGACCGTGT	TCATCCAGGA	GTTGATTAAAC	AACATTGCCA	450
	AGGCCACCGG	TGTTTTCTCC	GTTTTACCG	GTGTCGGTGA	GAGAACCAGA	500
	GAGGGTAACG	ATTTGTACCG	TGAAATGCAG	GAGACTGGTG	TCATCAACTT	550
	CGAGGGTGAC	TCCAAGGTCG	CCTTGTTTTT	CGGTCAGATG	AACGAGCCTC	600
	CAGGAGCTAG	AGCYAGAGTT	GCCTTGACCG	GTTTGACCAT	CGCCGAGTAC	650
25	TTCAGAGACG	AGGAGGGTCA	GGATGTGTTG	TTGTTTCGTCG	ACAACATTTT	700
	CAGATTCACC	CAAGCCGGTT	CTGAGGTGTC	TGCCTTGTTG	GGTCGTATTC	750
	CATCCGCTGT	CGGATACCAG	CCAACCTTGG	CCACCGATAT	GGGTGCCTTG	800
	CAGGAGAGAA	TTACCACCAC	CAAGAAGGGT	TCCGTCACCT	CCGTCCAGGC	850
	CGTCTACGTG	CCAGCCGATG	ACTTGACTGA	CCCTGCGCCA	GCCACCACTT	900
30	TCGCCCACCTT	GGACGCCACC	ACTGTGTTGT	CCAGAGGTAT	CTCTGAGTTG	950
	GGTATCTACC	CCGCTGTCTGA	CCCCTTGAC	TCCAACCTCA	GATTGTTGGA	1000
	CGCCACCGTT	GTTGGCCAGG	AGCACTACGA	CGTCGCCACC	AACGTCCAGC	1050
	AAACTTTACA	AGCTTACAAG	TCCTTGACAG	ATATCATTTG	CATTTTGGGT	1100
	ATGGATGAGT	TGTCCGAGAC	CCGACAAGTT	GACCCGTCGA	GAGAGCCAGA	1150
35	AAGATCCAGA	AGTTCTTGTC	CCAGCCATTT	GCCGTCGCCG	AGGTTTTTAC	1200
	CGGTATTGAG	GGTAGATTGG	TTAGATTGGA	GGACACCGTT	AGATCCTTTA	1250
	AGGAGGTTTT	GGAAGGTAAG	TACGACCACT	TG		1282

40

2) INFORMATION FOR SEQ ID NO: 487

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 482 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Penicillium marneffe*
(B) STRAIN: WSA-214

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 487

	TGTCTTTATC	CAGGAGTTGA	TTGTACGTCT	TTACCTTTCT	GCCTGACTGT	50
	TTACGACAAC	TAACGAAAGC	GTAGAACAAC	ATTGCCAAGG	CTCACGGTGG	100
	TTACTCTGTC	TTCACTGGTG	TCGGTGAACG	TACTCGTGAG	GGTAACGATT	150
60	TGTACCACGA	AATGCAGGAA	ACTGGTGTCA	TTCAGCTCGA	GGGTGAATCC	200

	AAGGTCGCCC	TCGTGTTCGG	TCAGATGAAC	GAGCCCCCGG	GTGCCCCGTGC	250
	CCGTGTCGCT	CTTACTGGTT	TGACCATTGC	CGAGTACTTC	CGTGACGAGG	300
	AAGGTCAGGA	CGTGCTTCTC	TTCATTGACA	ACATTTTCCG	TTTCACTCAG	350
	GCCGGTTCTG	AGGTGTCTGC	CCTTCTGGGT	CGTATCCCCT	CTGCCGTCGG	400
5	TTACCAGCCC	ACCCTTGCCG	TCGACATGGG	TATCATGCAG	GAGCGTATTA	450
	CCACCACCAC	CAAGGGTTCC	ATCACCTCCG	TC		482

10 2) INFORMATION FOR SEQ ID NO: 488

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 1290 bases
	(B)	TYPE: Nucleic acid
15	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Pichia anomala</i>
	(B)	STRAIN: ATCC 18205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 488

25	TCGAACAAGG	TAACCTACCA	GCTATCTTGA	ATGCTTTAGA	AATCAAAACC	50
	CCAAGTGGTA	CTCCATTAGT	TTTAGAAGTT	GCTCAACATT	TAGGTGAAAA	100
	CACTGTCAGA	ACTATTGCTA	TGGATGGTAC	TGAAGGTTTA	GTTCGTGGTG	150
	AACAAGTTAC	TGATACTGGT	TCTCCAATCA	CTGTCCCAGT	TGGTCGTGAA	200
30	ACTTTAGGTC	GTATTATCAA	CGTTGTTGGT	GAACCAATTG	ATGAACGTGG	250
	TCCAATTAAC	ACCAAACAAA	GAAACCCAAT	TCACGCTGAA	CCACCTTCAT	300
	TCAGTGAACA	ATCAACTGCT	GCTGAAGTTT	TAGAACTGG	TATCAAAGTT	350
	GTYGATTTAT	TAGCTCCATA	CGCTAGAGGT	GGTAAAATTG	GTTTATTCGG	400
	TGGTGCCGGT	GTCGGTAAAA	CTGTCTTTAT	CCAAGAATTG	ATTAACAACA	450
35	TTGCTAAAGC	TCATGGTGGT	TTCTCAGTTT	TCACCGGTGT	TGGTGAAAGA	500
	ACCAGAGAAG	GTAACGATTT	ATACCGTGAA	ATGAAAGAAA	CTGGTGTTAT	550
	TAACCTGGAA	GGTGATTCTA	AGGTCGCTTT	AGTTTTCGGT	CAAATGAATG	600
	AACCACCAGG	TGCTAGAGCT	CGTGTGCTT	TAACTGGTTT	GACCATTGCT	650
	GAATACTTCA	GAGATGAAGA	AGGTCAAGAT	GTCTTGTTAT	TCGTTGATAA	700
40	CATTTTCAGA	TTCACCCAAG	CCGGTTCAGA	AGTTTCTGCC	TTATTAGGTC	750
	GTATTCCATC	TGCTGTCGGT	TATCAACCAA	CTTTAGCAAC	TGATATGGGT	800
	TTGTTACAAG	AACGTATTAC	CACCACACAA	AAAGGTTTCA	TTACTTCTGT	850
	CCAAGCTGTT	TATGTCCCAG	CTGATGATTT	AACAGATCCT	GCTCCAGCTA	900
	CCACTTTCGC	CCATTGATG	GCTACTACTG	TCTTGTCTCG	TGGTATTTCA	950
45	GAATTAGGTA	TTTACCCAGC	TGTCGATCCA	TTAGATTCTA	AATCAAGATT	1000
	ATTAGATGCT	TCAGTTGTTG	GTCAAGAACA	TTATGATGTT	GCTACCAACG	1050
	TTCAACAAAC	TTTACAAGCT	TACAAATCTT	TACAAGATAT	TATTGCTATT	1100
	TTAGGTATGG	ATGAATTGTC	TGAACAAGAT	AAATTGACTG	TCGAAAGAGC	1150
	AAGAAAAATC	CAAAGATTCT	TATCTCAACC	ATTTGCTGTT	GCCGAAGTTT	1200
50	TCACTGGTAT	YCCAGGTAGA	TTGGTTAGAT	TAAAAGACAC	TATCAAATCA	1250
	TTCAAAGATG	TTTTGGAAGG	TAAATATGAT	CACTTACCAG		1290

55 2) INFORMATION FOR SEQ ID NO: 489

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 1291 bases
	(B)	TYPE: Nucleic acid
60	(C)	STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pichia anomala*

(B) STRAIN: ATCC 2149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 489

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10 CCAATTCGAA CAAGGTAAC TACCAGCTAT CTTGAATGCT TTAGAAATCA      50
   AAACCCCAAG TGGTACTCCA TTAGTTTTAG AAGTTGCTCA ACATTTAGGT      100
   GAAAACACTG TCAGAACTAT TGCTATGGAT GGTACTGAAG GTTTAGTCCG      150
   TGGTGAACAA GTTACTGATA CTGGTTCTCC AATCACTGTC CCAGTTGGTC      200
15  GTGAAACTTT AGGTCGTATT ATCAACGTTG TTGGTGAACC AATTGATGAA      250
   CGTGGTCCAA TTAACACCAA ACAAGAAAC CCAATTCACG CTGAACCACC      300
   TTCATTCACT GAACAATCAA CTGCTGCTGA AGTTTTAGAA ACTGGAATCA      350
   AAGTTGTTGA TTTATTAGCT CCATACGCTA GAGGTGGTAA AATTGGTTTA      400
   TTCGGTGGTG CCGGTGTCGG TAAAACTGTC TTTATCCAAG AATTGATTAA      450
20  CAACATTGCT AAAGCTCATG GTGGTTTCTC AGTTTTCACC GGTGTTGGTG      500
   AAAGAACCAG AGAAGGTAAC GATTTATACC GTGAAATGAA AGAAACTGGT      550
   GTTATTAAC TGAAGGTGA TTCTAAGGTC GCTTTAGTTT TCGGTCAAAT      600
   GAATGAACCA CCAGGTGCTA GAGCTCGTGT TGCTTAACT GGTTTGACCA      650
   TTGCTGAATA CTTCAGAGAT GAAGAAGGTC AAGATGTCTT GTTATTCGTT      700
25  GATAACATTT TCAGATTCAC CCAAGCCGGT TCAGAAGTTT CTGCCTTATT      750
   AGGTCGTATT CCATCTGCTG TCGGTTATCA ACCAACTTTA GCAACTGATA      800
   TGGGTTTGTT ACAAGAACGT ATTACCACCA CAAAAAAGG TTCAGTTACT      850
   TCTGTCCAAG CTGTTTATGT CCCAGCTGAT GATTTAACAG ATCCTGCTCC      900
   AGCTACCACT TTCGCCCATT TGGATGCTAC TACTGTCTTG TCTCGTGGTA      950
30  TTTCAGAATT AGGTATTTAC CCAGCTGTCG ATCCATTAGA TTCTAAATCA      1000
   AGATTATTAG ATGCTTCAGT TGTGTTGTC AAGCATTATG ATGTTGCTAC      1050
   CAACGTTCAA CAAACTTTAC AAGCTTACAA ATCTTTACAA GATATTATTG      1100
   CTATTTTAGG TATGGATGAA TTGTCTGAAC AAGATAAATT GACTGTGCGA      1150
   AGAGCAAGAA AAATCCAAAG ATTCTTATCT CAACCATTG CTGTTGCCGA      1200
35  AGTTTTCACT GGTATCCCAG GTAGATTGGT TAGATTAAA GACACTATCA      1250
   AATCATTCAA AGATGTTTTG GAAGGTAAAT ATGATCACTT A              1291

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40 2) INFORMATION FOR SEQ ID NO: 490

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 508 bases

(B) TYPE: Nucleic acid

45 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Rhodotorula minuta*

(B) STRAIN: ATCC 10658

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 490

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55 CGTATTGATT CGTGAGTGGC CGTTCCTTA CAGCAAGCTT ATAAAGGAGC      50
   GAAAAAGATC TGACATTCCG CTTATGTGCT ATACAGAGGA ACTCATCAAC      100
   AACGTCGCCA AGGTCATGG TGGTTACTCT GTCTTCACCG GTGTCGGAGA      150
   GCGAACACGT GAAGGTAACG ATCTCTACCA CGAAATGATT GAAACCGGTG      200
60 TCATTCACT CAAGAACGAC AAGTCCAAG CCGCTCTGGT CTTGCGACAG      250

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	ATGAACGAGC	CCCCCGGAGC	TCGTGCCCCGT	GTCGCTCTGA	CCGGTCTCAC	300
	CATCGCCGAG	TACTTCCGTG	ACGTCGAAGG	ACAGGATGTG	CTACTCTTCA	350
	TCGACAACAT	TTTCCGATTC	ACCCAGGCCG	GTTCAGAGGT	ATCTGCCCTG	400
	CTCGGACGTA	TCCCATCTGC	TGTCGGATAC	CAGCCCACAC	TCTCAACCGA	450
5	TATGGGTGGT	ATGCAAGAGC	GAATCACAAC	CACCAAGAAG	GGTTCGATTA	500
	CCTCCGTC					508

10 2) INFORMATION FOR SEQ ID NO: 491

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 686 bases
	(B)	TYPE: Nucleic acid
15	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Rhodotorula mucilaginosa</i>
	(B)	STRAIN: ATCC 66034

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 491

25	TGTCCTCATT	CAGGAGCTCA	TCAACAACAT	CGCCAAGGCC	CACGGTGGTT	50
	ACTCGGTCTT	CACCGGTGTC	GGCGAGCGTA	CCCGTGAGGG	TAACGGTGAG	100
	TCTCCCCCTT	CAAACCTTTG	GCCGGCTAGT	TGGCGCAGCG	CAAACCTGACG	150
	CGCGCGCCCT	GTCCAGACTT	GTACCACGAG	ATGATCGAGA	CTGGTGTCAT	200
30	CCAGCTCGAG	AACGACAAC	CGAAGTGCGC	TCTCGTGTTT	GGCCAGATGA	250
	ACGAGCCCCC	TGGTGCCCCG	GCCCGTGTCG	CTCTCACTGG	GTTTCGTCCTT	300
	TCTCTCTCTC	GAGCGTCCTG	GCTTGATACG	GAACGCTGAC	ACGTCACGCA	350
	GTCTCACTAT	TGCTGAGTAC	TTCCGTGACG	AGGAGGGCCA	GGACGTGCTC	400
	CTCTTCATCG	ACAACATCTT	CCGTTTCACC	CAGGGTGAGC	CGCCTCCGCG	450
35	GGCATTCTCC	CGTTTCTTTC	GCGCTGACGT	CTGTCCCGTA	TAGCCGGTTC	500
	GGAGGTGTCT	GCCCTTCTCG	GACGTATCCC	GTCCGCTGTC	GGATAACCAGC	550
	CGACTCTCTC	GACCGACATG	GGTCAGATGC	AGGAGCGTAT	CACGTAAGTT	600
	TGGCCGCAGC	TCCGTCCGCG	GCGCCCTTTG	TGTCTGACCG	TGTTCCACCG	650
40	CTCAGCACCA	CCAAGAAGGG	CTCGATCACC	TGTGTC		686

2) INFORMATION FOR SEQ ID NO: 492

45 (i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 625 bases
	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
50	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Sporobolomyces salmonicolor</i>
55	(B)	STRAIN: ATCC 32311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 492

	TGTCTTGATT	CAGGAGCTCA	TCAACAACGT	CGCCAAGGCC	CACGGTGGTT	50
60	ACTCCGTTTT	CACCGGTGTC	GGTGAGCGTA	CCCGTGAGGG	TAACGGTGAG	100

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CACACTTTTCG CCGACCTGGC CATTCCGGAA CGTGCGGACT GACGAGGACC 150
ACCTCGAACA GATCTCTACC ACGAGATGAT CGAGACCGGT GTCATTGAGC 200
TCGACAACGA CAAGTCGAAG ACTGCTCTCG TCTTCGGCCA GATGAACGAG 250
CCCCCTGGCG CCCGTGCCCG TGTCGCTCTT ACTGGTCTCA CCATCGCGGA 300
5 GTACTTCCGT GACGACGAGG GCCAGGACGT GCTTCTCTTC ATCGACAACA 350
TCTTCCGTTT CACCCAGGGT ACGTTCGATC CCGCCCGTCC AACACGAATG 400
TCGTGGTGAC TGACAACCTG TTGCGCGTGC AGCCGGTTTC GAGGTGTCTG 450
CCCTTCTCGG TCGTATCCCG TCCGCTGTGC GATACCAGCC CACTCTCTCG 500
ACCGACATGG GTGGCATGCA GGAGCGTATC ACGTACGCCC TCTTCTGCTT 550
10 TCTCTCGTTT CGCTCTGCAT CGCTCACGCA TGTTTCGCCC ACAGCACCAC 600
CAAGAAGGGT TCGATCACCT GTGTC 625

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15 2) INFORMATION FOR SEQ ID NO: 493

(i) SEQUENCE CHARACTERISTICS:

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20 (A) LENGTH: 1211 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

25

(vi) ORIGINAL SOURCE:

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    (A) ORGANISM: Sporothrix schenckii
    (B) STRAIN: WSA-148

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30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 493

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TCTCGTCCGT GGTGCTAAGG CCACTGACAC TGGTTCCCCC ATTACCATCC 50
CCGTGCGGCC CGGTACCCTC GGTGCGATCA TGAACGTCAC CGGTGACCCG 100
ATCGACGAGC GCGGTCCCAT CAAGACCGAC AAGTTCCGTC CCATCCACGC 150
35 TGAGGCTCCC GAGTTCGTTG ACCAGTCGAC CACCGCTGAG GTTCTCGTGA 200
CTGGTATCAA GGTGCTCGAT CTGCTTGCTC CCTACGCCCC TGGTGGTAAG 250
ATTGGTCTGT TTGGCGGTGC CGGTGTTGGC AAGACCGTGT TCATCCAGGA 300
GCTCATCAAC AACATCGCCA AGGCCACCG TGGTTACTCC GTCTTCACCG 350
GTGTGCGCGA GCGTACCCGT GAGGGTAACG ATCTGTACCA CGAAATGCAG 400
40 GAGACCTCTG TCATTAGCT TGACGGTGAC TCCAAGGTCG CCCTGGTGTT 450
CGGTGAGATG AACGAGCCCC CTGGTGCTCG TGCCCGTGTC GCCTTGACCG 500
GTTTGACTGT CGCTGAGTAC TTCCGTGACG AGGAGGGCCA GGATGGTATG 550
TTTTGAATTA TTTCTTGTC GTACAGTTCC AAATCGAAGA ATTACTAACT 600
TGTCAGTGCT TCTCTTCATC GACAACATTT TCCGCTTCAC CCAGGCCGGT 650
45 TCTGAGGTGT CTGCCCTTCT GGGTCGTATT CCCTCCGCTG TCGGTTACCA 700
GCCACGCTC GCCGTGGACA TGGGTCTGAT GCAGGAGCGT ATTACCACCA 750
CCCGCAAGGG CTCAATTACC TCCGTCCAGG CCGTCTACGT GCCCGCTGAC 800
GATCTGACGG ATCCCGCCCC CGCCACCACC TTCGCCCATC TGGACGCCAC 850
CACTGTGCTG TCCCGAGGTA TCTCTGAGCT GGGTATCTAC CCCGCTGTCT 900
50 ACCCCCTCGA CTCCAAGTCG CGTATGCTGG ACCCCCGTAT TGTCGGTGAC 950
GACCACTACG AGACCGCCAC TCGCGTCCAG CAGATCCTCC AAGAGTACAA 1000
GTCGCTGCAG GACATCATCG CCATTCTGGG TATGGACGAG CTGTCTGAGG 1050
CCGACAAGCT TACAGTCGAG CGTCTCGTA AGATCCAGCG TTTCTGAGC 1100
CAGCCGTTCA CCGTCGCGCA GGTCTTCACT GGTATCGAAG GCCAGCTGGT 1150
55 CGATCTGAAG GACACTATCG CTTCTGTTCAA GGCTATCCTG AGCGGTGAGG 1200
GTGACAGCCT T 1211

```

60 2) INFORMATION FOR SEQ ID NO: 494

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1133 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Stephanoascus ciferrii*
 (B) STRAIN: ATCC 52550

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 494

```

15 TCTTGTTAGA GGCACCCAG TCAAGGACAC TGGTGCTCCA ATTACCATTC      50
   CAGTTGGTAA CGGCACTTTG GGCCGTATCG TCAACGTTCT CGGTGAGCCA      100
   ATTGATGAGC GTGGACCAGT CAAGGCTGAC AAGTTCAGAC CTATTCACGC      150
   TGAGCCACCA ACCTTCGCTG ACCAGTCCAC CTCTGCCGAG GTTCTTGAGA      200
20 CCGGTATTAA GGTGTGCGAC TTGCTTGCCC CTTATGCCAG AGGTGGTAAG      250
   ATTGGTCTTT TCGGTGGTGC CGGTGTCGGT AAGACTGTGT TCATTCAGGA      300
   GCTTATTAAAC AACATTGCTA AGGCCACGG TGGTTACTCT GTCTTCACTG      350
   GTGTCGGTGA GCGAACTCGT GAAGGTAACG ATTTGTACCA CGAAATGATG      400
   GAGACCGGTG TCATCAACCT TGAGGGTGAC TCCAAGGTGT CTCTTGTGTT      450
25 CCGTCAGATG AACGAGCCTC CAGGAGCCCG TGCCCGTGTT GCCTTGACCG      500
   GTTTGACCAT TGCCGAGTAC TTCAGAGATG AGGAGGGCCA GGATGTCTTG      550
   TTGTTTCATTG ACAACATTTT CCGATTACCC CAGGCCGGTT CTGAGGTCTC      600
   TGCCTTGTTG GGTGCTATCC CATCTGCCGT CGGTTACCAA CCAACCTTGG      650
   CTACTGATAT GGGTGGTCTT CAAGAACGTA TTACCACCAC TCAAAAGGGT      700
30 TCCGTCACCT CTGTCCAGGC TGTCTACGTC CCAGCTGACG ATTTGACTGA      750
   TCCTGCCCCA GCTACCACCT TCGCCCATTT GGACGCCACC ACCGAATTGT      800
   CCCGATCTAT CTCTGAGTTG GGTATCTACC CAGCTGTCTG CCCTCTTGGT      850
   TCCAAGTCCC GTCTTTTGA TGCCTCCGTC GTCGGCCAAG AGCACTACGA      900
   CGTTGCCGCC AACGTCCAAC AGACCTTGCA GGCCTACAAG TCTCTCCAGG      950
35 ATATCATTGC CATTTTGGGT ATGGACGAAT TGTCTGAGGC TGATAAGCTC     1000
   ACTGTCGAGC GTGCTCGTAA GATGCAGAGA TTCCTTTCTC AGCCATTAC      1050
   CGTCGCTGAG GTCTTCACTG GTCTCGAGGG TAGACTCGTT TCTTTGAAGG     1100
   ACACCATCCG ATCCTTCAAG GAGATCCTTG ACG                          1133

```

2) INFORMATION FOR SEQ ID NO: 495

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 608 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichophyton mentagrophytes*
 (B) STRAIN: WSA-225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 495

```

GGAGTTGATT GTAAGTCATT TGAAACCCAG CCCCAAGAAA CAGAAGCTAG      50
GCGAAAATTG GACAATTGAG CAATTTAGCC ATTGGAGAAA AGAAATTTCTG     100
60 AGTATTAATT GTTTTTATAG AACAAATTG CCAAGGCTCA CGGTGGTTAC      150

```

```

TCTGTCTTCA CTGGTGTCCG AGAGCGTACC CGTGAAGGAA ACGATCTCTA 200
CCATGAAATG CAGGAGACCC GTGTCATTCA GCTTGATGGC GAGTCCAAGG 250
TCGCCCTGGT CTTCCGCCAG ATGAACGAGC CCCCAGGTGC CCGTGCCCGT 300
GTTGCTCTTA CTGGTTTGAC CATTGCTGAG TACTTCCGTG ATGAGGAAGG 350
5 TCAAGACGGT GAGTTTCTTA TGGATAAAAA AAAATTTTTT TTTTTTTTTT 400
TTTTTTTCAA GAAATTCATG TTCTAACAAA GTGTATTCTA GTGCTTCTCT 450
TCATCGACAA CATTTTCCGT TTTACTCAGG CTGGTTCCGA AGTGTCTGCC 500
CTGCTTGGTC GTATCCCATC TGCCGTCGGT TACCAACCCA CTCTTGCCGT 550
CGACATGGGT GGTATGCAGG AACGTATTAC CACCACCAAG AAGGGATCCA 600
10 TTACCTCC 608

```

2) INFORMATION FOR SEQ ID NO: 496

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 794 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Wangiella dermatitidis*
 (B) STRAIN: WSA-229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 496

```

30 GTTTATTCAA GAACTCATTG TGGGTGGCAT TCTCATAATG TTTCGGCCAC 50
AATTACTGAT TGAAAATAGA ACAACATTGC AAAGGCTCAT GGTGGTTACT 100
CCGTGTTTCA TGGTGTCCGC GAGCGAAGTC GTGAGGGTAA CGACTTGTAC 150
CACGAAATGC AGGAGACCTC TGTCAATCAG CTCGATGGCG AGTCCAAGGT 200
CGCGCTGGTG TTTGGTCAAA TGAACGAACC TCCTGGTGCT CGTGCTCGTG 250
35 TTGCTCTGAC TGGGTAAGTT GTTCCTTCGC TTCTTGCGCG TATCCACATC 300
CCCATCTTGA GAATACGTCT GCCACCATGT CATGTGATGT TGGGCTGGTT 350
CTGGTTTTTTG GGAGGCCCTC AAGTTCAATT TTTGGATGAC AGCACCAGCT 400
TTACAAGATT ATGCTAACTT AATGGAGTCT TACGGTGGCT GAGTTCTTCA 450
GGGATGAGGA GGGACAGGAT GGTAAGTTTG ATAACAATCT CGTCGGTGTC 500
40 AATATCGACG GCGTACTCTT CGCATCAAAA AACCAGAGAG GTGGTTTGGT 550
GTGAGAAGTG CGCCGGAAT AATGGCAACC ACGTGACAAT GACCACGTGT 600
GGGGCTCCCG TGCTAACACG TGACAGTCTT GCTCTTCATC GACAACATTT 650
TCCGATTAC TCAASCCGGT TCTGARGTGT CTGCCTTGCT TGGTCGTATT 700
CCATCTGCCG TCGGTTACCA ACCCACACTC GCCGTCGACA TGGGTCTCAT 750
45 GCAGGAACGT ATCACCACCA CCCGGAAGGG ATCCATCACA TCTG 794

```

2) INFORMATION FOR SEQ ID NO: 497

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1148 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yarrowia lipolytica*

(B) STRAIN: ATCC 38295

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 497

5	TCTTGTCCGA	GGCACCGCCG	TCGCTGACAC	CGGTGCTCCC	ATCACTATCC	50
	CCGTCGGCCG	AGGTACCCTT	GGTCGAATCA	TCAACGTCTG	TGGTGAGCCC	100
	ATTGACGAGC	GAGGACCCAT	CGAGGCTTCC	AAGTACCTCC	CCATCCACGC	150
	TGACCCCCCT	ACCTTCGCTG	AGCAGTCTAC	CTCCGCTGAG	GTTCTCGAGA	200
	CCGGTATTAA	GGTCGTCGAC	CTCCTCGCCC	CTTACGCCCG	AGGTGGTAAG	250
10	ATTGGTCTCT	TCGGTGGTGC	CGGTGTCGGT	AAGACTGTCT	TCATCCAGGA	300
	GCTGATTAAC	AACATTGCCA	AGGCCCATGG	TGGTTTCTCC	GTTTTCTGCG	350
	GTGTCGGTGA	GCGAACCCGA	GAGGGTAACG	ATCTTTACCG	AGAGATGAAG	400
	GAGACTGGTG	TCATCAACCT	CGAGGGTGAG	TCTAAGGTCA	CCCTCGTCTT	450
	CGGTCAGATG	AACGAGCCTC	CCGGAGCCCG	TGCCCGAGTC	GCCCTTACTG	500
15	GTCTGACCAT	TGCCGAGTAC	TTCCGAGACG	AGGAGGGTCA	GGATGTGTTG	550
	CTCTTCGTTG	ACAACATTTT	CCGATTACAC	CAGGCCGGTT	CCGAGGTGTC	600
	CGCTCTGCTT	GGTCGAATTG	CCTCCGCTGT	CGGTTACCAG	CCCACTCTGG	650
	CCACCGATAT	GGGTGCCCTC	CAGGAGCGAA	TTACCACCAC	CCAGAAGGGT	700
	TCCGTCACCT	CCGTCCAGGC	CGTCTACGTG	CCTGCCGATG	ATTTGACCGA	750
20	TCCTGCTCCC	GCCACCACCT	TCGCCCATCT	TGACGCCACC	ACCGTCCTGT	800
	CCCGAGGTAT	TTCCGAGCTG	GGTATCTACC	CCGCTGTCGA	TCCCCTTGAT	850
	TCCAAGTCTC	GACTTCTGGA	TATCGATGTT	GTCCGAAAGG	AGCACTACGA	900
	TGTTGCTTCC	AACGTCCAGC	AGACCCTCCA	GGCTTACAAG	TCTCTCCAGG	950
	ATATCATTGC	CATTCTTGGT	ATGGATGAGC	TGTCCGAGCA	GGACAAGCTG	1000
25	ACCGTCGAGC	GAGCTCGAAA	GATCCAGCGA	TTCCTGTCTC	AGCCCTTCAC	1050
	CGTCGCCGAG	GTTTTACCCG	GTATTGAGGG	ACGACTTGTC	TCTCTCAAGG	1100
	ACACTGTCCG	ATCCTTCAAG	GAGATCCTTG	ACGGTAAGCA	CGATGCTC	1148

30

2) INFORMATION FOR SEQ ID NO: 498

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 966 bases
35	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40

(vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Aspergillus fumigatus</i>
	(B)	STRAIN: WSA-172

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 498

	GCGCTATTGT	CGTTGTTGCT	GCCTCCGACG	GTCAGATGTA	GGTGGAACAT	50
	CTTGGGAAAT	ACGTCGTAAA	ACACGTCGCT	TACGTTTTTCG	CGAATAGGCC	100
	CCAGACTCGT	GAGCATTTGC	TGCTCGCCCCG	CCAGGTTGGT	GTCCAGAAGA	150
50	TCGTTGTCTT	CGTCAACAAA	ATCGATGCTA	TTGATGATCC	GGAGATGCTG	200
	GAACTGGTCG	AACTCGAGAT	GCGTGAGCTG	CTGAACAGCT	ACGGTTTCGA	250
	GGGTGAAGAG	ACTCCGATCA	TTTTTCGGTTC	CGCTCTCTGT	GCTCTCGAAG	300
	GACGCCGTGA	CGACATCGGT	AAAGACAGAA	TTGAGCAGCT	TATGAACGCT	350
	GTCGACACCT	GGATCCCCAC	TCCTCAGCGT	GACCTCGACA	AACCTTTCTT	400
55	GATGTCTGTC	GAGGAAGTGT	TCTCTATCGC	CGGCCGTGGT	ACCGTGGCTT	450
	CTGGTCGTGT	CGAGCGTGGT	ATCTTGAAGA	AGGACTCTGA	GGTTGAGATT	500
	GTTGGAGGCT	CCTTCGAACC	CAAGAAGACC	AAAGTCACCG	ACATTGAAAC	550
	CTTCAAGAAG	AGCTGTGATG	AATCGCGTGC	TGGTGACAAC	TCTGGTCTCC	600
	TCCTGCGTGG	TATCCGACGT	GAAGACGTCA	AGCGTGGTAT	GGTCATTGCT	650
60	GTTCCCGGCA	GCACCAAGGC	TCACGACAAG	TTCCTCGTCT	CCATGTACGT	700

	CCTGACCGAG	GCGGAGGGTG	GTCGTCGTAC	TGGCTTCGGT	GCCAACTACC	750
	GTCCCCAAGT	CTTCATCCGT	ACTGCAGGTA	AGTCCCCGCA	CACCGTGTCC	800
	AGATCTTCCG	AGAGATTAGC	GATATATGCT	AATGATTCAT	CAGACGAGGC	850
	TGCTGACCTC	AGCTTCCCTG	ACGGCGACCA	ATCTCGCAGA	GTTATGCCTG	900
5	GTGACAACGT	CGAGATGATC	CTGAAGACCC	ACCACCCTGT	TGCTGCTGAG	950
	GCTGGTCAAC	GCTTCA				966

10 2) INFORMATION FOR SEQ ID NO: 499

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Blastoschizomyces capitatus*
 (B) STRAIN: ATCC 10663

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 499

25	TGGTGCTATT	ATTGTTGTTG	CTGCTTCTGA	TGGTCAAATG	CCCCAAACCC	50
	GTGAGCACTT	GCTTCTTGCT	CGTCAAGTTG	GTGTTAAGCA	CATTGTTGTT	100
	TTCGTTAACA	AGATTGATAC	TATTGATGAT	CCTGAAATGT	TGGAACCTGT	150
	CGAAATGGAA	ATGAGAGAAC	TTCTTTCTTC	TTACGGTTTT	GATGGCGATA	200
30	ACACCCCTGT	CATTATGGGT	TCTGCTCTCT	GTGCTCTTGA	AGGTCGTGAA	250
	CCAGAAATTG	GTGAACAAAG	AATCAACCAA	CTCCTTGATG	CTATCGATGA	300
	ATACATTCTT	ACCCAGTTTC	GTGATATGGA	CCAACCTTTC	TTGATGCCAC	350
	TTGAAGGTGT	TTTCTCTATT	CCAGGTCGTG	GTACTGTTGC	CACTGGACGT	400
	GTCTATCGTG	GTACTTTGAA	GAGAGGTGAA	GAAGTTGAAG	TTGTTGGCTA	450
35	CAATGATGCT	CCAATCAAGA	CCACCGTTAC	TGGTATTGAA	ATGTTCAAGA	500
	AGGAACTTGA	TCAAGCTCAA	GCTGGTGACA	ACGCTGGTAT	TCTTTTGAGA	550
	GGTGTTAAGC	GTGAAGACCT	TAAGCGTGGT	ATGGTTGTTG	CTAAACCAGG	600
	TACCGTTAAG	CCACACACCA	AGTTCCTTGC	CTCCATCTAT	GTTTTGACTA	650
	AGGAAGAAGG	TGGCAGACAC	TCTGGCTTTG	GTCTTAACTA	CAGACCTCAA	700
40	CTTTTCCTTG	GTTCTGCTGA	TGTTACCCT	GTCTTGACCT	TCCCAGAGGG	750
	TGTTGACCAA	AGCACTCAAG	TCATGCCAGG	TGACAACACT	GAAATGGTTT	800
	GCGAACTTGT	TCACCCAGTT	GCTGTCTGAAC	AAGGCCAACG	TTTCAA	846

45 2) INFORMATION FOR SEQ ID NO: 500

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida rugosa*
 (B) STRAIN: ATCC 96275

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 500

```

GGTGCCATTA TTGTTGTTGC TGCCTCTGAT GGACAGATGC CCCAGACCCG      50
TGAGCATCTT TTGCTTGCCC GCCAAGTCGG TATGCAAAAG GTCGTTGTGT      100
TTGTTAACAA GATTGATACC ATTGATGACC CTGAAATGCT TGATCTTGTC      150
5  GAGATGGAGA TGCCTGAACT GTTGAATGAA TATGACTTCG ATGGAGATAA      200
CTCTCCTGTC ATTATGGGCT CTGCTCTTGC TGCTCTTGAG GACAAGAACC      250
CCGAGATTGG TAAGGACCGT ATCATGCAGC TCTTGGACGC TGTTGATGAA      300
TGGATCCCTA CCCCCGAGCG TGACCTTGAC AAGCCTTTCA TGATGCCTAT      350
TGAGGCCTCT TTCTCCATTT CTGGTCGTGG TACTGTTGCC ACTGGCCGTG      400
10 TCGAGCGTGG TATTCTCAAG AAGGGTGAGG AAGTCGAGAT CGTTGGTTTC      450
AACAAAGCAGC CCCTGAAATC TGTGTGTTACT GGTATTGAAA TGTTCAAGAA      500
GGAACCTTGAT CAGGCCCCAGG GCGGTGATAA TGCTGGTATC TTGCTTCGTG      550
GTATTCGTCG TGAGGACTTG CAGCGTGGTA TGGTTTTGGC CAAGCCTGGA      600
ACTGTTAAGG CTCACACCAA GTTCCTTTCC TCCATCTACG TTCTCTCCAA      650
15 GGAAGAGGGC GGCCGCTACT CTCCTTTCCG TATGAACTAT CGTCCCCAGA      700
TGTTTCGTTT TGCACCTGAT CTCACCGTTA CTCTTACTTT CCCTGAGGGT      750
GTTGAACAGC ACACTCAGGT CTTCCCTGGT GAGAACACCG AGATGGTTGG      800
CGAGCTCGTT CACCCTACTG CTATTGAGGT TGGTCAACGC TTCAAC      846

```

20

2) INFORMATION FOR SEQ ID NO: 501

```

25 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 944 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Coccidioides immitis
        (B) STRAIN: Silveira

```

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 501

```

AGTTGTCGTC GTTGCTGCTT CAGACGGTCA AATGTATGCA ACCGAGAGCA      50
CTCCCGGATC TTGGTTTAAA TGGCACTAAT ATAAGACAGG CCTCAAACCTC      100
40 GAGAGCATTT ACTTCTCGCC CGTCAGATCG GTATCCAAAA AATCGTCGTC      150
TTCGTGAACA AGGTTGATGC CATCGAGGAC AAAGAGATGT TGGAGCTTGT      200
TGAATTGGAG ATGCGTGAAC TCCTAACCAG CTACGGTTTC GAGGGTGAAG      250
AAACTCCCAT CATTTTGGC TCTGCTCTCT GTGCCCTCGA AGGAAGACAA      300
CCCGAGATCG GTGTTACCAA GATTGATGAG CTCTTGCAGG CCGTCGACAC      350
45 CTGGATTCCC ACTCCTCAGC GTGAGACTGA CAAGCCCTTC TTGATGTCCA      400
TTGAGGAAGT GTTCTCTATT TCCGACGAG GAACCGTTGT CTCCGGCCGT      450
GTGGAGCGTG GTATCCTCAA GAAGGACTCC GAAGTTGAAA TTGTCGGCGG      500
TTCGCCCAG CCAATCAAAA CCAAGGTTAC CGATATCGAA ACCTTTAAGA      550
AGTCTTGCGA CGAGTCTCGC GCTGGTGATA ACTCCGGCTT GCTCCTACGA      600
50 GGCCTTAAGC GTGAAGATAT TAGCCGTGGC ATGGTCGTCG CTGTACCAGG      650
AAGTGTC AAG GCCCATACTG AATTCTTAGT TTCGCTTTAC GTCCTCACC      700
AAGCTGAGGG TGGGCGCAAA TCTGGATTCA GCAGCAAGTA CCGCCCACAG      750
ATGTTCAATC GCACTGCCGG TATGTAATAC TGTGATAATT TCGTTGACAT      800
GGTACTGATT GAATTCTATA GACGAAGCGG CTCAGCTCAG CTGGCCCAGG      850
55 GAAGATCAAG ACAAGATGGC TATGCCAGGA GACAATATCG AAATGATTTG      900
CACCACCTTG CACCCAGTTG CCGCCGAGGC TGGCCAGCGA TTCA      944

```

60 2) INFORMATION FOR SEQ ID NO: 502

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 849 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fusarium oxysporum*
 (B) STRAIN: WSA-212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 502

```

15  GCTATCATCG TCGTTGCTGC CTCCGATGGA CAGATGCCCC AGACCCGTGA      50
    ACACTTGCTC CTCGCTCGTC AGGTCGGTGT CCAGCGAATT GTCGTCTTCG      100
    TCAACAAGGT CGATGCCATT GATGACCCCG AGATGCTTGA GCTCGTCGAG      150
    ATGGAGATGC GCGAGCTTCT TAACACCTAC GGCTTCGAAG GCGACGACAC      200
20  TCCCGTCATG ATGGGCTCTG CTCCTATGTC TCTCCAGAAC CAGCGCCCCG      250
    AGATTGGCAC CGAGAAGATC GATGAGCTCC TTGCTGCCGT CGACGAGTGG      300
    ATCCCAACCC CCGAGCGTGA CCTTGACAAG CCCTTCCTTA TGTCCGTCGA      350
    GGATGTCTTC TCCATTGCCG GCCGTGGTAC CGTCGTGTCT GGCCGTGTGG      400
    AGCGTGGTAT TCTGAAGCGT GATCAGGAGA TCGAGCTTGT CGGAAAGGGG      450
25  CAGGAGGTTA TCAAGACCAA GGTACCGAC ATTGAGACCT TCAAGAAGTC      500
    TTGTGAGCAG TCCCAGGCTG GTGACAACCT TGGTCTCCTC ATCCGAGGTG      550
    TTCGCCGTGA GGATGTCCGC CGTGGTATGG TTGTCTGCGC TCCTGGCACC      600
    GTCAAGTCTC ATACCCAGTT TCTCGCTTCC CTCTACGTCC TCACCAAGGA      650
    GGAGGGTGGC CGACACACCG GTTTCCAGGA GCACTACCGA CCCCAGCTCT      700
30  ATCTCCGAAC TGCAGATGAG TCCATTGACC TGACTTTCCC CGAGGGTACT      750
    GAGGATGCCT CCAGTAAGAT GGTCAATGCCT GGTGACAACA CCGAGATGGT      800
    TGTCACCATG GGTCAACCCA ATGCCATCGA GGTGAGTCAG CGATTCAAC      849

```

2) INFORMATION FOR SEQ ID NO: 503

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1064 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Histoplasma capsulatum*
 (B) STRAIN: G186A5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 503

```

55  TGGTGCTATT GTCGTTGTTG CTGCTGCTGA CGGCCAAATG TAAGACGCCG      50
    CGAGGGACTG CTGAGGGTTT TATGCTTTTT AGGCCCCCTT GTTTCTGAGA      100
    GCATGATGAT ACTAATATTC GGAAACGTAT CTATTAGGCC TCAAACACGT      150
    GAGCATTTGC TCCTTGCCCG ACAGGTCGGT GTCCAAAAGA TCGTCGTTTT      200
    CGTGAACAAA GTCGACGCCC TTGAGGACAA GGAGATGTTG GAGCTTGTCTG      250
    AGTTAGAAAT GAGAGAGCTC TTAAACACCT ACGGCTTCGA GGGTGAAGAG      300
    ACACCCATCA TCTTTGGTTC TGCCCTTTGC GCCATGGAAG GCCGTGAGCC      350
    TGAGTTGGGA GAAAAGAAAA TTGATGAATT GCTGGAGGCT GTTGATACTT      400
60  GGATCCCCAC ACCACAACGT GATACCGAAA AACCTTTCTT GATGTCCGTT      450

```



```

GAGGAAGTAT TCTCTATCTC CGGCCGTGGA ACCGTTGCCT CCGGTCGTGT 500
TGAGCGCGGT GTCCTCAAGA AGGATTCAGA AGTCGAGCTA ATTGGGGGCG 550
GCTCCACCCC CATCAGGACG AAGGTAAGT ATATCGAAAC TTTCAAGAAA 600
TCCTGTGACG AGTCTAGAGC TGGGGACAAC TCCGGTCTTT TATTGCGTGG 650
5 TATCAAGCGT GAAGATATCC GCCGTGGTAT GGTAGTTGCC GTTCCTGGCA 700
GCGTCAAGGC CCACGACAAG TTCTTGGTGT CGATGTATGT CCTGACCGAA 750
GCTGAGGGTG GTCGCCGAAC CGGATTCGGC CAGAACTATC GTCCTCAAAAT 800
GTTTCATCCGC ACAGCTGGTA TGTCAAAATG GGACCCCTTT TCATAATCCT 850
TTCTTTTTTTT CCTTTTCCTC TCTATCTCTC TTTCTGTTTC CTTTCAACTC 900
10 GCCTGATTCA CGAAATTAAC TAACCCGTTT GATTATAGAC GAAGCCGCCC 950
ATCTCAGCTT CCCTAGTGGA GCAGATGAAA GCAAACCTCGT TATGCCTGGT 1000
GACAACGTCG AGATGATCCT CCAGACACAC CGCCCCGTGG CTGCTGAGGC 1050
CGGCCAGCGA TTCA 1064

```

15

2) INFORMATION FOR SEQ ID NO: 504

```

20 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 982 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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    (A) ORGANISM: Paracoccidioides brasiliensis
    (B) STRAIN: ATCC 32071

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30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 504

```

TGGTGCTATC GTCGTTGTTG CTGCCTCTGA CGGCCAAATG TAGGGATTTT 50
GCAAGACTGG TGAAAAAATC TAAAGAAAAT AGAAAAGATT GTGCTGATGT 100
35 TTGGTATCAG GCCCCAAACA CGCGAGCATC TGCTTCTTGC CAGACAAGTC 150
GGTGTTTCA GAATCGTTGT TTTCGTCAAC AAGGTCGATG CTGTAGAGGA 200
TAAGGAGATG TTGGAGCTTG TCGAATTGGA GATGAGAGAG CTCTTGACCA 250
CCTATGGGTT CGAGGGTGAG AAGACACCTA TCATCTTTGG TTCTGCGCTC 300
TGTGCTATGG AGGGCCGTCA GCGCGAGTTG GGAGAGCAGA AAATTGATGA 350
40 ATTACTCGAG GCTGTGGATA CTTGGATCCC TACGCCACAG CGTGATACTG 400
ACAAGCCCTT CCTGATGTCC ATTGAGGAGG TGTTCTCTAT CTCTGGACGA 450
GGAACCGTTG CCTCCGGCCG CGTTGAGCGT GGTATCCTCA AGAAGGACTC 500
CGAAGTTGAA ATTATTGGCG GCGGTGTTCC CACAATCCTG ACCAAGGTGA 550
CTGATATCGA AACCTTCAAG AAGTCTTGCG ACGAGTCCAG AGCCGGGGAC 600
45 AACTCCGGCC TCTTGTTGCG CGGTGTCAAG CGTGAGGATA TCCGCCGTGG 650
TATGGTCGTT GCAGTTCCCG GAAGCGTCAA AGCACATGAC AGATTCTTGG 700
TGTCGATGTA CGTTCTGACC GAGGCTGAGG GTGGTCGCCG CACTGGCTTC 750
GGTCAGAACT ATCGTCCTCA AATGTTTCAT CGCACAGCTG GTACGTTTCAT 800
TCTTTTACTA TATTCCTATA TGCATAGCCC GATCCTCCCA TTAATAATT 850
50 GACACAGACG AGGCTGCTGA ACTCAGCTGG CCTGATGGAG ACGACGAAGC 900
CAAAATGGTC ATGCCCGGTG ACAATGTTGA AATGGTCCTG AAGTCACACC 950
GCCCCGGGGC GCTGAGGCTG GACAGCGATT CA 982

```

55

2) INFORMATION FOR SEQ ID NO: 505

```

60 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 931 bases
    (B) TYPE: Nucleic acid

```

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Penicillium marneffei*

(B) STRAIN: ATCC 58950

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 505

	CGCTGTTGTT	GTCGTCGCTG	CTTCTGATGG	TCAAATGTAA	CATATCCACG	50
	AGCTGCCAAT	TATGGACACT	GCTGATAAGA	ATAGGCCCCA	AACCCGTGAG	100
	CACTTGCTCC	TCGCCCCGTC	GGTCGGTGTT	CAAAAGATCG	TCGTCTTCGT	150
15	CAACAAGGTT	GATGCCGTCG	AGGACCCCGA	GATGTTGGAA	CTTGTCGAAT	200
	TGGAAATGCG	TGAACCTTTG	ACCACCTACG	GTTTCGAGGG	TGAAGAGACC	250
	CCTATCATTT	TCGGATCCGC	TCTTTGCGCC	TTGGAAGGCC	GCAAGCCCGA	300
	GATTGGCGAA	CAGAAGATTG	ACGAGCTCAT	GAACGCCGTT	GATACCTGGA	350
	TCCCCACCCC	CCAGCGTGAC	CTTGACAAGC	CCTTCTTGAT	GTCCGTTGAG	400
20	GAAGTTTTCT	CCATCTCTGG	TCGTGGTACC	GTTGCATCTG	GTCGTGTTGA	450
	GCGTGGTATT	TTGCGCAAGG	ATTCTGAGGT	TGAGATTATC	GGATACCAGA	500
	AGAACCCTAT	CAAGACCAAG	GTTACCGACA	TTGAGACCTT	CAAGAAGTCT	550
	TGCGATGAAT	CTCGTGCTGG	TGACAACTCT	GGCTTGCTTC	TCCGTGGTAT	600
	CAAGCGTGAG	GACATTGCTC	GTGGTATGGT	TATCGCTGCT	CCTGGAACCA	650
25	CCAAGGCTCA	TGACAACTTC	TTGGTCTCCA	TGTATGTCTT	GACTGAGGCT	700
	GAAGGTGGTC	GTCGTAAGTG	ATTGCGCGCC	AACTACCGTC	CTCAAGCTTT	750
	CATCCGTAAT	GCCGGTATGT	TCCCTTTCAA	AGTCAATTAA	TGAGCGATTT	800
	GCTAACGAGT	TATAGATGAG	GCTGCTACTC	TCAGCTTCCC	CGGTGACGAT	850
	CAGTCCAAGC	AGGTCATGCC	CGGTGACAAC	GTTGAGATGA	TCTTGAAGAC	900
30	ACACCGTCCC	GTTGCCGCCG	AAGCTGGTCA	G		931

2) INFORMATION FOR SEQ ID NO: 506

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 846 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

40 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

45 (A) ORGANISM: *Pichia anomala*

(B) STRAIN: ATCC 18205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 506

50	TGGTGCTATT	ATTGTTGTTG	CTGCTTCTGA	TGGTCAAATG	CCTCAAACCA	50
	GAGAACATTT	RTTATTGGCT	AGACAAGTTG	GTGTTCAACA	CATTGTTGTC	100
	TTTGTTAACA	AAGTTGATAC	TATTGATGAC	CCAGAAATGT	TGGAATTAGT	150
	TGAAATGGAA	ATGAGAGAAT	TGTTAAGTAC	TTATGGTTTT	GATGGTGATA	200
	ACGTCCCAGT	TGTTATGGGT	TCTGCTTTAT	GTGCCTTGGA	AGGTCGTGAA	250
55	GAAGAAATTG	GTGTCAAAGC	TATTGATAAA	TTATTAGCTG	CTGTTGATGA	300
	ATATATCCCA	ACCCACAAA	GAGATTTAGA	AAAACCATTC	TTGATGGGTG	350
	TTGAAGATGT	CTTYTCAATC	TCAGGTAGAG	GTACCGTTGT	TACTGGTCGT	400
	GTTGAACGTG	GTAACCTGAA	GAAAGGTGAT	GAAGTTGAAA	TTGTTGGTTT	450
	AAACAAAAC	CCATTGAAAA	CTACTGTYAC	NGGTATTGAA	ATGTTCAAAA	500
60	AAGAATTGGA	CCAAGCTATG	GCTGGTGATA	ACTGTGGTAT	CTTATTACGT	550

	GGTATCAAAA	GAGATGACAT	YAAAAGAGGT	ATGGTTATTG	CTAAAACCGG	600
	TACCATCTCW	GCTCACACTA	AATTCTTAGC	CTCAATGTAT	ATTTTGACTA	650
	AAGAAGAAGG	TGGTCGTCAC	TCAGGTTTTG	GTGAACATTA	CAGACCTCAA	700
	TTATTTCATCA	GAAGTGGTGA	TGTTACCGTT	GTTTAAACCT	TYCCAGAAGG	750
5	TGGTGATTCA	TCTCAACAAA	TCTTACCAGG	TGACAATGTC	GAAATGGTTT	800
	GTGAATTGGT	TCACCCAAC	GCTTTAGAAG	CTGGTCAAAG	ATTCAA	846

10 2) INFORMATION FOR SEQ ID NO: 507

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 964 bases
	(B)	TYPE: Nucleic acid
15	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Trichophyton mentagrophytes</i>
	(B)	STRAIN: WSA-225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 507

25	GGAGCTGTTG	TCGTTGTCGC	AGCTTCTGAC	GGTCAAATGT	AATTGAATGC	50
	CCGCCCAGAC	GGATGAAAGG	ATTTGACGTT	TCTAACATCA	GTCTAGGCCT	100
	CAGACCAGAG	AACATTTGCT	CCTTGCCCGC	CAGGTCGGTG	TCCAGAAGCT	150
	GGTCGTTTTC	GTTAACAAGG	TCGATGCCGT	TGAGGACCCA	GAGATGTTGG	200
30	AGCTTGTCGA	ACTTGAAATG	CGTGAACCTC	TCAGCCACTA	CAGTTTTGAG	250
	GGTGAGGAGA	CCCCCATCAT	TTTTGGCTCT	GCTCTCTGTG	CCCTCGAGTC	300
	CCGTTCGACCT	GAGCTTGGTG	TCGAGAAGAT	TGACGAGCTA	TTGAACGCCG	350
	TCGACACCTG	GATCCCCACC	CCCGAGCGCG	CCACTGATAA	GCCTTTCCTC	400
	ATGTCCATTG	AGGAAGTGTT	CTCTATCTCT	GGTCGTGGTA	CCGTCGTCTC	450
35	CGGTTCGTGTT	GAGCGTGGTA	TCCTCAAGAA	GGATTCGGAC	GTGCGAAATTG	500
	TTGGTGGCTC	TACCACCCCT	ATCAAGACCA	AGGTCACAGA	TATCGAAACC	550
	TTCAAGAAGT	CCTGCGATGA	ATCTCGAGCT	GGTGACAACT	CTGGTCTCCT	600
	TCTCCGAGGT	ATCAAGCGTG	AGGACTTGAA	CCGTGGAATG	GTTGTTGCTG	650
	CCCCCGGATC	CACCAAGGCT	CACACCGACT	TCATGGTCTC	CCTCTACGTC	700
40	CTGACTGAGG	CTGAGGGTGG	TCGTTCCAAC	GGCTTCACCC	ACAAGTACCG	750
	CCCTCAAATG	TTCATCCGTA	CTGCTGGTAT	GTAACCAAAG	TTTCCGCTAT	800
	TTACTAAGTA	GATCATTGCT	AACTTGATAT	CCCTTCGGTA	GACGAAGCCG	850
	CATCTTTCAG	CTGGCCTGGA	GAAGACCAAG	ACAAGAAGGC	TATGCCTGGT	900
	GACAACGTCG	AGATGATTTG	CAAAACCCCTC	CACCCCATTTG	CTGCCGAGGC	950
45	TGGCCAACGA	TTCA				964

2) INFORMATION FOR SEQ ID NO: 508

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 844 bases
	(B)	TYPE: Nucleic acid
55	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

60	(A)	ORGANISM: <i>Yarrowia lipolytica</i>
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(B) STRAIN: ATCC 38295

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 508

5	GGTGCTATCA	TTGTCGTTGC	TGCTGGAGAC	GGTTCCAAGC	CCCAGACCCG	50
	AGAGCATCTG	CTGCTTGCTC	GACAGGTCGG	TGTCCAGAAC	CTGGTTGTGT	100
	TTGTTAACAA	GGTTGATCAG	ATTGATGATA	AGGAGATTCT	TGAGCTCGTT	150
	GACATGGAGA	TGCGAGATCT	GCTGACCCAG	TACGGTTTTG	ATGGTGACAA	200
	CACCCCGT	GTCATGGGCT	CTGCTCTGTG	CGCTCTTGAG	GGCAAGCAGA	250
10	AGGATATTGG	AGAGGACGCC	ATCATGGCCC	TTATGGATGC	CGTTGATGAG	300
	CACATCCCTA	CCCCTAACC	TGACCTTGAG	AAGCCCTTCC	TGATGCCCCG	350
	TGAGGACGTT	TTCTCCATCT	CTGGCCGAGG	AACTGTTGTT	ACTGGCCGAG	400
	TCGAGCGAGG	AAACCTGAAG	AAGGGTGAGG	AAATCGAGAT	TGTTGGCTAC	450
	AACAACAAGC	CCATCAAGGC	TGTTGTTACC	GGTATTGAGA	TGTTCAAGAA	500
15	GGAGCTCGAG	TCCGCCATGG	CCGGTGACAA	CGCCGGTATC	CTGCTCCGAG	550
	GTATCAAGCG	AGACGAGATC	AAGCGAGGTA	TGGTCATGTG	CAAGCCTGGC	600
	ACCGTCAACG	CCCACACCAA	GTTCTTGTCT	TCTCTTTACA	TCATCCCCAC	650
	CGAGGAGGGT	GGTCGAACCA	GCTCTTTCGG	CGCCAACTAC	CGACCCGAGA	700
	TGTTTCATCCG	AACCTTCTCC	GTCACCGCCA	CTCTCACCTT	CCCCGAGGGT	750
20	ACCGACGAGT	CCCAGACCGT	CAACCCCGGT	GACAACACTG	AGATGGTTCT	800
	CGAGCTTGTT	CACCCTACCG	CCATTGAGGT	CAACCAGCGA	TTCA	844

25 2) INFORMATION FOR SEQ ID NO: 509

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 1067 bases
	(B)	TYPE: Nucleic acid
30	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Babesia bigemina</i>
	(B)	STRAIN: Suarez-2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 509

40	CTTGGACAAG	CTGAAGAGCG	AGCGTGAGCG	TGGTATCACC	ATTGACATTA	50
	CCCTGTGGAA	GTTCTGAACT	GGCAAGTACT	ACTACACCGT	CATTGACGCC	100
	CCCGGTCACC	GTGACTTTCAT	TAAGAACATG	ATTACGGGTA	CCTCCCAGGC	150
	CGATGTTGCT	ATGCTTGTCG	TGCCCCGCCA	GGCTGGTGTT	TTCGAAGCTG	200
45	CCTTCTCTAA	GGAAGGTCAG	ACCCGTGAGC	ACGCTCTTTT	GGCCTTCACC	250
	CTTGGTGTCA	AGCAGATCAT	TTGCGCCATC	AACAAGATGG	ACAAGTGCGA	300
	CTACAAGGAG	GACCGTTACA	GCGAAATCCA	GAAGGAAGTT	CAGGGTTACC	350
	TGAAGAAGGT	CGGTTACAAC	ATCGAGAAGG	TGCCTTTCGT	CGCCATCTCC	400
	GGTTTCATGG	GTGACAACAT	GGTTGAGCGC	TCCACCAACA	TGCCGTGGTA	450
50	CAAGGGCAAG	ACCTTGGTG	AGGCCCTCGA	CATGATGGAG	CCCCCGAAGA	500
	GGCCCGTCGA	CAAGCCCCTG	CGTCTTCCCC	TCCAGGGTGT	GTACAAGATC	550
	GGTGGTATCG	GTACCTGCTC	TGTCGGTCGT	GTGGAGACTG	GTCAGCTCAA	600
	GGCCGGTATG	GTCCTCACCT	TCGCCCCCAA	CCCGATCACT	ACTGAGTGCA	650
	AATCCGTCGA	AATGCACCAC	GAAGTTATCG	ATGTTGCCAG	CCCTGGTGAC	700
55	AACGTTGGTT	TCAACGTGAA	GAACGTGTCC	ACCTCTGACA	TCCGCACTGG	750
	TCACGTCGCT	TCTGACTCCA	AGAACGACCC	CGCCAAGGCC	GCCGTGTCCT	800
	TCACCGCCCA	GGTCATCATC	TTGAACCACC	CTGGTACCAT	CAAGGCCGGT	850
	TACTCCCTG	TGGTTGACTG	CCACACTGCC	CACATCTCGT	GCAAATTCTGA	900
	CGAGATCACC	AGCCGTATGG	ACAAGCGTAC	CGGTAAGGCC	CTTGAGGAGA	950
60	ACCCCAAGAC	CATCAAGAAC	GGCGACGCCG	CTATGGTCGT	CCTGAAGCCG	1000

TGCAAGCCCA TGGTCGTCGA GGCCTTCACT GAATACGCTC CCCTTGGTGC 1050
 TTTCCGCCGTG CGTGACG 1067

5

2) INFORMATION FOR SEQ ID NO: 510

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1049 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Babesia bovis*
 (B) STRAIN: Suarez-3

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 510

GTGAACGTGA ACGTGGTATT ACTATTGATA TTACCTTATG GAAGTTCGAG 50
 ACCACCAAGT ACTACTACAC CGTCATTGAT GCCCCTGGTC ACCGTGACTT 100
 CATCAAGAAC ATGATTACGG GTACTTCTCA AGCCGATGTT GCTATGCTTG 150
 25 TTGTACCAGC TGAGGCTGGT GGTTCGAGG CCGCTTTCTC CAAGGAAGGA 200
 CAGACCCGTG AGCACGCTCT TTTGGCTTTC ACCCTTGGTG TCAAACAGAT 250
 CATCTGTGCC ATTAACAAGA TGGACAAGTG CGACTACAAG GAGGACCGTT 300
 ACAGTGAAAT CCAGAAGGAA GTCCAGGGTT ACCTCAAGAA GGTCGGTTAC 350
 AATATTGAGA AGGTGCCCTT CGTTGCCATC TCCGGTTTCA TGGGAGACAA 400
 30 CATGGTTGAG CGTTCCACCA ACATGCCCTG GTATAAGGGA AAGACATTGG 450
 TCGAGGCCCT TGATCAGATG GAACCCCAA AGAGGCCCGT TGACAAGCCA 500
 CTTCTCTTTC CCCTCCAGGG TGTCTACAAG ATCGGTGGTA TCGGTACCGT 550
 CCCCCTCGGT CGTGTTGAAA CTGGTATGTT GAAGGCTGGT ATGATTCTAA 600
 CCTTTGCTCC TAACCCAATC ACCACTGAAT GCAAATCCGT TGAAATGCAC 650
 35 CACGAAACCG TTGAGGTTGC TTACCCCGGT GACAACGTCG GTTTCAACGT 700
 AAAGAACGTT TCTACTTCTG ACATTCGCAG TGGTCACGTT GCCTCTGATT 750
 CTAAGAACGA CCCTGCCAAG GCTGCTGTTT CCTTCACTGC CCAGGTCATT 800
 GTGCTCAACC ACCCTGGTAC CATTAAAGGC GGTACTGCC CCGTCGTCGA 850
 TTGCCACACC GCTCACATT CTGTAAATT CGAAGAGATC ACCAGCCGTA 900
 40 TGGACAAGCG TACCGGTAAA TCTCTTGAGG AAAACCCCAA GACCATCAAG 950
 AACGGTGACG CTGCCATGGT TGTGCTCAAG CCAATGAAGC CCATGGTTGT 1000
 CGAATCCTTC ACTGAGTATG CTCCTCTTGG TCGTTTCGCT GTTCGTGAC 1049

45

2) INFORMATION FOR SEQ ID NO: 511

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1070 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Crithidia fasciculata*
 (B) STRAIN: ATCC 11745

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 511

	TGGACAAGCT	GAAGGCGGAG	CGCGAGCGCG	GTATCACGAT	CGATATTGCC	50
	CTGTGGAAGT	TGCAGTCGCC	CAAGTCCGTG	TTCACGATCA	TCGATGCCCC	100
	CGGCCACCCG	GACTTCATCA	AGAACATGAT	CACCGGCACC	TCCCAGGCCG	150
5	ATGCCGCCAT	TCTGATGATT	GACTCGACCC	AGGGTGGCTT	CGAGGCTGGC	200
	ATCTCCAAGG	ACGGCCAGAC	CCGCGAGCAC	GCCCTGCTTG	CCTTCACGCT	250
	GGGCGTGAAG	CAGATGGTTG	TGTGCTGCAA	CAAGATGGAC	GACAAGACGG	300
	TGCAGTACGC	CCAGGCCCGC	TACGAGGAGA	TCAGCAAGGA	GGTCGGCGCG	350
	TACCTGAAGC	GCGTGGGCTA	CAACCCGGAG	AAGGTGCGCT	TCATCCCCGAT	400
10	CTCGGGCTGG	CAGGGCGACA	ACATGATCGA	GAAGTCCGAC	AACATGTCTG	450
	GGTACAAGGG	TCCCACGCTG	CTGGAGGCGC	TCGACCTGCT	GGAGGCCCCC	500
	GTCGCTCCGG	TGGACAAGCC	GCTGCGCCTG	CCCCTGCAGG	ACGTGTACAA	550
	GATCGGCGGT	ATCGGCACTG	TGCCCGTGGG	CCGTGTGGAG	ACCGGCGTGA	600
	TGAAGCCGGG	CGACGTTGTG	GTGTTTCGCG	CTGCCAACGT	GACGACCGAG	650
15	GTGAAGTCGA	TCGAGATGCA	CCACGAGCAG	CTGGCTGAGG	CCGTGCCCCG	700
	CGACAACGTG	GGCTTCAACG	TGAAGAACGT	GTCCGTGAAG	GATATCCGCC	750
	GTGGTAACGT	GTGCGGCAAC	ACGAAGAGCG	ACCCCCGAA	GGAGGCGGCC	800
	GACTTCACTG	CCCAGGTGAT	CGTGCTGAAC	CACCCCGGCC	AGATCAGCAA	850
	CGGCTACCGG	CCGGTGCTGG	ACTGCCACAC	GAGCCACATC	GCGTGCAAGT	900
20	TCGCGGACAT	CGAGTCCAAG	ATCGACCGCC	GCTCTGGCAA	GGAGCTGGAG	950
	AAGAGCCCGA	AGGCCATCAA	GTCCGGCGAT	GCGGCCATCG	TGAAGATGAT	1000
	CCCGCAGAAG	CCGATGTGCG	TGGAGGTGTT	CAACGACTAC	CCGCCGCTGG	1050
	GCCGCTTCGC	TGTCCGCGAT				1070

25

2) INFORMATION FOR SEQ ID NO: 512

(i) SEQUENCE CHARACTERISTICS:

30	(A)	LENGTH: 1052 bases
	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Entamoeba histolytica</i>
	(B)	STRAIN: HM1-IMMS

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 512

	GCTGAAAGAG	AAAGAGGAAT	TACTATTGAT	ATTTCAATTAT	GGAAATTCGA	50
	AACATCTAAA	TACTACTTCA	CTATTATTGA	TGCCCCAGGT	CAYAGAGATT	100
45	TCATTAAGAA	CATGATTACT	GGAACCTTCA	AAGCTGATGT	TGCCATCCTT	150
	ATTGTTGCTG	CTGGTACTGG	WGAATTTGAA	GCTGGTATTT	CAAAGAATGG	200
	ACAAACCAGA	GAACAYATTC	TTCTTTTATA	CACTCTTGGA	GTTAAACAAA	250
	TGATTGTTGG	WGTTAACAAG	ATGGATGCTA	TTCAATATAA	ACAAGAAAGA	300
	TATGAAGAAA	TTAAGAAAGA	AATTAGTGCA	TTCCTTAAGA	AGACWGGATA	350
50	TAATCCAGAC	AAGATTCCAT	TTGTCCCAAT	TTCAGGATTC	CAAGGAGATA	400
	ATATGATTGA	ACCATCAACC	AACATGCCAT	GGTACAAAGG	ACCAACATTA	450
	ATTGGAGCAC	TTGATTTCAGT	CACACCACCA	GAAAGACCAG	TTGATAAACC	500
	ACTTAGACTT	CCACTTCAAG	ATGTTTAYAA	GATTTTCAGT	ATTGGAACCTG	550
	TACCATGTGG	AAGAGTTGAA	ACTGGAGTTC	TTAGACCAGG	AACTATTGTT	600
55	CAATTTGCAC	CATCAGGAGT	TTCATCTGAA	TGTAAATCAG	TTGAAATGCA	650
	TCACACAGCA	CTTGCTCAAG	CTATTCCAGG	TGATAATGTT	GGATTCAATG	700
	TTAGAAAYTT	AACAGTTAAA	GATATTAAGA	GAGGAAATGT	AGCATCAGAT	750
	GCTAAGAATC	AACCAGCTGT	TGGATGTGAA	GATTTCACTG	CTCAAGTCAT	800
	TGTCATGAAC	CATCCAGGAC	AAATTAGAAA	GGGATATACA	CCAGTTCTTG	850
60	ATTGCCATAC	ATCACACATT	GCATGTAAAT	TCGAAGAATT	ATTAAGCAAG	900

ATTGATAGAA	GAACAGGTAA	ATCCATGGAA	GGAGGAGAAC	CAGAATATAT	950
TAAGAATGGA	GATTGAGCAC	TTGTTAAGAT	TGTTCCAAC	AAACCACTTT	1000
GTGTTGAAGA	ATTTGCTAAA	TTCCCAACAT	TGGGAAGATT	TGCTGTTAGA	1050
GA					1052

5

2) INFORMATION FOR SEQ ID NO: 513

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1082 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

20 (A) ORGANISM: *Giardia lamblia*
 (B) STRAIN: Faubert-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 513

GACGAGCGCG	AGCGCGGGAT	CACGATCAAC	ATCGCGCTCT	GGAAGTTCGA	50
GACGAAGAAG	TACATCGTCA	CGATCATCGA	CGCCCCGGGC	CACCGCGACT	100
TCATCAAGAA	CATGATCACG	GGGACGTCCC	AGGCCGACGT	CGCGATCCTC	150
GTCGTCGCGG	CGGGCCAGGG	CGAGTTCGAG	GCCGGGATCT	CGAAGGACGG	200
CCAGACGCGC	GAGCACGCGA	CCCTTGCGAA	CACGCTCGGG	ATCAAGACGA	250
TGATCATCTG	CGTCAACAAG	ATGGACGACG	GCCAGGTCAA	GTACTCGAAG	300
GAGCGCTACG	ACGAGATCAA	GGGCGAGATG	ATGAAGCAGC	TCAAGAACAT	350
CGGCTGGAAG	AAGGCCGAGG	AGTTCGACTA	CATCCCGACG	TCCGGCTGGA	400
CCGGGGACAA	CATCATGGAG	AAGTCCGACA	AGATGCCCTG	GTACGAGGGC	450
CCGTGCCTGA	TCGACGCGAT	CGACGGGCTC	AAGGCCCCGA	AGCGCCCGAC	500
CGACAAGCCC	CTCCGCCTCC	CGATCCAGGA	CGTCTACAAG	ATCTCGGGCG	550
35 TCGGGACCGT	CCCCGCGGGC	CGCGTCGAGA	CGGGCGAGCT	CGCGCCCGGG	600
ATGAAGGTCG	TCTTCGCCCC	GACGTCCAG	GTCTCGGAGG	TCAAGTCCGT	650
CGAGATGCAC	CACGAGGAGC	TCAAGAAGGC	CGGGCCCGGG	GACAACGTCG	700
GCTTCAACGT	CCGCGGGCTC	GCCGTCAAGG	ACCTCAAGAA	GGGCTACGTC	750
GTCGGGGACG	TGACGAACGA	CCCCCCGTC	GGCTGCAAGA	GCTTCACCGC	800
40 CCAGTTCATC	GTCATGAACC	ACCCGAAGAA	GATCCAGCCC	GGCTACACGC	850
CCGTTCATCGA	CTGCCACACC	GCGCACATCG	CGTGCCAGTT	CCAGCTCTTC	900
CTCCAGAAGC	TCGACAAGCG	CACGCTCAAG	CCCAGATGG	AGAACCCGCC	950
CGACGCAGGC	CGCGGCGATT	GCATCATCGT	CAAGATGGTC	CCCCAGAAGC	1000
CCCTGTGCTG	CGAGACGTTT	AACGACTACG	CGCCCCCTCGG	CCGCTTCGCC	1050
45 GTCCGCGACA	TGCGCCAAAC	CGTTGCCGTC	GG		1082

2) INFORMATION FOR SEQ ID NO: 514

50

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1098 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

60 (A) ORGANISM: *Leishmania tropica*

(B) STRAIN: ATCC 30816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 514

5	ACGCGTGGGT	GCTCGACAAG	CTGAAGGCGG	AGCGCGAGCG	CGGCATCACG	50
	ATCGACATTG	CGCTGTGGAA	GTTTCGAGTCG	CCCAAGTCCG	TGTTTCACGAT	100
	CATCGATGCG	CCCGGCCACC	GCGACTTCAT	CAAGAACATG	ATCACGGGCA	150
	CGTCGCAGGC	GGACGCCGCC	ATCCTGATGA	TCGACTCGAC	GCATGGTGGC	200
	TTCGAGGCTG	GCATCTCGAA	GGACGGCCAG	ACCCGCGAGC	ACGCGCTGCT	250
10	TGCCTTCACT	CTTGGCGTGA	AGCAGATGGT	GGTGTGCTGC	AACAAGATGG	300
	ACGACAAGAC	GGTGACGTAC	GCGCAGTCGC	GCTACGATGA	GATCAGCAAG	350
	GAGGTGGGCG	CGTACCTGAA	GCGCGTGGGC	TACAACCCGG	AGAAGGTGCG	400
	CTTCATCCCG	ATCTCGGGCT	GGCAGGGCGA	CAACATGATC	GAGAAGTCGG	450
	ACAACATGCC	GTGGTACAAG	GGTCCACGC	TGCTGGACGC	GCTCGACATG	500
15	CTGGAGCCGC	CGGTGCGCCC	GGTGGACAAG	CCGCTGCGCC	TGCCCCCTGCA	550
	GGACGTGTAC	AAGATCGGCG	GTATCGGGAC	GGTGCCCGTG	GGGCGCGTGG	600
	AGACCGGCAT	CTGAAGCCG	GCGCAGTGG	TGACGTTCGC	GCCCCGCCAAC	650
	GTGACGACTG	AGGTGAAGTC	GATCGAGATG	CACCACGAGC	AGCTGGCGGA	700
	GGCGCAGCCC	GGCGACAACG	TCGGCTTCAA	CGTGAAGAAC	GTGTCGGTGA	750
20	AGGACATCCG	CCGTGGTAAC	GTGTGCGGCA	ACTCGAAGAA	CGACCCGCCG	800
	AAGGAGGCGG	CCGACTTCAC	GGCGCAGGTG	ATCGTGCTGA	ACCACCCCGG	850
	CCAGATCAGC	AACGGCTACG	CGCCGGTGCT	GGACTGCCAC	ACGAGCCACA	900
	TTGCGTGCCG	CTTCGCGGAA	ATCGAGTCCA	AGATCGACCG	CCGCTCCGGC	950
	AAGGAGCTGG	AGAAGAACCC	CAAGGCGATC	AAGTCTGGCG	ATGCCGCGAT	1000
25	CGTGAAGATG	GTGCCGCAGA	AGCCGATGTG	CGTGGAGGTG	TTCAACGACT	1050
	ACGCGCCGCT	GGGCCGCTTT	GCCGTGCGCG	ACATGCGCCA	AACCGTTG	1098

30 2) INFORMATION FOR SEQ ID NO: 515

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 1104 bases
	(B)	TYPE: Nucleic acid
35	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Leishmania aethiopica</i>
	(B)	STRAIN: ATCC 50119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 515

45	TACGCGTGGG	TGCTCGACAA	GCTGAAGGCG	GAGCGCGAGC	GCGGCATCAC	50
	GATCGACATT	GCGCTGTGGA	AGTTCGAGTC	GCCCAAGTCC	GTGTTTCACGA	100
	TCATCGATGC	GCCCGGCCAC	CGCGACTTCA	TCAAGAACAT	GATCACGGGC	150
	ACGTCGCAGG	CGGACGCCGC	CATCCTGATG	ATCGACTCGA	CGCATGGTGG	200
50	CTTCGAGGCT	GGCATCTCGA	AGGACGGCCA	GACCCGCGAG	CACGCGCTGC	250
	TTGCCTTCAC	TCTTGCGGTG	AAGCAGATGG	TGGTGTGCTG	CAACAAGATG	300
	GACGACAAGA	CGGTGACGTA	CGCGCAGTCG	CGCTACGAGG	AGATCAGCAA	350
	GGAGGTGGGC	GCGTACCTGA	AGCGCGTGGG	CTACAACCCG	GAGAAGGTGC	400
	GCTTCATCCC	GATCTCGGGC	TGGCAGGGCG	ACAACATGAT	CGAGAAGTCG	450
55	GACAACATGC	CGTGGTACAA	GGTCCACG	CTGCTGGACG	CGCTCGACAT	500
	GCTGGAGCCG	CCGGTGCGCC	CGGTGGACAA	GCCGCTGCGC	CTGCCCCCTGC	550
	AGGACGTGTA	CAAGATCGGC	GGTATCGGGA	CGGTGCCCCG	GGGCCGCGTG	600
	GAGACCGGCA	TCATGAAGCC	GGGCGACGTG	GTGACGTTCG	CGCCCCGCAA	650
	CGTGACGACT	GAGGTGAAGT	CGATCGAGAT	GCACCACGAG	CAGCTGGCGG	700
60	AGGCGCAGCC	CGGCGACAAC	GTCGGCTTCA	ACGTGAAGAA	CGTGTGCGTG	750

	AAGGACATCC	GCCGTGGCAA	CGTGTGCGGC	AACTCGAAGA	ACGACCCGCC	800
	GAAGGAGGCG	GCCGACTTCA	CGGCGCAGGT	GATCGTGCTG	AACCACCCCG	850
	GCCAGATCAG	CAACGGCTAC	GCGCCGGTGC	TGGACTGCCA	CACGAGCCAC	900
	ATTGCGTGCC	GCTTCGCGGA	AATCGAGTCC	AAGATCGACC	GCCGCTCCGG	950
5	CAAGGAGCTG	GAGAAGAACC	CCAAGGCGAT	CAAGTCTGGC	GATGCCGCGA	1000
	TCGTGAAGAT	GGTGCCGCAG	AAGCCGATGT	GCGTGGAGGT	GTTCAACGAC	1050
	TACGCGCCGC	TGGGCCGCTT	TGCCGTGCGC	GACATGCGCC	AAACCGTTGC	1100
	CGTC					1104

10

2) INFORMATION FOR SEQ ID NO: 516

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 1106 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania tropica*
 (B) STRAIN: ATCC 30815

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 516

	TACGCGTGGG	TGCTCGACAA	GCTGAAGGCG	GAGCGCGAGC	GCGGCATCAC	50
	GATCGACATT	GCGCTGTGGA	AGTTCGAGTC	GCCCAAGTCC	GTGTTACGA	100
30	TCATCGATGC	GCCCGGCCAC	CGCGACTTCA	TCAAGAACAT	GATCACGGGC	150
	ACGTCGCAGG	CGGACGCCGC	CATCCTGATG	ATCGACTCGA	CGCATGGTGG	200
	CTTCGAGGCT	GGCATCTCGA	AGGACGGCCA	GACCCGCGAG	CACGCGCTGC	250
	TTGCCTTCAC	KCTTGGCGTG	AAGCAGATGG	TGGTGTGCTG	CAACAAGATG	300
	GACGACAAGA	CGGTGACGTA	CGCGCAGTCG	CGCTACGATG	AGATCAGCAA	350
35	GGAGGTGGGC	GCGTACCTGA	AGCGCGTGGG	CTACAACCCG	GAGAAGGTGC	400
	GCTTCATCCC	GATCTCGGGC	TGGCAGGGCG	ACAACATGAT	CGAGAAGTCG	450
	GACAACATGC	CGTGGTACAA	GGGTCCCACG	CTGCTGGACG	CGCTCGACAT	500
	GCTGGAGCCG	CCGGTGCGCC	CGGTGGACAA	GCCGCTGCGC	CTGCCCCCTG	550
	AGGACGTGTA	CAAGATCGGC	GGTATCGGGA	CGGTGCCCCG	GGGGCGCGTG	600
40	GAGACCGGCA	TCATGAAGCC	GGGCGACGTG	GTGACGTTTC	CGCCCGCCAA	650
	CGTGACGACT	GAGGTGAAGT	CGATCGAGAT	GCACCACGAG	CAGCTGGCGG	700
	AGGCGCAGCC	CGGCGACAAC	GTCGGCTTCA	ACGTGAAGAA	CGTGTCCGTG	750
	AAGGACATCC	GCCGTGGTAA	CGTGTGCGGC	AACTCGAAGA	ACGACCCGCC	800
	GAAGGAGGCG	GCCGACTTCA	CGGCGCAGGT	GATCGTGCTG	AACCACCCCG	850
45	GCCAGATCAG	CAACGGCTAC	GCGCCGGTGC	TGGACTGCCA	CACGAGCCAC	900
	ATTGCGTGCC	GCTTCGCGGA	AATCGAGTCC	AAGATCGACC	GCCGCTCCGG	950
	CAAGGAGCTG	GAGAAGAACC	CCAAGGCGAT	CAAGTCTGGC	GATGCCGCGA	1000
	TCGTGAAGAT	GGTGCCGCAG	AAGCCGATGT	GCGTGGAGGT	GTTCAACGAC	1050
	TACGCGCCGC	TGGGCCGCTT	TGCCGTGCGC	GACATGCGCC	AAACCGTTGC	1100
50	CGTCGG					1106

2) INFORMATION FOR SEQ ID NO: 517

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 1099 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Leishmania donovani* subsp. *donovani*
 (B) STRAIN: ATCC 50212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 517

```

10 TACGCGTGGG TGCTCGACAA GCTGAAGGCG GAGCGCGAGC GCGGCATCAC      50
   GATCGACATT GCGCTGTGGA AGTTCGAGTC GCCCAAGTCC GTGTTACGA      100
   TCATCGATGC GCCCGGCCAC CGCGACTTCA TCAAGAACAT GATCACGGGC      150
   ACGTCGCAGG CGGACGCCGC CATCCTGATG ATCGACTCGA CGCATGGTGG      200
   CTTCGAGGCT GGCATCTCGA AGGACGGCCA GACCCGCGAG CACGCGCTGC      250
15 TTGCCTTCAC GCTTGCGGTG AAGCAGATGG TGGTGTGCTG CAACAAGATG      300
   GACGACAAGA CCGTGACGTA CGCGCAGTCG CGCTACGATG AGATCAGCAA      350
   GGAGGTGGGC GCGTACCTGA AGCGCGTGGG CTACAACCCG GAGAAGGTGC      400
   GCTTCATCCC GATCTCGGGC TGGCAGGGCG ACAACATGAT CGAGAGGTGC      450
   GACAACATGC CGTGGTACAA GGGTCCCACG CTGCTGGACG CGCTCGACAT      500
20 GCTGGAGCCG CCGGTGCGCC CGGTGGACAA GCCGCTGCGC CTGCCCTGC      550
   AGGACGTGTA CAAGATCGGC GGTATCGGGA CTGTGCCCGT GGGCCGCGTG      600
   GAGACCGGCA TCATGAAGCC GGGCGACGTG GTGACGTTTC CGCCCGCCAA      650
   CGTGACGACT GAGGTGAAGT CGATCGAGAT GCACCACGAG CAGCTGGCGG      700
   AGGCGCAGCC CGGCGACAAC GTCGGCTTCA ACGTGAAGAA CGTGTCGGTG      750
25 AAGGACATCC GCCGTGGCAA CGTGTGCGGC AACTCGAAGA ACGACCCGCC      800
   GAAGGAGGCG GCCGACTTCA CGGCGCAGGT GATCGTGCTG AACCACCCCG      850
   GCCAGATCAG CAACGGCTAC GCGCCGTTGC TGGACTGCCA CACGAGCCAC      900
   ATTGCGTGCC GCTTCGCGGA AATCGAGTCC AAGATCGACC GCCGCTCCGG      950
   CAAGGAGCTG GAGAAGAACC CCAAGGCGAT CAAGTCTGGC GATGCCGCGA     1000
30 TCGTGAAGAT GGTGCCCGAG AAGCCGATGT GCGTGGAGGT GTTCAACGAC     1050
   TACGCGCCGC TGGGCCGCTT TGCCGTGCGC GACATGCGCC AAACCGTTG     1099

```

35 2) INFORMATION FOR SEQ ID NO: 518

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1098 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Leishmania donovani* subsp. *infantum*
 (B) STRAIN: MOU

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 518

```

50 TACGCGTGGG TGCTCGACAA GCTGAAGGCG GAGCGCGAGC GCGGCATCAC      50
   GATCGACATT GCGCTGTGGA AGTTCGAGTC GCCCAAGTCC GTGTTACGA      100
   TCATCGATGC GCCCGGCCAC CGCGACTTCA TCAAGAACAT GATCACGGGC      150
   ACGTCGCAGG CGGACGCCGC CATCCTGATG ATCGACTCGA CGCATGGTGG      200
55 CTTCGAGGCT GGCATCTCGA AGGACGGCCA GACCCGCGAG CACGCGCTGC      250
   TTGCCTTCAC GCTTGCGGTG AAGCAGATGG TGGTGTGCTG CAACAAGATG      300
   GACGACAAGA CCGTGACGTA CGCGCAGTCG CGCTACGATG AGATCAGCAA      350
   GGAGGTGGGC GCGTACCTGA AGCGCGTGGG CTACAACCCG GAGAAGGTGC      400
   GCTTCATCCC GATCTCGGGC TGGCAGGGCG ACAACATGAT CGAGAGGTGC      450
60 GACAACATGC CGTGGTACAA GGGTCCCACG CTGCTGGACG CGCTCGACAT      500

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5  GCTGGAGCCG CCGGTGCGCC CGGTGGACAA GCCGCTGCGC CTGCCCCTGC 550
   AGGACGTGTA CAAGATCGGC GGTATCGGGA CTGTGCCCCG GGGCCGCGTG 600
   GAGACCGGCA TCATGAAGCC GGGCGACGTG GTGACGTTTC CGCCCGCCAA 650
   CGTGACGACT GAGGTGAAGT CGATCGAGAT GCACCACGAG CAGCTGGCGG 700
   AGGCGCAGCC CGGCGACAAC GTCGGCTTCA ACGTGAAGAA CGTGTCGGTG 750
   AAGGACATCC GCCGTGGCAA CGTGTGCGGC AACTCGAAGA ACGACCCGCC 800
   GAAGGAGGCG GCCGACTTCA CGGCGCAGGT GATCGTGCTG AACCACCCCG 850
   GCCAGATCAG CAACGGCTAC GCGCCGGTGC TGGACTGCCA CACGAGCCAC 900
   ATTGCGTGCC GCTTCGCGGA AATCGAGTCC AAGATCGACC GCCGCTCCGG 950
10 CAAGGAGCTG GAGAAGAACC CCAAGGCGAT CAAGTCTGGC GATGCCGCGA 1000
   TCGTGAAGAT GGTGCCGCGA AAGCCGATGT GCGTGGAGGT GTTCAACGAC 1050
   TACGCGCCGC TGGGCCGCTT TGCCGTGCGC GACATGCGCC AAACCGTT 1098

```

15

2) INFORMATION FOR SEQ ID NO: 519

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20  (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 1071 bases
     (B) TYPE: Nucleic acid
     (C) STRANDEDNESS: Double
     (D) TOPOLOGY: Linear

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25  (ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

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     (A) ORGANISM: Leishmania enriettii
     (B) STRAIN: ATCC 50120

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30  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 519

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```

   CTCGACAAGC TGAAGGCGGA GCGCGAGCGC GGCATCACGA TCGACATTGC 50
   GCTGTGGAAG TTCGAGTCGC CCAAGTCTGT GTTCACGATC ATCGATGCGC 100
   CCGGCCACCG CGACTTCATC AAGAACATGA TCACCGGCAC GTCGCAGGCC 150
35  GACGCCGCCA TCCTGATGAT CGACTCGACC CAGGGCGGCT TCGAGGCTGG 200
   CATCTCGAAG GACGGCCAGA CCCGCGAGCA CGCGCTGCTC GCCTTCACGC 250
   TTGGTGTGAA GCAGATGGTG GTGTGCTGCA ACAAGATGGA CGACAAGACG 300
   GTGCAGTACT CGCAGGCGCG CTACGAGGAG ATCAGCAAGG AGGTGGGCGC 350
   GTACCTGAAG CGCGTCGGCT ACAACCCGGA GAAGGTGCGC TTCATCCCGA 400
40  TCTCGGGCTG GCAGGGCGAC AACATGATCG ACAAGTCGGA CAGCATGCCG 450
   TGGTACAAGG GGCCACGCT GCTGGACGCG CTCGACATGC TGGAGGCGCC 500
   GGTGCGCCCG GTGGACAAGC CGCTGCGCCT GCCCCTGCAG GACGTGTACA 550
   AGATCGGCGG TATCGGGACG GTGCCCCTGG GCCGCGTGGA GACCGGCATC 600
   ATGAAGCCTG GCGACGTGGT GACGTTTGCG CCCGCCAACG TGACGACGGA 650
45  GGTGAAGTCG ATCGAGATGC ACCACGAGCA GTGGCGGAG GCGGTGCCCG 700
   GCGACAACGT CGGCTTCAAC GTGAAGAACG TGTCGGTGAA GGACATCCGC 750
   CGTGGTAAAC TGTGCGGCAA CTCGAAGAAC GACCCGCCGA AGGAGGCGGC 800
   CGACTTCACG GCGCAGGTGA TCGTGCTGAA CCACCCTGGC CAGATCAGCA 850
   ACGGCTACGC GCCGGTGCTG GACTGCCACA CGAGCCACAT CGCGTGCCGC 900
50  TTCCGCGGATA TCGAGTCCAA GATCGACCGC CGCTCTGGCA AGGAGCTGGA 950
   GAAGAACCCC AAGGCGATCA AGTCCGGCGA TGCGGCCATC GTGAAGATGG 1000
   TGCCGCAGAA GCCGATGTGC GTGGAGGTGT TCAACGACTA CCCGCCGCTG 1050
   GGGCGCTTCG CTGTGCGCGA C 1071

```

55

2) INFORMATION FOR SEQ ID NO: 520

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60  (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 1071 bases

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(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania gerbilli*

(B) STRAIN: ATCC 50121

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 520

	CTCGACAAGC	TGAAGGCGGA	GCGCGAGCGC	GGCATCACGA	TCGACATTGC	50
	GCTGTGGAAG	TTCGAGTCGC	CCAAGTCCGT	GTTCACGATC	ATCGATGCGC	100
15	CCGGCCACCG	CGACTTCATC	AAGAACATGA	TCACGGGCAC	GTCGCAGGCG	150
	GACGCCGCCA	TCCTGATGAT	CGACTCGACG	CATGGTGGCT	TCGAGGCTGG	200
	CATCTCGAAG	GACGGCCAGA	CCCGCGAGCA	CGCGCTGCTT	GCCTTCACTC	250
	TTGGCGTGAA	GCAGATGGTG	GTGTGCTGCA	ACAAGATGGA	CGACAAGACG	300
	GTGACGTACG	CGCAGTCGCG	CTACGATGAG	ATCAGCAAGG	AGGTGGGCGC	350
20	GTACCTGAAG	CGCGTGGGCT	ACAACCCGGA	GAAGGTGCGC	TTCATCCCGA	400
	TCTCGGGCTG	GCAGGGCGAC	AACATGATCG	AGAAGTCGGA	CAACATGCCG	450
	TGGTACAAGG	GTCCACGCT	GCTGGACGCG	CTCGACATGC	TGGAGCCGCC	500
	GGTGCGCCCG	GTGGACAAGC	CGCTGCGCCT	GCCCCTGCAG	GACGTGTACA	550
	AGATCGGCGG	TATCGGGACG	GTGCCCCTGG	GCCGCGTGGA	GACCGGCATC	600
25	ATGAAGCCCG	GCGACGTGGT	GACGTTCCGC	CCCGCCAACG	TGACGACTGA	650
	GGTGAAGTCG	ATCGAGATGC	ACCACGAGCA	GCTGGCGGAG	GCGCAGCCCG	700
	GCGACAACGT	CGGCTTCAAC	GTGAAGAACG	TGTCGGTGAA	GGACATCCGC	750
	CGTGGTAACG	TGTGCGGCAA	CTCGAAGAAC	GACCCGCCGA	AGGAGGCGGC	800
	CGACTTCACG	GCGCAGGTGA	TCGTGCTGAA	CCACCCCGGC	CAGATCAGCA	850
30	ACGGCTATGC	GCCGGTGCTG	GACTGCCACA	CGAGCCACAT	TGCGTGCCGC	900
	TTCGCGGAAA	TCGAGTCCAA	GATCGACCGC	CGCTCCGGCA	AGGAGCTGGA	950
	GAAGAACCCC	AAGGCGATCA	AGTCTGGCGA	TGCCGCGATC	GTGAAGATGG	1000
	TGCCGCAGAA	GCCGATGTGC	GTGGAGGTGT	TCAACGACTA	CGCGCCGCTG	1050
35	GGCCGCTTTG	CCGTGCGCGA	C			1071

2) INFORMATION FOR SEQ ID NO: 521

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1114 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania hertigi* subsp. *hertigi*

50 (B) STRAIN: ATCC 50125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 521

	TCGTTCAAGT	ACGCGTGGGT	GCTCGACAAG	CTGAAGGCGG	AGCGCGAGCG	50
55	CGGTATCACG	ATCGACATTG	CGCTGTGGAA	GTTTCGAGTCG	CCCAAGTCGG	100
	TGTTACGAT	CATCGATGCG	CCCGGCCACC	GCGACTTCAT	CAAGAACATG	150
	ATCACCGGCA	CGTCGCAGGC	GGATGCTGCC	ATTCTGATGA	TCGATTTCGAC	200
	GCAGGGTGGC	TTGAGGCTG	GCATCTCGAA	GGACGGCCAG	ACGCGCGAGC	250
	ACGCGCTGCT	GGCCTTCACG	CTGGGCGTGA	AGCAGATGGT	TGTGTGCTGC	300
60	AACAAGATGG	ACGACAAGAC	GGTGCACTAC	GCGCAGGCGC	GCTACGAGGA	350

	GATCAGCAAG	GAGGTGGGCG	CGTACCTGAA	GCGCGTGGGC	TACAACCCGG	400
	AGAAGGTGCG	CTTCATCCCG	ATCTCGGGCT	GGCAGGGCGA	CAACATGATC	450
	GAGAAGTCCG	ACAACATGTC	GTGGTACAAG	GGTCCCACGC	TGCTGGAGGC	500
	GCTGGACATG	CTGGAGGCGC	CGGTGCGCCC	GGTGGACAAG	CCGCTGCGCC	550
5	TGCCCCCTGCA	GGACGTGTAC	AAGATCGGCG	GCATTGGCAC	GGTGCCGGTG	600
	GGCCGTGTGG	AGACCGGCAT	CATGAAGCCC	GGCGACGTGG	TGACGTTTCGC	650
	GCCCCGCCAAC	GTGACGACGG	AGGTGAAGTC	GATCGAGATG	CACCACGAGC	700
	AGCTGCAGGA	GGCTGTGCCC	GGCGACAACG	TCGGCTTCAA	CGTGAAGAAC	750
	GTGTGCGTGA	AGGACATCCG	CCGTGGTAAC	GTGTGTGGCA	ACTCGAAGAA	800
10	CGACCCGCCG	AAGGAGGCGG	CTGACTTCAC	GGCGCAGGTG	ATCGTGCTGA	850
	ACCACCCCGG	CCAGATCAGC	AACGGCTACG	CGCCGGTGCT	GGACTGCCAC	900
	ACCAGCCACA	TCGCGTGCCG	CTTCGCGGAC	ATCGAGTCGA	AGATCGACCG	950
	CCGCTCCGGC	AAGGAGCTGG	AGAAGAACCC	CAAGTCCATC	AAGTCCGGCG	1000
	ACGCCGCCAT	CGTGAAGATG	GTGCCGCAGA	AGCCGATGTG	CGTGGAGGTG	1050
15	TTCAACGACT	ACCCGCCGCT	GGGCCGCTTT	GCGGTGCGCG	ACATGCGCCA	1100
	AACCGTTGCC	GTCG				1114

20 2) INFORMATION FOR SEQ ID NO: 522

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1106 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania major*
 (B) STRAIN: ATCC 50122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 522

35	TACGCGTGGG	TGCTCGACAA	GCTGAAGGCG	GAGCGCGAGC	GCGGCATCAC	50
	GATCGACATT	GCGCTGTGGA	AGTTCGAGTC	GCCCAAGTCC	GTGTTACGA	100
	TCATCGATGC	CCCCGGCCAC	CGCGACTTCA	TCAAGAACAT	GATCACGGGC	150
	ACGTCCGAGG	CGGACGCCGC	CATTCTGATG	ATCGACTCGA	CGCATGGCGG	200
40	CTTCGAGGCT	GGCATCTCGA	AGGACGGCCA	GACCCGCGAG	CACGCGCTGC	250
	TTGCCTTCAC	TCTTGGCGTG	AAGCAGATGG	TGGTGTGCTG	CAACAAGATG	300
	GACGACAAGA	CGGTGACGTA	CGCGCAGTCR	CGCTACGATG	AGATCAGCAA	350
	GGAGGTGGGC	GCGTACCTGA	AGCGCGTGGG	CTACAACCCG	GAGAAGGTGC	400
	GCTTCATCCC	GATCTCGGGC	TGGCAGGGCG	ACAACATGAT	CGAGAAGTCG	450
45	GACAACATGC	CGTGGTACAA	GGGTCCCACG	CTGCTGGACG	CGCTCGACAT	500
	GCTGGAGCCG	CCGGTGCGCC	CGGTGGACAA	GCCGCTGCGC	CTGCCCCCTGC	550
	AGGACGTGTA	CAAGATCGGC	GGTATCGGGA	CGGTGCCCCG	GGGCCGCGTG	600
	GAGACCGGCA	TCATGAAGCC	GGGCGACGTG	GTGACGTTTC	CGCCCGCCAA	650
	CGTGACGACT	GAGGTGAAGT	CGATCGAGAT	GCACCACGAG	CAGCTGGCGG	700
50	AGGCGCAGCC	CGGCGACAAC	GTCGGCTTCA	ACGTGAAGAA	CGTGTCGGTG	750
	AAGGACATCC	GCCGTGGTAA	CGTGTGCGGC	AACTCGAAGA	ACGACCCGCC	800
	GAAGGAGGCG	GCCGACTTCA	CGGCGCAGGT	GATCGTGCTG	AACCACCCCG	850
	GCCAGATCAG	CAACGGCTAT	GCGCCGGTGC	TGGACTGCCA	CACGAGCCAC	900
	ATTGCGTGCC	GCTTCGCGGA	AATCGAGTCC	AAGATCGACC	GCCGCTCCGG	950
55	CAAGGAGCTG	GAGAAGAACC	CCAAGGCGAT	CAAGTCTGGC	GATGCCGCGA	1000
	TCGTGAAGAT	GGTGCCGCAG	AAGCCGATGT	GCGTGGAGGT	GTTC AACGAC	1050
	TACGCGCCGC	TGGGCCGCTT	TGCCGTGCGC	GACATGCGCC	AAACCGTTGC	1100
	CGTCCG					1106

60

2) INFORMATION FOR SEQ ID NO: 523

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1105 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania amazonensis*
 (B) STRAIN: ATCC 50131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 523

```

TACGCGTGGG TGCTCGACAA GCTGAAGGCG GAGCGCGAGC GCGGCATCAC      50
GATCGACATT GCGCTGTGGA AGTTCGAGTC GCCGAAGTCC GTGTTACGCA      100
TCATCGATGC GCCCGGCCAC CGCGACTTCA TCAAGAACAT GATCACGGGC      150
ACGTTCGAGG CGGACGCGGC CATCCTGATG ATCGACTCGA CGCATGGTGG      200
CTTCGAGGCT GGCATCTCGA AGGACGGCCA GACCCGCGAG CACGCGCTGC      250
TTGCCTTCAC TCTTGGCGTG AAGCAGATGG TGGTGTGCTG CAACAAGATG      300
GACGACAAGA CGGTGATGTA CGCGCAGTCG CGCTACGATG AGATCAGCAA      350
GGAGGTGAGC GCGTACCTGA AGCGCGTGGG CTACAACCCG GAGAAGGTGC      400
GCTTCATCCC GATCTCGGGG TGGCAGGGCG ACAACATGAT CGACAAGTCG      450
GACAACATGC CGTGGTACAA GGGTCCACG CTGCTGGACG CGCTCGACAT      500
GCTGGAGCCG CCGGTGCGCC CGGTGGACAA GCCGCTGCGC CTGCCCCTGC      550
AGGACGTGTA CAAGATCGGC GGTATCGGGA CGGTGCCCCG GGGCCGCGTG      600
GAGACCGGGA TCATGAAGCC GGGCGACGTG GTGACGTTTC CGCCCGCCAA      650
CGTGACGACT GAGGTGAAGT CGATCGAGAT GCACCACGAG CAGCTGGCGG      700
AGGCGCAGCC CGGCGACAAC GTCGGCTTCA ACGTGAAGAA CGTGTGCGTG      750
AAGGACATCC GCCGTGGTAA CGTGTGCGGC AACTCGAAGA ACGACCCGCC      800
GAAGGAGGCG GCCGACTTCA CGGCGCAGGT GATCGTGCTG AACCACCCCG      850
GCCAGATCAG CAACGGCTAC GCGCCGGTGC TGGACTGCCA CACGAGCCAC      900
ATCGCGTGCC GCTTCGCGGA GATCGAGTCC AAGATCGACC GCCGCTCCGG      950
CAAGGAGCTG GAGAAGAACC CCAAGGCGAT CAAGTCTGGC GACGCCGCGA     1000
TCGTGAAGAT GGTGCCGCAG AAGCCGATGT GCGTGGAGGT GTTCAACGAC     1050
TACGCGCCGC TGGGCCGCTT TGCCGTGCGC GACATGCGCC AAACCGTTGC     1100
CGTCG                                         1105

```

2) INFORMATION FOR SEQ ID NO: 524

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1098 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania mexicana*
 (B) STRAIN: ATCC 50156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 524

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TACGCGTGGG TGCTCGACAA GCTGAAGGCG GAGCGCGAGC GCGGCATCAC      50

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	GATCGACATT	GCGCTGTGGA	AGTTCGAGTC	GCCGAAGTCC	GTGTTACGA	100
	TCATCGATGC	GCCCGGCCAC	CGCGACTTCA	TCAAGAACAT	GATCACGGGC	150
	ACGTCGCAGG	CGGACGCGGC	CATCCTGATG	ATCGACTCGA	CGCATGGTGG	200
	CTTCGAGGCT	GGCATCTCGA	AGGACGGCCA	GACCCGCGAG	CACGCGCTGC	250
5	TTGCCTTCAC	TCTTGGCGTG	AAGCAGATGG	TGGTGTGCTG	CAACAAGATG	300
	GACGACAAGA	CGGTGATGTA	CGCGCAGTCG	CGCTACGATG	AGATCAGCAA	350
	GGAGGTGAGC	GCGTACCTGA	AGCGCGTGGG	CTACAACCCG	GAGAAGGTGC	400
	GCTTCATCCC	GATCTCGGGG	TGGCAGGGCG	ACAACATGAT	CGACAAGTCG	450
	GACAACATGC	CGTGGTACAA	GGGTCCCACG	CTGCTGGACG	CGCTCGACAT	500
10	GCTGGAGCCG	CCGGTGCGCC	CGGTGGACAA	GCCGCTGCGC	CTGCCCCTGC	550
	AGGACGTGTA	CAAGATCGGC	GGTATCGGGA	CGGTGCCCCG	GGGCCGCGTG	600
	GAGACCGGGA	TCATGAAGCC	GGGCGACGTG	GTGACGTTTC	CGCCCGCCAA	650
	CGTGACGACT	GAGGTGAAGT	CGATCGAGAT	GCACCACGAG	CAGCTGGCGG	700
	AGGCGCAGCC	CGGCGACAAC	GTCGGCTTCA	ACGTGAAGAA	CGTGTCGGTG	750
15	AAGGACATCC	GCCGTGGTAA	CGTGTGCGGC	AACTCGAAGA	ACGACCCGCC	800
	GAAGGAGGCG	GCCGACTTCA	CGGCGCAGGT	GATCGTGCTG	AACCACCCCG	850
	GCCAGATCAG	CAACGGCTAC	GCGCCGGTGC	TGGACTGCCA	CACGAGCCAC	900
	ATCGCGTGCC	GCTTCGCGGA	GATCGAGTCC	AAGATCGACC	GCCGCTCCGG	950
	CAAGGAGCTG	GAGAAGAACC	CCAAGGCGAT	CAAGTCTGGC	GACGCCGCGA	1000
20	TCGTGAAGAT	GGTGCCGCAG	AAGCCGATGT	GCGTGGAGGT	GTTC AACGAC	1050
	TACGCGCCGC	TGGGCCGCTT	TGCCGTGCGC	GACATGCGCC	AAACCGTT	1098

25 2) INFORMATION FOR SEQ ID NO: 525

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 1081 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania tarentolae*
 (B) STRAIN: II WT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 525

40	GCTGAAGGCG	GAGCGCGAGC	GCGGCATCAC	GATCGACATT	GCGCTGTGGA	50
	AGTTCGAGTC	GCCCAAGTCG	GTGTTACGA	TCATCGATGC	GCCCGGCCAC	100
	CGCGACTTCA	TCAAGAACAT	GATCACGGGC	ACGTCGCAGG	CGGACGCGGC	150
	CATCCTGATG	ATCGACTCGA	CGCACGGTGG	GTTCGAGGCT	GGCATCTCGA	200
45	AGGACGGGCA	GACGCGCGAG	CACGCGCTGC	TTGCCTTCAC	TCTTGGCGTG	250
	AAGCAGATGG	TTGTGTGCTG	CAACAAGATG	GACGACAAGA	CGGTGATGTA	300
	CGCGCAGTCG	CGCTACGATG	AGATCAGCAA	GGAGGTGGGC	GCGTACCTGA	350
	AGCGCGTGGG	CTACAACCCG	GAGAAGGTGC	GCTTCATCCC	GATCTCGGGC	400
	TGGCAGGGCG	ACAACATGAT	CGAGAAGTCG	GACAACATGC	CGTGGTACAA	450
50	GGGTCCACG	CTGCTGGACG	CGCTCGACAT	GCTGGAGGCG	CCGGTGCGCC	500
	CGGTGGACAA	GCCGCTGCGC	CTGCCCCTGC	AGGACGTGTA	CAAGATCGGC	550
	GGCATCGGCA	CGGTGCCCCG	GGGCCGCGTG	GAGACCGGCA	TCATGAAGCC	600
	GGGCGACGTG	GTGACGTTTC	CGCCCGCGAA	CGTGACGACG	GAGGTGAAGT	650
	CGATCGAGAT	GCACCACGAG	CAGCTGGCGG	AGGCGCAGCC	CGGCGACAAC	700
55	GTCGGCTTCA	ACGTGAAGAA	CGTGTGCGTG	AAGGACATCC	GCCGTGGGAA	750
	CGTGTGCGGT	AACTCGAAGA	ACGACCCGCC	GAAGGAGGCC	GCCGACTTCA	800
	CGGCGCAGGT	GATCGTGCTG	AACCACCCCG	GCCAGATCAG	CAACGGCTAC	850
	GCGCCGCTGC	TGGACTGCCA	CACGAGCCAC	ATCGCGTGCC	GGTTCGCGGA	900
	CATCGAGTCC	AAGATTGACC	GCCGCTCCGG	CAAGGAGCTG	GAGAAGAACC	950
60	CCAAGGCGAT	CAAGTCCGGC	GATGCCGCGA	TCGTGAAGAT	GGTGCCGCAG	1000

AAGCCGATGT GCGTGGAGAT GTTCAACGAC TACGCGCCGC TTGGCCGCTT 1050
 TGCTGTGCGC GACATGCGCC AAACCGTTGC C 1081

5

2) INFORMATION FOR SEQ ID NO: 526

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 1102 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania tropica*
 (B) STRAIN: ATCC 50129

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 526

AAATACGCGT GGGTGCTCGA CAAGCTGAAG GCGGAGCGCG AGCGCGGCAT 50
 CACGATCGAC ATTGCGCTGT GGAAGTTCGA GTCGCCCAAG TCCGTGTTCA 100
 CGATCATCGA TGCGCCCGGC CACCGCGACT TCATCAAGAA CATGATCACG 150
 25 GGCACGTCGC AGGCGGACGC CGCCATCCTG ATGATCGACT CGACGCATGG 200
 TGGCTTCGAG GCTGGCATCT CGAAGGACGG CCAGACCCGC GAGCACGCGC 250
 TGCTTGCCCTT CACKCTTGGC GTGAAGCAGA TGGTGGTGTG CTGCAACAAG 300
 ATGGACGACA AGACGGTGAC GTACGCGCAG TCGCGCTACG ATGAGATCAG 350
 CAAGGAGGTG GGC GCGTACC TGAAGCGCGT GGGCTACAAC CCGGAGAAGG 400
 30 TGC GCTTCAT CCCGATCTCG GGCTGGCAGG GCGACAACAT GATCGAGAAG 450
 TCGGACAACA TGCCGTGGTA CAAGGGTCCC ACGCTGCTGG ACGCGCTCGA 500
 CATGCTGGAG CCGCCGGTGC GCCCGGTGGA CAAGCCGCTG CGCCTGCCCC 550
 TGCAGGACGT GTACAAGATC GGCGGTATCG GGACGGTGCC CGTGGGGCGC 600
 GTGGAGACCG GCATCATGAA GCCGGGCGAC GTGGTGACGT TCGCGCCCGC 650
 35 CAACGTGACG ACTGAGGTGA AGTCGATCGA GATGCACCAC GAGCAGCTGG 700
 CGGAGGCGCA GCCCGGCGAC AACGTCGGCT TCAACGTGAA GAACGTGTCTG 750
 GTGAAGGACA TCCGCCGTGG TAACGTGTGC GGCAACTCGA AGAACGACCC 800
 GCCGAAGGAG GCGGCCGACT TCACGGCGCA GGTGATCGTG CTGAACCACC 850
 CCGGCCAGAT CAGCAACGGC TACGCGCCGG TGCTGGACTG CCACACGAGC 900
 40 CACATTGCGT GCCGCTTCGC GGAAATCGAG TCCAAGATCG ACCGCCGCTC 950
 CGGCAAGGAG CTGGAGAAGA ACCCCAAGGC GATCAAGTCT GGCGATGCCG 1000
 CGATCGTGAA GATGGTGCCG CAGAAGCCGA TGTGCGTGGA GGTGTTCAAC 1050
 GACTACGCGC CGCTGGGCCG CTTTGCCGTG CGCGACATGC GCCAAACCGT 1100
 TG 1102

45

2) INFORMATION FOR SEQ ID NO: 527

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 1105 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

60 (A) ORGANISM: *Neospora caninum*
 (B) STRAIN: Suarez-4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 527

	GGACRAACTT	AAAGCTGAAC	GTGAGCGTGG	TATCACCATT	GATATCTCCC	50
5	TGTGGAAATT	TGAGACCAGC	AAGTACTATG	TTACCATCAT	TGATGCCCCA	100
	GGACACAGAG	ACTTCATCAA	AAACATGATT	ACAGGCACAT	CCCAGGCTGA	150
	CTGTGCTGTC	CTGATTGTTG	CTGCTGGTGT	TGGTGAATTT	GAAGCCGGTA	200
	TCTCCAAGAA	CGGGCAGACC	CGTGAGCATG	CCCTTNTGGC	TTACACCCTG	250
	GGTGTGAAAC	AACTAATTGT	TGGCGTTAAC	AAAAGKGATT	CCACTGAGCC	300
10	ACCCTATAGC	CARAAGAGAT	ACGARGAAAT	TGTTAAGGAA	GTCAGCMCCT	350
	AYNTTAAAAA	AATTGGYTAC	AACCCCGACA	CAGTANCATT	TGKGCCAATT	400
	TNTGGCTGGA	ATGGTGACAA	CATGCTGGAN	CCAAGTGCTA	ATATGCCATG	450
	GTTCAAGGGA	TGGAAGTCM	CCCGTAAGGA	CGGCAATGCC	AGKGGAACCM	500
	CCCTGCTTGA	AGCTYTGAT	TGCATTYTGC	CACCAAYTTG	CCCAACTGAC	550
15	AAACCCCTTG	GTTTGCCTYT	CCAGGATGTC	TATAAAATTG	GKGGTATTGG	600
	TACTGTCCCT	GTGGGTCGTG	TGGAGACTGG	TGTTCTCAA	CCTGGCATGG	650
	TGGTCACCTT	TGCTCCAGTC	AATGTAACAA	CTGAAGTGAA	GTCTGTAGAA	700
	ATGCACCATG	AAGCATTGAG	TGAAGCCCTT	CCTGGGGACA	ATGTGGGCTT	750
	CAATGTCAAG	AACGTGTCTG	TCAAAGATGT	CCGTCGTGGC	AATGTGGCTG	800
20	GTGACAGCAA	AAATGATCCA	CCCATGGAAG	CTGCTGGCTT	CACAGCTCAG	850
	GTGATTATTT	TGAACCATCC	AGGCCAAATC	AGTGCTGGAT	ATGCACCTGT	900
	GCTGGATTGT	CACACAGCTC	ACATTGCTTG	CAAGTTTGCT	GAGCTGAAGG	950
	AGAAGATTGA	TCGTCGTTCT	GGGAAAAAGC	TGGAAGATGG	CCCTAAATTC	1000
	TTGAAATCTG	GTGACGCTGC	CATCGTTGAT	ATGTTTCCTG	GCAAGCCCAT	1050
25	GTGTGTCGAG	AGCTTCTCTG	ATTATCCTCC	CCTGGGCCGT	TTTGCTGTGC	1100
	GTGAC					1105

30 2) INFORMATION FOR SEQ ID NO: 528

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 935 bases
 (B) TYPE: Nucleic acid
 35 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichomonas vaginalis*
 (B) STRAIN: ATCC 30001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 528

45	GCACATCCCA	GGCTGATGCT	GCTATCCTTG	TCATCGACTC	CACACTCGGT	50
	GGYTTCGAAG	CCGGTATCGC	TGAACAAGGC	CAGACACGTG	AACACGCTCT	100
	TCTTGCCTTC	ACACTCGGCA	TCAAGCAGGT	CATTGTGCGC	GTCAACAAGA	150
	TGGATGACAA	GACAGTCAAC	TACAACAAGG	CYCGTTTCGA	CGAAATCACA	200
50	GCCGAAATGA	CACGCATCCT	TACAGGCATC	GGCTACAAGC	CAGAAATGTT	250
	CCGCTTCGTC	CCAATCTCCG	GCTGGGCTGG	CGACAACATG	ACAGAGAAGT	300
	CTCCAAACAT	GCCATGGTAC	AATGGCCCAT	ACCTTCTTGA	AGCCCTCGAT	350
	TCCCTTCAGC	CACCAAAGCG	CCCATTCGAC	AAGCCACTCC	GTCTTCCACT	400
	CCAGGATGTC	TACAAGATCA	ACGGTATCGG	TACAGTTCCA	GTCGGCCGTG	450
55	TCGAATCCGG	CACAATGAAG	CCAGGCATGA	TCGTTAACCT	CGCCCCATCC	500
	ACAGTTACAG	CTGAAGTTAA	GTCCATCGAA	ATGCACCACG	AATCCCTTCC	550
	AGAGGCTCTT	CCAGGTGACA	ACATCGGCTT	CAACGTCAAG	AACGTTTCCA	600
	CAGCTGATGT	CAAGCGTGCC	TACGTCGTTG	GTGATACAAA	GCGTGACCCA	650
	CCAGTCGAAT	CGCCTTCCTT	CACAGCTCAR	ATGATCATCT	CCAACCACCC	700
60	AGGCAAGATC	CACGCCGGCT	ACCAGCCAGT	TTTCGACTGC	CACACAGCTC	750

ACATCGCCTG	CAAGTTCGAC	AAGCTCATCC	AGCGTATCGA	TCGTCGCCAC	800
GGCAAGAAGG	CTACAGAGAA	CCCAGAATAC	ATTCAGAAGG	ATGATGCCGC	850
TATCGTCGAG	GTTGTCCCAT	CCAAGCCACT	CGTCGTCGAG	TCCTTCCAGG	900
AGTACCCACC	ACTCGGCCGT	TTCGCCATCC	GTGAT		935

5

2) INFORMATION FOR SEQ ID NO: 529

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1065 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma brucei* subsp. *brucei*
- (B) STRAIN: EATRO795

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 529

AAGCTGAAGG	CTGAGCGCGA	ACGTGGTATC	ACGATCGACA	TTGCACTGTG	50
GAAATTCGAG	TCACCCAAGT	CTGTCTTCAC	TATTATTGAT	GCTCCTGGGC	100
ACCGTGACTT	CATCAAGAAC	ATGATCACCG	GCACATCGCA	AGCCGACGCA	150
GCCATCCTCA	TCATTGCCTC	TGCGCAGGGT	GAGTTCGAGG	CTGGTATCTC	200
CAAGGATGGA	CAGACCCGCG	AGCACGCGTT	GCTGGCCTTC	ACTTTGGGTG	250
TGAAGCAGAT	GGTTGTGTGC	TGCAACAAGA	TGGACGACAA	GACTGTGAAC	300
TACGGACAGG	AGCGGTATGA	CGAGATTGTG	AAGGAGGTGT	CTGCTTACAT	350
CAAGAAGGTT	GGGTACAACG	TGGAGAAGGT	GCGCTTCGTC	CCCATCTCCG	400
GATGGCAGGG	CGACAACATG	ATTGAGAAAT	CCGAGAAGAT	GCCATGGTAC	450
AAGGGTCCAA	CGCTCCTGGA	GGCACTAGAC	ATGCTGGAGC	CACCAGTGCG	500
TCCGAGCGAC	AAGCCCCTGC	GTCTGCCACT	GCAGGACGTG	TACAAGATCG	550
GTGGTATTGG	CACCGTGCCC	GTTGGTCGTG	TGGAGACCGG	CGTGATGAAG	600
CCTGGTGATG	TGGTGACGTT	TGCCCCCGCC	AACGTGACGA	CCGAGGTGAA	650
ATCGATCGAG	ATGCACCACG	AGCAGCTCGC	TGAGGCGACC	CCCGGTGACA	700
ACGTCCGGCTT	TAACGTGAAG	AACGTTTCTG	TAAAGGACAT	CCGCCGTGGC	750
AACGTCTGCG	GTAACACCAA	GAACGACCCC	CCAAAGGAGG	CCGCCGACTT	800
CACGGCACAG	GTGATCATCC	TGAACCACCC	CGGACAGATT	GGAAACGGTT	850
ATGCGCCCGT	GCTGGACTGC	CACACATCGC	ACATTGCCTG	CAAGTTCGCG	900
GAGATCGAGT	CGAAGATCGA	CCGTCGCTCT	GGCAAGGAGC	TGGAGAAGGC	950
TCCCAAGTCG	ATCAAGTCTG	GCGACGCCGC	GATCGTGCGC	ATGGTGCCGC	1000
AGAAGCCTAT	GTGCGTGGAG	GTCTTCAACG	ACTACGCGCC	ACTCGGCCGC	1050
TTTGCCGTGC	GTGAC				1065

45

2) INFORMATION FOR SEQ ID NO: 530

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1297 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Crithidia fasciculata*

60

(B) STRAIN: ATCC 11745

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 530

5	TTTCGCGGAGG	GCGTGCCGCC	GGTGCTGACG	GCGCTGGACG	TGACGGAGGA	50
	CCTCGGCCCG	GACGAGCCGC	TGACGCTGGA	GATTGTGCAG	CACTTGGACG	100
	CGAACACCGG	CCGCTGCATT	GCCATGCAGA	CGACGGATCT	GCTGAAGCTG	150
	AAGTCAAGG	TTGTGTGAC	GGGCGGCAAC	ATCTCCGTGC	CGGTGGCCG	200
	CGAGACGCTG	GGCCGCATCT	TCAACGTGCT	CGGCGACGCG	ATCGACCAGC	250
10	GCGGTGTGGT	GGGCGAGAAG	ATGCGCATGC	CGATCCACGC	CGAGGCGCCG	300
	AAGCTGGCGG	ACCAGGCCGC	GGAGGACGCG	ATTCTGACGA	CCGGCATCAA	350
	GGTGATCGAC	CTGATTCTGC	CGTACTGCAA	GGGTGGCAAG	ATCGGGCTGT	400
	TCGGCGGTGC	TGGTGTGGGC	AAGACTGTGA	TCATCATGGA	GCTGATCAAC	450
	AACGTGGCCA	AGGGCCACCG	TGGTTTCTCC	GTGTTCGCCG	GCGTTGGCGA	500
15	GCGCACCCGC	GAGGGCACCG	ATCTGTACCT	GGAGATGATG	CAGTCGAAGG	550
	TCATTGACCT	GAAGGGCGAG	TCGAAGTGCG	TGCTGGTGTA	CGGCCAGATG	600
	AACGAGCCCC	CGGGTGCGCG	TGCGCGTGTT	GCGCAGTCTG	CGCTGACGAT	650
	GGCGGAGTAC	TTCCGTGACG	TGGAGGGCCA	GAACGTGCTG	CTGTTCATCG	700
	ACAACATCTT	CCGCTTCACC	CAGGCCAACT	CCGAGGTGTC	CGCCCTGCTG	750
20	GGCCGCATTC	CCGCCGCCGT	GGGCTACCA	CCGACGCTTG	CCGAGGATCT	800
	TGGTATGCTG	CAGGAGCGCA	TTACGTGCGA	GACGAAGGGC	TCGATTACGT	850
	CTGTGCAGGC	CGTGTACGTG	CCGGCCGATG	ATATCACGGA	TCCGGCGCCG	900
	GCGACGACCT	TCTCGCACCT	GGATGCGACG	ACGGTGCTGG	ACCGCGCGGT	950
	TGCCGAGTCT	GGCATCTACC	CCGCCGTGAA	CCCGCTGGAG	TGCGCGTCGC	1000
25	GTATCATGGA	CCCCGATGTG	ATCGACGTGG	ACCACTACAA	CGTTGCGCAG	1050
	GATATCGTGC	AGATGCTGAC	CAAGTACAAG	GAGCTGCAGG	ATATCATTCG	1100
	CGTGCTGGGT	ATCGACGAGC	TGAGCGAGGA	GGACAAGCTT	GTGGTGGACC	1150
	GCGCTCGCAA	GGTGACGCGC	TTCCTGTGCG	AGCCGTTCCA	GGTGGCCGAG	1200
	GTGTTACCG	GCATGACGGG	CCACTACGTG	CAGCTGGAGG	ACACAGTGGA	1250
30	GTCGTTCTCT	GGCCTGCTGA	TGGGCTCGTA	CGACCAGATC	CCGGAGA	1297

2) INFORMATION FOR SEQ ID NO: 531

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1298 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

45

- (A) ORGANISM: *Leishmania tropica*
 (B) STRAIN: ATCC 30816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 531

50	CTTCTCGGAG	GGCGTGCCGC	CCGTGCTGAC	GGCGCTGGAT	GTGACGGAGG	50
	ACCTTGGCCG	CGATGAGCCG	CTGACGCTGG	AGATCGTGCA	GCACTTGGAC	100
	GCGAACACCG	GCCGCTGCAT	TGCGATGCAG	ACGACGGACC	TGCTGAAGCT	150
	GAAGTCGAAG	GTCGTGTCGA	CCGGCGGCAA	CATCTCTGTG	CCGGTGGGCC	200
	GTGAGACGCT	GGGCCGCATC	TTCAAYGTTT	TGGGCGACGC	GATCGACCAG	250
55	CGCGGCCCCG	TGGGCGAGAA	GATGCGCATG	GCGATCCACG	CCGAGGCCCC	300
	GAAGCTGGCG	GATCAGGCCG	CGGAGGACAC	GATCCTGACG	ACCGGCATCA	350
	AGGTGATCGA	CCTGATTCTG	CCCTACTGCA	AGGGTGGCAA	GATCGGCCTG	400
	TTCGGCGGTG	CCGGTGTGGG	CAAGACTGTG	ATCATCATGG	AGCTGATCAA	450
	CAACGTCGCG	AAGGGCCACG	GCGGTTTCTC	CGTGTTTGCC	GGCGTTGGCG	500
60	AGCGCACGCG	CGAGGGCACG	GACCTGTACC	TGGAGATGAT	GCAGTCGAAG	550

	GTGATTGACC	TGAAGGGCGA	GTCGAAGTGY	GTGCTTGTGT	ATGGGCAGAT	600
	GAACGAGCCC	CCGGGTGCGC	GCGCGCGCGT	TGCGCAGTCT	GCGCTGACGA	650
	TGGCGGAGTA	CTTCCGCGAC	GTGGAGGGCC	AGAACGTGCT	GCTGTTCATC	700
	GACAACATCT	TCCGCTTCAC	GCAGGCGAAC	TCCGAGGTGT	CTGCGCTGCT	750
5	GGGCCGCATT	CCGGCCGCGG	TGGGCTACCA	GCCGACGCTT	GCGGAGGATC	800
	TTGGTATGCT	GCAGGAGCGC	ATCACGTCGA	CAACGAAGGG	GTCGATCACG	850
	TCCGTGCAGG	CCGTGTACGT	GCCAGCGGAT	GATATCACGG	ATCCCGCGCC	900
	CGCGACGACG	TTCTCGCACC	TGGACGCGAC	GACTGTGCTG	GACCGCGCGG	950
	TGGCGGAGTC	GGGCATCTAC	CCTGCCGTGA	ACCCGCTGGA	GTGCGCGTCC	1000
10	CGTATCATGG	ACCCTGATGT	GATCGATGTG	GACCACTACA	ACGTTGCGCA	1050
	GGATATCGTG	CAGATGCTGA	CCAAGTACAA	GGAGCTGCAG	GATATCATTG	1100
	CGGTGCTTGG	CATCGACGAG	CTGAGCGAGG	AAGACAAGGT	TGTTGTGGAC	1150
	CGCGCGCGCA	AGGTGACCCG	GTTCTGTGCG	CAGCCGTTCC	AGGTTGCGGA	1200
	GGTGTTCACG	GGCATGACGG	GCCACTACGT	GCAGCTGGTC	GACACGGTGG	1250
15	AGTCGTTCTC	TGGCCTGCTG	ATGGGGTTCG	ACGACCAGAT	CCCGGAGA	1298

2) INFORMATION FOR SEQ ID NO: 532

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1297 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania aethiopica*
 (B) STRAIN: ATCC 50119

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 532

35	TTCTCGGAGG	GCGTGCCGCC	CGTGCTGACG	GCGCTGGATG	TGACGGAGGA	50
	CCTTGGCCGC	GATGAGCCGC	TGACGCTGGA	GATCGTGCAG	CACTTGGACG	100
	CGAACACCGG	CCGCTGCATT	GCGATGCAGA	CGACGGACCT	GCTGAAGCTG	150
	AAGTCGAAGG	TTGTGTCGAC	CGGCGGCAAC	ATCTCTGTGC	CGGTGGGCCG	200
	TGAGACGCTG	GGCCGCATCT	TCAACGTTCT	GCGCGACGCG	ATCGACCAGC	250
40	GCGGCCCCGT	GGGCGAGAAG	ATGCGCATGG	CGATCCACGC	CGAGGCCCCA	300
	AAGCTGGCGG	ATCAGGCCGC	GGAGGACACG	ATCCTGACGA	CCGGCATCAA	350
	GGTGATCGAC	CTGATTCTGC	CCTACTGCAA	GGGTGGCAAG	ATCGGCCTGT	400
	TCCGCGGTGC	CGGTGTGGGC	AAGACTGTGA	TCATCATGGA	GCTGATCAAC	450
	AACGTCGCGA	AGGGCCACGG	TGGTTTCTCC	GTGTTTGCCG	GCGTTGGCGA	500
45	GCGCACGCGC	GAGGGCACGG	ACCTGTACCT	GGAGATGATG	CAGTCGAAGG	550
	TGATTGACCT	GAAGGGCGAG	TCGAAGTGCG	TGCTTGTTGTA	CGGGCAGATG	600
	AACGAGCCCC	CGGGTGCGCG	CGCGCGCGTT	GCGCAGTCTG	CGCTGACGAT	650
	GGCGGAGTAC	TTCCGCGACG	TGGAGGGCCA	GAACGTGCTG	CTGTTTCATCG	700
	ACAACATCTT	CCGCTTCACG	CAGGCGAACT	CCGAGGTGTC	TGCGCTGCTG	750
50	GGCCGCATTG	CAGCCGCCGT	GGGCTACCAG	CCGACGCTTG	CGGAGGATCT	800
	TGGTATGCTG	CAGGAGCGCA	TCACGTCGAC	AACGAAGGGG	TCGATCACGT	850
	CCGTGCAGGC	CGTGATACGT	CCAGCGGATG	ATATCACGGA	TCCCGCGCCC	900
	GCGACGACGT	TCTCGCACCT	GGACGCGACG	ACTGTGCTGG	ACCGCGCGGT	950
	GGCGGAGTCG	GGCATCTACC	CTGCCGTGAA	CCCGCTGGAG	TGCGCGTCGC	1000
55	GTATCATGGA	CCCCGACGTG	ATCGATGTGG	ACCACTACAA	CGTTGCGCAG	1050
	GATATCGTGC	AGATGCTGAC	CAAGTACAAG	GAGCTGCAGG	ATATCATTGC	1100
	GGTGCTTGGC	ATCGACGAGC	TGAGCGAGGA	AGACAAGGTT	GTTGTGGACC	1150
	GCGCGCGCAA	GGTGACCCGG	TTCTGTGTCG	AGCCGTTCCA	GGTTGCGGAG	1200
	GTGTTTCACG	GCATGACGGG	CCACTACGTG	CAGCTGGTCC	ACACGGTGGA	1250
60	GTCGTTCTCT	GGCCTGCTGA	TGGGGTTCGTA	CGACCAGATC	CCGGAGA	1297

2) INFORMATION FOR SEQ ID NO: 533

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1298 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania donovani* subsp. *donovani*
 (B) STRAIN: ATCC 50212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 533

20	CTTCTCGGAG	GGCGTGCCGC	CCGTACTGAC	GGCGCTGGAT	GTGACGGAGG	50
	ACCTTGGCCG	CGATGAGCCG	CTGACGCTGG	AGATCGTGCA	GCACTTGGAT	100
	GCGAACACCG	GCCGCTGCAT	TGCGATGCAG	ACGACGGACC	TGCTGAAGCT	150
	GAAGTCGAAG	GTTGTGTCTGA	CCGGCGGCAA	CATCTCTGTG	CCGGTGGGCC	200
	GTGAGACGCT	GGGCCGCGATC	TTCAACGTTC	TGGGCGACGC	GATCGACCAG	250
25	CGCGGCCCCG	TGGGCGAGAA	GATGCGCATG	GCGATCCACG	CCGAGGCCCC	300
	GAAGCTGGCG	GACCAGGCCG	CGGAGGACAC	GATCCTGACG	ACCGGCATCA	350
	AGGTGATCGA	CCTCATTCTG	CCCTACTGCA	AGGGCGGCAA	GATCGGCCTG	400
	TTCGGCGGTG	CCGGTGTGGG	CAAGACTGTG	ATCATCATGG	AGCTGATCAA	450
	CAACGTCGCG	AAGGGCCACG	GTGGCTTCTC	CGTGTTTGCC	GGCGTTGGCG	500
30	AGCGCACGCG	CGAGGGCACG	GACCTATACC	TGGAGATGAT	GCAGTCGAAG	550
	GTGATTGACC	TGAAGGGCGA	GTCGAAGTGC	GTGCTTGTGT	ACGGGCAGAT	600
	GAACGAGCCC	CCGGGTGCGC	GCGCGCGCGT	TGCGCAGTCT	GCGCTGACGA	650
	TGGCGGAGTA	CTTCCGCGAC	GTGGAGGGCC	AGAACGTGCT	GCTGTTTCATC	700
	GACAACATCT	TCCGCTTCAC	GCAGGCGAAG	TCCGAGGTGT	CTGCGCTGCT	750
35	GGGCCGCATT	CCGGCCGCCG	TGGGCTACCA	GCCGACGCTT	GCCGAGGATC	800
	TTGGTATGCT	GCAGGAGCGC	ATCACATCGA	CGACGAAGGG	GTCGATCACG	850
	TCCGTGCAGG	CCGTGTACGT	GCCGGCGGAT	GATATCACGG	ATCCCGCGCC	900
	CGCGACGACG	TTCTCGCACC	TGGACGCGAC	GACTGTGCTG	GACCGCGCGG	950
	TGGCGGAGTC	GGGCATCTAC	CCTGCCGTGA	ACCCGCTGGA	GTGCGCGTCG	1000
40	CGTATCATGG	ACCCCGATGT	GATCGATGTG	GACCACTACA	ACGTTGCGCA	1050
	GGATATCGTG	CAGATGCTGA	CCAAGTACAA	GGAGCTGCAG	GATATCATTG	1100
	CGGTGCTTGG	CATCGACGAG	CTGAGCGAGG	AGGACAAGGT	TGTGGTGGAC	1150
	CGCGCGCGCA	AGGTGACCCG	GTTCTGTGTC	CAGCCGTTCC	AGGTTGCGGA	1200
	GGTGTTCACG	GGCATGACGG	GCCACTACGT	GCAGCTGGCC	GACACGGTGG	1250
45	AGTCGTTCTC	TGGCCTGCTG	ATGGGGTCGT	ACGACCAGAT	CCCGGAGA	1298

2) INFORMATION FOR SEQ ID NO: 534

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1298 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania donovani* subsp. *infantum*

(B) STRAIN: MOU

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 534

```

5  CTTCTCGGAG GGCCTGCCGC CCGTACTGAC GGCCTGGAT GTGACGGAGG      50
   ACCTTGCCCG CGATGAGCCG CTGACGCTGG AGATCGTGCA GCACTTGGAT      100
   GCGAACACCG GCCGCTGCAT TGCATGACAG ACGACGGACC TGCTGAAGCT      150
   GAAGTCGAAG GTTGTGTCTGA CCGGCGGCAA CATCTCTGTG CCGGTGGGCC      200
   GTGAGACGCT GGGCCGCATC TTCAACGTTT TGGGCGACGC GATCGACCAG      250
10  CGCGGCCCCG TGGGCGAGAA GATGCGCATG GCGATCCACG CCGAGGCCCC      300
   AAAGCTGGCG GACCAGGCCG CGGAGGACAC GATCCTGACG ACCGGCATCA      350
   AGGTGATCGA CCTCATTCTG CCCTACTGCA AGGCGGCAA GATCGGCCTG      400
   TTCGGCGGTG CCGGTGTGGG CAAGACTGTG ATCATCATGG AGCTGATCAA      450
   CAACGTCCGC AAGGGCCACG GTGGCTTCTC CGTGTGTTGCC GGCCTTGGCG      500
15  AGCGCACGCG CGAGGGCACG GACCTATACC TGGAGATGAT GCAGTCGAAG      550
   GTGATTGACC TGAAGGGCGA GTCGAAGTGC GTGCTTGTGT ACGGGCAGAT      600
   GAACGAGCCC CCGGGTGCGC GCGCGCGCGT TCGCAGTCT GCGCTGACGA      650
   TGGCGGAGTA CTTCCGCGAC GTGGAGGGCC AGAACGTGCT GCTGTTTCATC      700
   GACAACATCT TCCGCTTCAC GCAGGCGAAG TCCGAGGTGT CTGCGCTGCT      750
20  GGGCCGCATT CCGGCCGCGG TGGGCTACCA GCCGACGCTT GCCGAGGATC      800
   TTGGTATGCT GCAGGAGCGC ATCACATCGA CGACGAAGGG GTCGATCAGC      850
   TCCGTGCAGG CCGTGTACGT GCCGGCGGAT GATATCACTG ATCCCGCGCC      900
   CGCGACGACG TTCTCGCACC TGGACGCGAC GACTGTGCTG GACCGCGCGG      950
   TGGCGGAGTC GGGCATCTAC CCTGCCGTGA ACCCGCTGGA GTGCGCGTCG      1000
25  CGTATCATGG ACCCCGATGT GATCGATGTG GACCACTACA ACGTTGCGCA      1050
   GGATATCGTG CAGATGCTGA CCAAGTACAA GGAGCTGCAG GATATCATTG      1100
   CCGTGCTTGG CATCGACGAG CTGAGCGAGG AGGACAAGGT TGTGGTGGAC      1150
   CGCGCGCGCA AGGTGACCCG GTTCCTGTCT CAGCCGTTCC AGGTTGCGGA      1200
   GGTGTTTACG GGCATGACGG GCCACTACGT GCAGCTGGCC GACACGGTGG      1250
30  AGTCGTTCTC TGGCCTGCTG ATGGGGTCTG ACGACCAGAT CCCGGAGA      1298

```

2) INFORMATION FOR SEQ ID NO: 535

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1301 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

45

- (A) ORGANISM: *Leishmania gerbilli*
- (B) STRAIN: ATCC 50121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 535

```

50  GCACTTCTCG GAGGGCGTGC CGCCCGTGCT GACGGCGCTG GATGTGACGG      50
   AGGACCTTGG CCGCGATGAG CCGCTGACGC TGGAGATCGT GCAGCACTTG      100
   GACGCGAACA CCGGCCGCTG CATTGCGATG CAGACGACGG ACCTGCTGAA      150
   GCTGAAGTCG AAGGTTGTGT CGACCGGTGG CAACATCTCT GTGCCGGTGG      200
   GCCGTGAGAC CCGTGGGCCG ATCTTCAACG TTCTGGGCGA TGCGATCGAC      250
55  CAGCGCGGCC CCGTGGGCGA GAAGATGCGC ATGGCGATCC ACGCCGAGGC      300
   CCCGAAGCTG GCGGATCAGG CCGCGGAGGA CACGATCCTG ACGACCGGCA      350
   TCAAGGTGAT CGACCTGATT CTGCCCTACT GCAAGGGTGG CAAGATCGGY      400
   CTGTTCCGGC GTGCCGGTGT GGGCAAGACT GTGATCATCA TGGAGCTGAT      450
   CAACAACGTC GCGAAGGGCC ACGGTGGTTT CTCCGTGTTT GCCGGCGTTG      500
60  GCGAGCGCAC GCGCGAGGGC ACGGACCTGT ACCTGGAGAT GATGCAGTCG      550

```

	AAGGTGATTG	ACCTGAAGGG	CGAGTCGAAG	TGCGTGCTTG	TGTACGGGCA	600
	GATGAACGAG	CCCCCGGGTG	CGCGCGCGCG	CGTTGCGCAG	TCTGCGCTGA	650
	CGATGGCGGA	GTACTTCCGC	GACGTGGAGG	GCCAGAACGT	GCTGCTGTTC	700
	ATCGACAACA	TCTTCCGCTT	CACGCAGGCG	AACTCCGAGG	TGTCCGCGCT	750
5	GCTGGGCCGC	ATTCCGGCCG	CCGTGGGCTA	CCAGCCGACG	CTTGCGGAGG	800
	ATCTTGGTAT	GCTGCAGGAG	CGCATCACGT	CGACAACGAA	GGGGTTCGATC	850
	ACGTCCGTGC	AGGCCGTGTA	CGTGCCAGCG	GATGATATCA	CGGATCCCCG	900
	GCCCCGCGACG	ACGTTCTCGC	ACCTTGACGC	GACGACTGTG	CTGGACCGCG	950
	CGGTGGCGGA	GTCGGGCATC	TACCCTGCCG	TGAACCCGCT	GGAGTGCGCG	1000
10	TCGCGTATCA	TGGACCCCGA	TGTGATCGAT	GTGGACCACT	ACAACGTTGC	1050
	GCAGGATATC	GTGCAGATGC	TGACCAAGTA	CAAGGAGCTG	CAGGACATCA	1100
	TTGCGGTGCT	TGGCATCGAC	GAGCTGAGCG	AGGAAGACAA	GGTTGTGGTG	1150
	GACCGCGCGC	GCAAGGTGAC	CCGGTTCCTG	TCGCAGCCGT	TCCAGGTTGC	1200
	GGAGGTGTTT	ACGGGCATGA	CGGGCCACTA	CGTGCACTG	GTCGACACGG	1250
15	TGGAGTCGTT	CTCTGGCTTG	CTGATGGGGT	CGTACGACCA	GATCCCGGAG	1300
	A					1301

20 2) INFORMATION FOR SEQ ID NO: 536

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1298 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania hertigi* subsp. *hertigi*
 (B) STRAIN: ATCC 50125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 536

35	CTTCGCGGAG	GGCGTGCCGC	CGGTGCTGAC	GTCGCTGGAT	GTGACGGAGA	50
	ACCTCGGCCG	CGATGAGCCG	CTGACGCTGG	AGATTGTGCA	GCACTTGGAC	100
	GCGAACACCG	GTCGCTGCAT	TGCGATGCAG	ACGACGGACC	TGCTGAAGCT	150
	GAAGTCGAAG	GTCGTGTCGA	CCGGTGGCAA	CATCTCTGTG	CCTGTTGGCC	200
40	GCGAGACGCT	GGGTGCGATC	TTCAACGTGC	TTGGCGATGC	GATTGACCAG	250
	CGCGGCCCTG	TGGGTGAGAA	GATGCGCATG	GCGATCCACG	CCGAGGCGCC	300
	GAAGCTGGCG	GATCAGGCGG	CAGAGGACAC	GATCCTGACG	ACCGGCATCA	350
	AGGTGATCGA	TCTTATTCTG	CCGTACTGCA	AGGGTGGTAA	GATCGGTCTG	400
	TTCCGGTGGTG	CCGGTGTAGG	CAAGACTGTG	ATTATTATGG	AGCTGATCAA	450
45	TAACGTGGCG	AAGGGCCACG	GTGGGTTTTC	CGTGTTTGCT	GGCGTGGGCG	500
	AGCGCACGCG	CGAGGGCACT	GACCTGTACC	TGGAGATGAT	GCAGTCGAAG	550
	GTGATTGACC	TGAAGGGCGA	ATCAAAGTGC	GTGCTTGTTG	ACGGACAGAT	600
	GAACGAGCCC	CCGGGTGCGC	GTGCGCGCGT	TGCGCAGTCT	GCGCTGACGA	650
	TGGCCGAGTA	CTTCCGCGAT	GTGGAGGGCC	AGAACGTGCT	GCTGTTTATT	700
50	GACAACATCT	TCCGCTTCAC	GCAGGCGAAC	TCCGAGGTGT	CTGCGCTGCT	750
	GGGTCGCATT	CCTGCCGCCG	TGGGCTACCA	GCCGACGCTT	GCGGAGGATC	800
	TGGGCATGCT	GCAGGAGCGC	ATTACGTCGA	CGACGAAGGG	CTCGATTACG	850
	TCTGTGCAGG	CCGTGTACGT	GCCTGCGGAT	GATATCACGG	ACCCGGCGCC	900
	CGCGACGACG	TTCTCGCACC	TGGACGCGAC	GACTGTGCTG	GACCGTGCGG	950
55	TGGCAGAGTC	GGGCATTTAC	CCTGCGGTGA	ACCCGCTGGA	GTGCGCGTCG	1000
	CGTATCATGG	ACCCCGATGT	GATCGATGTG	GACCACTACA	ACGTTGCGCA	1050
	GGATATCGTG	CAGATGCTGA	CCAAGTACAA	GGAGCTGCAG	GATATCATTT	1100
	CCGTGCTTGG	TATCGACGAG	CTGAGCGAGG	AGGACAAGGT	TGTGGTGGAC	1150
	CGCGCGCGCA	AGGTGACCCG	GTTCTGTGTC	CAGCCGTTCC	AGGTTGCGGA	1200
60	GGTGTTCACT	GGCATGACGG	GTCACTACGT	TCAGCTGGAG	GACACGGTGG	1250

AGTCGTTCTC TGGCCTACTG ATGGGGTCAT ACGACCAGAT CCCGGAGA

1298

5 2) INFORMATION FOR SEQ ID NO: 537

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 1297 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania major*
 (B) STRAIN: ATCC 50122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 537

20 CTTCTCGGAG GGCCTGCCGC CCGTGCTGAC GCGCTGGAT GTGACGGAGG 50
 ACCTTGGCCG TGATGAGCCG CTGACGCTGG AGATCGTGCA GCACTTGGAC 100
 GCGAACACCG GCCGCTGCAT TGCATGACAG ACGACGGACC TGCTGAAGCT 150
 GAAGTCGAAG GTTGTGTCTGA CCGGCGGCAA CATCTCTGTG CCGGTGGGCC 200
 25 GTGAGACGCT GGGCCGCATC TTCAACGTTT TGGGCGATGC GATCGACCAG 250
 CGCGGCCCCG TGGGCGAGAA GATGCGCATG GCGATCCACG CCGAGGCCCC 300
 GAAGCTGGCG GATCAGGCCG CAGAGGACAC GATCCTGACG ACCGGCATCA 350
 AGGTGATCGA CTTGATCCTG CCCTACTGCA AGGGTGGCAA GATCGGCCTG 400
 TTCGGCGGTG CCGGTGTGGG CAAGACTGTG ATCATCATGG AGCTGATCAA 450
 30 CAATGTGCGC AAGGGCCACG GTGGTTTCTC CGTGTGTTGCC GGCGTTGGCG 500
 AGCGCACGCG CGAGGGCACG GACCTGTACC TGGAGATGAT GCAGTCGAAG 550
 GTGATTGACC TGAAGGGCGA GTCGAAGTGC GTGCTTGTGT ACGGGCAGAT 600
 GAACGAGCCC CCGGGTGCGC GCGCGCGCGT TCGCGAGTCT GCGCTGACGA 650
 TGGCGGAGTA CTTCCGCGAC GTGGAGGGCC AGAACGTGCT GCTGTTCATC 700
 35 GACAACATCT TCCGCTTCAC GCAGGCGAAC TCCGAGGTGT CCGCGCTGCT 750
 GGGCCGCATT CCGGCCGCCG TGGGCTACCA GCCGACGCTT GCGGAGGATC 800
 TTGGTATGCT GCAGGAGCGC ATCACGTCGA CAACGAAGGG GTCGATCACG 850
 TCCGTGCAGG CCGTGTACGT GCCAGCGGAT GATATCACGG ATCCCGCGCC 900
 CGCGACGACG TTCTCGCACC TGGATGCGAC GACTGTGCTG GACCGCGCGG 950
 40 TGGCGGAGTC GGGCATCTAC CCTGCCGTGA ACCCGCTGGA GTGCGCGTCG 1000
 CGTATCATGG ACCCCGATGT GATCGATGTG GACCACTACA ACGTTGCGCA 1050
 GGATATCGTG CAGATGCTGA CCAAGTACAA GGAGCTGCAG GACATCATTTG 1100
 CCGGTGCTTGG CATCGACGAG CTGAGCGAGG AAGACAAGGT TGTGGTGGAC 1150
 CGCGCGCGCA AGGTGACCCG GTTCCTGTCT CAGCCGTTCC AGGTTGCGGA 1200
 45 GGTGTTTACG GGCATGACGG GCCACTACGT GCAGCTGGTC GACACGGTGG 1250
 AGTCGTTCTC TGGCCTGCTG ATGGGGTCGT ACGACCAGAT CCCGGAG 1297

50 2) INFORMATION FOR SEQ ID NO: 538

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 1297 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania amazonensis*
 (B) STRAIN: ATCC 50131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 538

```

5      TTCTCGGAGG GCGTGCCGCC CGTGCTGACG GCGCTGGATG TGACGGAGGA      50
      CCTTGGCCGC GATGAGCCGC TGACGCTGGA GATCGTGCAG CACCTGGACG      100
      CGAACACCGG CCGCTGCATT GCGATGCAGA CGACGGACCT GTTGAAGCTG      150
      AAGTCGAAGG TTGTGTCGAC CGGCGGCAAC ATCTCTGTGC CGGTGGGCCG      200
10     TGAGACGCTG GGCCGCATCT TCAACGTGCT GGGCGACGCG ATCGACCAGC      250
      GCGGCCCCGT GGGTGAGAAG ATGCGCATGG CGATCCACGC CGAGGCCCCG      300
      AAGCTGGCGG ATCAGGCCGC GGAGGACACG ATCCTGACGA CCGGCATCAA      350
      GGTGATCGAC CTGATTCTGC C'TACTGCAA GGGTGGCAAG ATCGGCCTGT      400
      TTGGTGGCGC CGGTGTGGGC AAGACCGTGA TCATCATGGA GTTGATTAAC      450
15     AACGTCGCGA AGGGCCACGG TGGTTTCTCG GTGTTTGCCG GCGTTGGCGA      500
      GCGCACGCGC GAGGGCACGG ACCTGTACCT GGAGATGATG CAGTCGAAGG      550
      TGATTGACCT GAAGGGCGAG TCGAAGTGCG TGCTTGTA TA CGGGCAGATG      600
      AACGAGCCCC CGGGTGCGCG CGCGCGCGTT GCGCAGTCTG CGCTGACGAT      650
      GGCGGAGTAC TTCCGAGACG TGGAGGGCCA GAATGTGCTG CTGTTTCATCG      700
20     ACAACATCTT CCGCTTCACG CAGGCGAACT CCGAGGTGTC TGCGCTGCTG      750
      GGCCGCATTC CGGCCGCCGT GGGCTACCAG CCGACGCTTG CCGAGGATCT      800
      TGGTATGCTG CAGGAGCGCA TCACGTCGAC GACGAAGGGG TCGATCACGT      850
      CCGTGCAGGC CGTGTACGTG CCTGCGGATG ATATCACGGA TCCGGCGCCC      900
      GCGACGACGT TCTCGCACCT GGACGCGACG ACTGTGCTGG ACCGCGCGGT      950
25     GGCGGAGTCG GGGATCTACC CTGCCGTGAA CCCGCTGGAG TGCGCGTCGC      1000
      GTATCATGGA CCCCGATGTG ATCGACGTGG ACCACTACAA CGTTGCGCAG      1050
      GATATCGTGC AGATGCTGAC CAAGTACAAG GAGCTGCAGG ATATCATTGC      1100
      GGTGCTTGGT ATCGACGAGC TGAGCGAGGA GGACAAGGTC GTGGTGGACC      1150
      GCGCGCGCAA GGTGACCCGG TTCCTGTCGC AGCCGTTCCA GGTGCGGAG      1200
30     GTGTTACCGG GCATGACGGG CCACTACGTG CAGCTGGCCG ACACGGTGGA      1250
      GTCGTTCTCT GGGCTGCTGA TGGGGTCGTA CGACCAGATC CCGGAGA      1297
  
```

35 2) INFORMATION FOR SEQ ID NO: 539

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 bases
 (B) TYPE: Nucleic acid
 40 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 539

CCITACATCC TBGTYGCICT IAACAAG

27

50

2) INFORMATION FOR SEQ ID NO: 540

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases
 55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 540

GGDGCITCYT CRTCGWAITC CTG

23

5

2) INFORMATION FOR SEQ ID NO: 541

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 541

GTKGAAATGT TCCGCAAGCT GCT

23

20

2) INFORMATION FOR SEQ ID NO: 542

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 542

CGGAARTAGA ACTGSGGACG GTAG

24

35

2) INFORMATION FOR SEQ ID NO: 543

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 543

ATCTTAGTAG TTTCTGCTGC TGA

23

50

2) INFORMATION FOR SEQ ID NO: 544

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

55

60

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 544

AYGTTGTCGC CMGGCATTMC CAT

23

10

2) INFORMATION FOR SEQ ID NO: 545

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 545

TACATCCTBG TYGCICTIAA CAAGTG

26

25

2) INFORMATION FOR SEQ ID NO: 546

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 546

CCRCGICCGG TRATGGTGAA GAT

23

40

2) INFORMATION FOR SEQ ID NO: 547

45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 547

55 GTACAGTTGC TTCAGGACGT ATC

23

60

2) INFORMATION FOR SEQ ID NO: 548

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 548

ACGTTTCGATT TCATCACGTT G

21

2) INFORMATION FOR SEQ ID NO: 549

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 549

GAACGTGATA CTGACAAACC TTTA

24

2) INFORMATION FOR SEQ ID NO: 550

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 550

GAAGAAGAAC ACCAACGTTG

20

2) INFORMATION FOR SEQ ID NO: 551

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria gonorrhoeae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 551

GAAGAAAAAA TCTTCGAACT GGCTA

25

2) INFORMATION FOR SEQ ID NO: 552

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria gonorrhoeae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 552

TACACGGCCG GTGACTACG

19

2) INFORMATION FOR SEQ ID NO: 553

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 553

GGCCGTGTTG AACGTGGTCA AATCA

25

2) INFORMATION FOR SEQ ID NO: 554

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Chlamydia trachomatis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 554

G TTCCTTACA TCGTTGTTTT TCTC

24

5

2) INFORMATION FOR SEQ ID NO: 555

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Chlamydia trachomatis*

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 555

TCTCGAACTT TCTCTATGTA TGCA

24

25

2) INFORMATION FOR SEQ ID NO: 556

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 556

CGGCGCNATC YTS GTTGTTG C

21

40

2) INFORMATION FOR SEQ ID NO: 557

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 557

CCMAGGCATR ACCATCTCGG TG

22

55

2) INFORMATION FOR SEQ ID NO: 558

60 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 558

10 TCITTYAART AYGCTGGGT

20

2) INFORMATION FOR SEQ ID NO: 559

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 559

25

CCGACRGCRA YIGTYTGICK CAT

23

2) INFORMATION FOR SEQ ID NO: 560

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 560

40

GAYTTCATYA ARAAYATGAT YAC

23

2) INFORMATION FOR SEQ ID NO: 561

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 561

55

ACIGTICGGC CRCCCTCACG GAT

23

60

2) INFORMATION FOR SEQ ID NO: 562

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 562

CARATGRAYG ARCCICCIGG IGYIMGIATG

30

2) INFORMATION FOR SEQ ID NO: 563

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 563

GGYTGRTAIC CIACIGCIGA IGGCAT

26

2) INFORMATION FOR SEQ ID NO: 564

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 564

TAYGGICARA TGAAYGARCC ICCIGGIAA

29

2) INFORMATION FOR SEQ ID NO: 565

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 565

GGYTGRTAIC CIACIGCIGA IGGDAT

26

5

2) INFORMATION FOR SEQ ID NO: 566

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 566

TTYGGIGGIG CIGGIGTIGG IAARAC

26

20

2) INFORMATION FOR SEQ ID NO: 567

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 567

TCRTCIGCIG GIACRTAIAY IGCYTG

26

35

2) INFORMATION FOR SEQ ID NO: 568

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 568

50 RTIATIGGIG CIGTIRTIGA YGT

23

2) INFORMATION FOR SEQ ID NO: 569

55

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 569

5

RTIRTIGGIS CIGTIRTIGA TAT

23

10 2) INFORMATION FOR SEQ ID NO: 570

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

15

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 570

RTIRYIGGIC CIGTIRTIGA YGT

23

25

2) INFORMATION FOR SEQ ID NO: 571

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

30

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 571

RTIRTIGGIC CIGTIRTIGA TGT

23

40

2) INFORMATION FOR SEQ ID NO: 572

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

45

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 572

RTIRTIGGIS CIGTIRTIGA

20

55

2) INFORMATION FOR SEQ ID NO: 573

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 573

10 CCICCIACCA TRTARAAIGC

20

2) INFORMATION FOR SEQ ID NO: 574

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

20

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 574

25

ATIGCIATGG AYGGIACIGA RGG

23

2) INFORMATION FOR SEQ ID NO: 575

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 575

40

TIACCATTTC AGTACCTTCT GGTA

25

2) INFORMATION FOR SEQ ID NO: 576

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 576

55

AACTTCRTCA AGAAGGTYGG TTACAA

26

60

2) INFORMATION FOR SEQ ID NO: 577

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida albicans*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 577

CATGATTGAA CCATCCACCA

20

2) INFORMATION FOR SEQ ID NO: 578

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Candida dubliniensis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 578

CATGATTGAA GCTTCCACCA

20

2) INFORMATION FOR SEQ ID NO: 579

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 579

GAAGGCCGTG CTGGTGAGAA

20

2) INFORMATION FOR SEQ ID NO: 580

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 580

GCTAAACCAG CTACAATCAC TCCAC

25

2) INFORMATION FOR SEQ ID NO: 581

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus influenzae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 581

ACATCGGTGC ATTATTACGT GG

22

2) INFORMATION FOR SEQ ID NO: 582

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 582

TTTCAACTTC GTCGTTGACA CGAACAGT

28

2) INFORMATION FOR SEQ ID NO: 583

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 bases
- (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus agalactiae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 583

CAACTGCTTT TTGGATATCT TCTTTAATAC CAACG

35

2) INFORMATION FOR SEQ ID NO: 584

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 584

ACATGACACA TCTAAAACAA

20

2) INFORMATION FOR SEQ ID NO: 585

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 585

ACCACATACT GAATTCAAAG

20

2) INFORMATION FOR SEQ ID NO: 586

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 586

CAGAAGTATA CGTATTATCA

20

2) INFORMATION FOR SEQ ID NO: 587

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 587

CGTATTATCA AAAGACGAAG

20

2) INFORMATION FOR SEQ ID NO: 588

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 588

TCTTCTCAAA CTATCGTCCA

20

2) INFORMATION FOR SEQ ID NO: 589

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus epidermidis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 589

5 GCACGAAACT TCTAAAACAA

20

2) INFORMATION FOR SEQ ID NO: 590

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

15

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

20

(A) ORGANISM: *Staphylococcus epidermidis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 590

25 TATACGTATT ATCTAAAGAT

20

25

2) INFORMATION FOR SEQ ID NO: 591

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

35

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

40

(A) ORGANISM: *Staphylococcus epidermidis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 591

45 TCCTGGTTCT ATTACACCAC

20

45

2) INFORMATION FOR SEQ ID NO: 592

(i) SEQUENCE CHARACTERISTICS:

50

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus epidermidis*

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 592

CAAAGCTGAA GTATACGTAT

20

5

2) INFORMATION FOR SEQ ID NO: 593

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus epidermidis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 593

20

TTCACCTAACT ATCGCCCACA

20

25 2) INFORMATION FOR SEQ ID NO: 594

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus haemolyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 594

40

ATTGGTATCC ATGACACTTC

20

45 2) INFORMATION FOR SEQ ID NO: 595

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

55 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus haemolyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 595

60

TTAAAGCAGA CGTATACGTT

20

2) INFORMATION FOR SEQ ID NO: 596

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus hominis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 596

GAAATTATTG GTATCAAAGA

20

2) INFORMATION FOR SEQ ID NO: 597

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus hominis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 597

ATTGGTATCA AAGAACTTC

20

2) INFORMATION FOR SEQ ID NO: 598

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus hominis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 598

AATTACACCT CACACAAAAT

20

2) INFORMATION FOR SEQ ID NO: 599

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 599

CGGTGAAGAA ATCGAAATCA

20

2) INFORMATION FOR SEQ ID NO: 600

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 600

ATGCAAGAAG AATCAAGCAA

20

2) INFORMATION FOR SEQ ID NO: 601

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 601

GTTTCACGTG ATGATGTACA

20

2) INFORMATION FOR SEQ ID NO: 602

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases

(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecium*

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 602

AAGTTGAAGT TGTGGTATT

20

15

2) INFORMATION FOR SEQ ID NO: 603

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

20

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 603

30

GGTATTAAAG ACGAAACATC

20

35 2) INFORMATION FOR SEQ ID NO: 604

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

40

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

45

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus gallinarum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 604

50

GGTGATGAAG TAGAAATCGT

20

55

2) INFORMATION FOR SEQ ID NO: 605

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

60

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 605

5 GAAATGTTCC GTAAATTATT 20

10 2) INFORMATION FOR SEQ ID NO: 606

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 606

ATTAGACTAC GCTGAAGCTG 20

25 2) INFORMATION FOR SEQ ID NO: 607

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 821 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecalis*
(B) STRAIN: ATCC 29212

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 607

	CGGAGCTATC	TTAGTAGTTT	CTGCTGCTGA	TGGTCCTATG	CCTCAAACAC	50
	GTGAACATAT	CTTATTATCA	CGTAACGTTG	GTGTACCATA	CATCGTTGTA	100
	TTCTTAAACA	AAATGGATAT	GGTTGATGAC	GAAGAATTAT	TAGAATTAGT	150
45	AGAAATGGAA	GTTTCGTGACT	TATTATCAGA	ATACGATTTC	CCAGGCGATG	200
	ATGTTCCAGT	TATCGCAGGT	TCTGCTTTGA	AAGCTTTAGA	AGGCGACGAG	250
	TCTTATGAAG	AAAAAATCTT	AGAATTAATG	GCTGCAGTTG	ACGAATATAT	300
	CCCAACTCCA	GAACGTGATA	CTGACAAACC	ATTCATGATG	CCAGTCGAAG	350
	ACGTATTCTC	AATCACTGGA	CGTGGTACTG	TTGCTACAGG	ACGTGTTGAA	400
50	CGTGGTGAAG	TTCGCGTTGG	TGACGAAGTT	GAAATCGTTG	GTATTAAAGA	450
	CGAAACATCT	AAAACAACTG	TTACAGGTGT	TGAAATGTTT	CGTAAATTAT	500
	TAGACTACGC	TGAAGCAGGC	GACAACTTCG	GTGCTTTATT	ACGTGGTGTA	550
	GCACGTGAAG	ATATCGAACG	TGGACAAGTA	TTAGCTAAAC	CAGCTACAAT	600
	CACTCCACAC	ACAAAATTCA	AAGCTGAAGT	ATACGTATTA	TCAAAAGAAG	650
55	AAGGCGGACG	TCACACTCCA	TTCTTCACTA	ACTACCGTCC	TCAATTCTAC	700
	TTCCGTACAA	CAGACGTTAC	TGGTGTGTA	GAATTGCCAG	AAGGTACTGA	750
	AATGGTAATG	CCTGGTGATA	ACGTTGCTAT	GGACGTTGAA	TTAATTCACC	800
	CAATCGCTAT	CGAAGACGGA	A			821

60

2) INFORMATION FOR SEQ ID NO: 608

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
 (B) STRAIN: ATCC 19434

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 608

CGGAGCTATC	TTGGTAGTTT	CTGCTGCTGA	CGGCCCAATG	CCTCAAACCTC	50
GTGAACACAT	CCTATTGTCT	CGTCAAGTTG	GTGTCCTTA	CATCGTTGTA	100
TTCTTGAACA	AAGTAGACAT	GGTTGATGAC	GAAGAATTAC	TAGAATTAGT	150
TGAAATGGAA	GTTTCGTGAC	TATTAACAGA	ATACRAATTC	CCTGGTGRCG	200
ATGTTTCCTGT	AGTTGCTGGA	TCAGCTTTGA	AAGCTCTAGA	AGGCGACGCT	250
TCATACGAAG	AAAAAATTCT	TGAATTAATG	GCTGCAGTTG	ACGAATACAT	300
CCCAACTCCA	GAACGTGACA	ACGACAAACC	ATTCATGATG	CCAGTTGAAG	350
ACGTGTTCTC	AATTACTGGA	CGTGGTACTG	TTGCTACAGG	TCGTGTTGAA	400
CGTGGACAAG	TTCGCGTTGG	TGACGAAGTT	GAAGTTGTTG	GTATTGCTGA	450
AGAAACTTCA	AAAACAACAG	TTACTGGTGT	TGAAATGTTT	CGTAAATTGT	500
TAGACYACGC	TGAAGCTGGA	GACRACATTG	GTGCTTTACT	ACGTGGTGTT	550
GCACGTGAAG	ACATCCAACG	TGGACAAGTT	TTAGCTAAAC	CAGGTACAAT	600
CACACCTCRT	ACAAAATTCT	CTGCAGAAGT	ATACGTGTTG	ACAAAAGAAG	650
AAGGTGGACG	TCATACTCCA	TTCTTCACTA	ACTACCGTCC	ACAATTCTAC	700
TTCCGTACAA	CTGACGTAAC	AGGTGTTGTT	GAATTACCAG	AAGGAACTGA	750
A					751

2) INFORMATION FOR SEQ ID NO: 609

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus gallinarum*
 (B) STRAIN: ATCC 49573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 609

CGGTGCGATC	TTAGTAGTAT	CTGCTGCTGA	CGGTCCTATG	CCTCAAACCTC	50
GTGAACACAT	CTTGTTATCA	CGTAACGTTG	GCGWACCATA	CATCGTTGTT	100
TTCTTGAACA	AAATGGATAT	GGTTGAYGAC	GAAGAATTGC	TAGAATTAGT	150
TGAAATGGAA	GTTTCGTGAC	TATTGTCTGA	ATATGACTTC	CCAGGCGACG	200
ATGTTTCCTGT	AATCGCCGGT	TCTGCTTTGA	AAGCTCTTGA	AGGAGATCCT	250
TCATACGAAG	AAAAAATCAT	GGAATTGATG	GCTGCAGTTG	ACGAATACGT	300
TCCAACCTCCA	GAACGTGATA	CTGACAAACC	ATTCATGATG	CCAGTCGAAG	350
ACGTATTCTC	AATCACTGGA	CGTGGTACTG	TTGCTACAGG	CCGTGTTGAA	400

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CGTGGACAAG TTCGCGTTGG TGATGAAGTA GAAATCGTTG GTATTGCTGA 450
CGAAACTGCT AAAACAACTG TAACAGGTGT TGAAATGTTT CGTAAATTGT 500
TAGACTATGC TGAAGCAGGG GATAACATTG GTGCATTGCT ACGTGGGGTT 550
GCTCGTGAAG ACATCCAACG TGGACAAGTA TTGGCTAAAG CTGGTACRAT 600
5 CACACCTCAT ACAAATTC AAGCTGAAGT TTATGTTTTG ACAAAGAAG 650
AAGGTGGRCG TCACACTCCA TTCTTCACTA ACTACCGTCC TCAGTTCTAC 700
TTCCGTACAA CTGACGTAAC TGGTGTGTT GAATTACCAG AAGGAACTGA 750
A 751

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10

2) INFORMATION FOR SEQ ID NO: 610

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 891 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

20 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus influenzae*
 (B) STRAIN: Rd
 25 (C) ACCESSION NUMBER: extracted from U32848

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 610

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AATATGATTA CTGGTGCGGC ACAAATGGAT GGTGCTATTT TAGTAGTAGC 50
30 AGCAACAGAT GGTCTTATGC CACAACTCG TGAACACATC TTATTAGGTC 100
GCCAAGTAGG TGTTCCATAC ATCATCGTAT TCTTAAACAA ATGCGACATG 150
GTAGATGACG AAGAGTTATT AGAATTAGTC GAAATGGAAG TTCGTGAACT 200
TCTATCTCAA TATGACTTCC CAGGTGACGA TACACCAATC GTACGTGGTT 250
CAGCATTACA AGCGTTAAAC GCGGTAGCAG AATGGGAAGA AAAAAATCCTT 300
35 GAGTTAGCAA ACCACTTAGA TACTTACATC CCAGAACCAG AACGTGCGAT 350
TGACCAACCG TTCCTTCTTC CAATCGAAGA TGTGTTCTCA ATCTCAGGTC 400
GTGGTACTGT AGTAACAGGT CGTGTAGAAC GAGGTATTAT CCGTACAGGT 450
GATGAAGTAG AAATCGTCGG TATCAAAGAT ACAGCGAAAA CTACTGTAAC 500
GGGTGTTGAA ATGTTCCGTA AATTACTTGA CGAAGGTCGT GCAGGTGAAA 550
40 ACATCGGTGC ATTATTACGT GGTACCAAAC GTGAAGAAAT CGAACGTGGT 600
CAAGTATTAG CGAAACCAGG TTCAATCACA CCACACACTG ACTTCGAATC 650
AGAAGTGTA GATTATCAA AAGATGAAGG TGGTCGTCAT ACTCCATTCT 700
TCAAAGGTTA CCGTCCACAA TTCTATTTCC GTACAACAGA CGTGAAGGTT 750
ACAATCGAAT TACCAGAAGG CGTGGAAATG GTAATGCCAG GCGATAACAT 800
45 CAAGATGACA GTAAGCTTAA TCCACCCAAT TGCGATGGAT CAAGGTTTAC 850
GTTTCGCAAT CCGTGAAGGT GGCCGTACAG TAGGTGCAGG C 891

```

50 2) INFORMATION FOR SEQ ID NO: 611

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 818 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus epidermidis*
 (B) STRAIN: ATCC 14990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 611

```

5      CGGCGGTATC TTAGTTGTAT CTGCTGCTGA CGGTCCAATG CCACAAACTC      50
      GTGAACACAT CTTATTATCA CGTAACGTTG GTGTACCAGC ATTAGTTGTA      100
      TTCTTAAACA AAGTTGACAT GGTAGACGAC GAAGAATTAT TAGAATTAGT      150
      TGAAATGGAA GTTCGTGACT TATTAAGCGA ATATGACTTC CCAGGTGACG      200
10     ATGTACCTGT AATCGCTGGT TCTGCATTAA AAGCATTAGA AGGCGATGCT      250
      GAATACGAAC AAAAAATCTT AGACTTAATG CAAGCAGTTG ATGATTACAT      300
      TCCAACCTCA GAACGTGATT CTGACAAACC ATTCATGATG CCAGTTGAGG      350
      ACGTATTCTC AATCACTGGT CGTGGTACTG TTGCTACAGG CCGTGTTGAA      400
      CGTGGTCAAA TCAAAGTTGG TGAAGAAGTT GAAATCATCG GTATGCACGA      450
15     AACTTCTAAA ACAACTGTTA CTGGTGTAGA AATGTTCCGT AAATTATTAG      500
      ACTACGCTGA AGCTGGTGAC AACATCGGTG CTTTATTACG TGGTGTGCA      550
      CGTGAAGACG TACAACGTGG TCAAGTATTA GCTGCTCCTG GTTCTATTAC      600
      ACCACACACA AAATTCAAAG CTGAAGTATA CGTATTATCT AAAGATGAAG      650
      GTGGACGCTCA CACTCCATTC TTCATTAAC ATCGCCCACA ATTCTATTTC      700
20     CGTACTACTG ACGTAACTGG GTTGTAAAC TTACCAGAAG GTACAGAAAT      750
      GGTATGCTCT GGCACAAACG TTGAAATGAC AGTTGAATTA ATCGCTCCAA      800
      TCGCTATCGA AGACGGAA                                     818
  
```

25

2) INFORMATION FOR SEQ ID NO: 612

```

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 825 bases
          (B) TYPE: Nucleic acid
          (C) STRANDEDNESS: Double
          (D) TOPOLOGY: Linear

      (ii) MOLECULE TYPE: Genomic DNA

35     (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Salmonella choleraesuis subsp. choleraesuis
              serotype paratyphi A
          (B) STRAIN: ATCC 9150
  
```

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 612

```

      GCGCGATCC TGGTTGTTGC TGCGACTGAC GGCCCGATGC CGCAGACCCG      50
      TGAGCACATC CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT      100
45     TCCTGAACAA ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTT      150
      GAAATGGAAG TTCGTGAACT TCTGTCTCAG TACGACTTCC CGGGCGACGA      200
      CACGCCGATC GTTCGTGGTT CTGCTCTGAA AGCGCTGGAA GGCGACGCAG      250
      AGTGGGAAGC GAAAATCATC GAACTGGCTG GCTTCCTGGA TTCTTACATC      300
      CCGGAACCAG AGCGTGCGAT TGACAAGCCG TTCTGTCTGC CGATCGAAGA      350
50     CGTATTCTCC ATCTCCGGTC GTGGTACCGT TGTTACCGGT CGTGTAGAAC      400
      GCGGTATCAT CAAAGTGGGC GAAGAAGTTG AAATCGTTGG TATCAAAGAG      450
      ACTCAGAAGT CTACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA      500
      CGAAGGCCGT GCCGGTGAGA ACGTAGGTGT TCTGCTGCGT GGTATCAAAC      550
      GTGAAGAAAT CGAACGTGGT CAGGTACTGG CTAAGCCGGG CACCATCAAG      600
55     CCGCACACCA AGTTCGAATC TGAAGTGATC ATTCTGTCCA AAGATGAAGG      650
      CGGCCGTCAT ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC      700
      GTACTACTGA CGTGAAGTGC ACCATCGAAC TGCCGGAAGG CGTAGAGATG      750
      GTAATGCCCG GCGACAACAT CAAAATGGTT GTTACCCTGA TCCACCCGAT      800
      CGCAATGGAC GACGGTCTGC GTTTC                                     825
  
```

60

2) INFORMATION FOR SEQ ID NO: 613

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 778 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 10 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Serratia ficaria*
 15 (B) STRAIN: ATCC 33105
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 613

20	GGCGCTATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCAATGC	CTCAGACCCG	50
	TGAGCACATC	CTGCTGGGTC	GYCAGGTTGG	CGTTCCTTTC	ATCATCGTRT	100
	TCATGAACAA	ATGCGACATG	GTTGATGATG	AAGAGCTGCT	GGAAGTGGTA	150
	GAAATGGAAG	TTCGCGAACT	GCTGTCCGCT	TACGACTTCC	CTGGCGATGA	200
	CCTGCCGGTG	ATTGCGGGTT	CCGCGCTGAA	AGCGCTGGAA	GGCGAAGCCG	250
	AGTGGAAGC	TAAAATCATC	GAGCTGGCTG	AMCMSCTGGA	TACTTACATC	300
25	CCAGAACCAG	AGCGCGCTAT	CGACAAGCCG	TTCCTGCTGC	CAATCGAAGA	350
	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	GGTTACCGGT	CGTGTTGAGC	400
	GCGGTATCAT	CAAAGTTGGC	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAC	450
	ACCGTCAAGT	CTACCTGTAC	CGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCCGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAGC	550
30	GTGAAGACAT	CGAACGTGGT	CAGGTTCTGG	CTAAACCAGG	TTCCATCAAG	600
	CCGCACACCC	AGTTTCGATTC	AGAAGTGTAC	ATCCTGAGCA	AAGAAGAAGG	650
	TGGTCGTCAC	ACKCCATTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700
	GTACTACTGA	CGTGACCGGT	ACCATCGAAC	TGCCAGAAGG	CGTTGAGATG	750
35	GTAATGCCTG	GCGACAACGT	GAACATGA			778

2) INFORMATION FOR SEQ ID NO: 614

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 653 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- 45 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Enterococcus malodoratus*
 50 (B) STRAIN: ATCC 43197
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 614

55	GTGCGATCTT	AGTAGTATCA	GCTACTGATG	GTCCAATGCC	TCAAACCTCGT	50
	GAACACATTT	TGTTATCACG	TCAAGTTGGT	GTAAAGCACT	TGATCGTTTT	100
	CTTGAACAAA	GTAGATTTAG	TTGATGACGA	AGAATTGATC	GACTTAGTTG	150
	AAATGGAAGT	ACGTGAATTA	CTTTCTGAAT	ATGGTTTCCC	AGGTGATGAT	200
	ATTCCAGTGC	TTAAAGGTTC	TGCTTTGAAA	GCATTAGAAG	GCGATCCAGA	250
	ACAAGAACAA	GTTATTCTTG	ATTTGATGGA	TACCGTTGAT	GAATATATCC	300
60	CAACACCTGA	ACGTGACAAT	GACAAACCGT	TCTTGTTACC	AGTTGAGGAT	350

	GTTTTCTCGA	TCACAGGACG	TGGTACTGTA	GCTTCTGGTC	GTATCGACCG	400
	TGGCGAAGTT	AAAGTCGGCG	ATGAAATTGA	AATCATCGGG	ATCAAACCTG	450
	AAGTTCAAAA	AGCAATCGTT	ACTGGACTTG	AAATGTTCCG	TAAACATTG	500
	GATTATGGTG	AAGCTGGCGA	TAACGTTGGG	GTTCTATTAC	GTGGGATTAC	550
5	ACGTGATGAA	ATCGAACGTG	GCCAAGTATT	AGCTAAACCA	GGTTCAATCA	600
	CACCACATAC	TAAGTTCAAA	GCCGAAGTAT	ATGTGTTGAC	GAAAGAAGAA	650
	GGT					653

10

2) INFORMATION FOR SEQ ID NO: 615

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 669 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus durans*
- (B) STRAIN: ATCC 19432

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 615

	GGAGCCATTC	TAGTTGTATC	TGCAACAGAT	GGACCAATGC	CACAAACACG	50
	TGAACATATT	TTATTGTCAC	GTCAAGTAGG	TGTTAAATAT	TTGATCGTCT	100
	TCTTGAACAA	AATCGACTTA	GTAGATGATG	AAGAATTGAT	TGATCTTGTC	150
30	GAAATGGAAG	TTCGTGAATT	ATTAAGCGAA	TATGGTTTCC	CAGGTGACGA	200
	TACACCAGTC	ATCAAAGGTT	CAGCATTAAA	AGCTTTACAA	GGAGATCCTG	250
	ATGCAGAAGC	AGCTATCATG	GAATTGATGG	ATACTGTTGA	TGAATATATC	300
	CCAACACCAG	AACGTGATAC	AGACAAACCA	TTATTGTTAC	CAGTGGGAAGA	350
	TGTCTTCTCA	ATCACAGGTC	GTGGGACTGT	TGCTTCAGGT	CGTATCGATC	400
35	GTGGTGCAGT	TCGTGTAGGT	GATGAAATCG	AAATCGTCGG	TATCAAACCT	450
	GAAACACAAA	AAGCTGTTGT	AACTGGGGTC	GAAATGTTCC	GCAAGACATT	500
	AGACTATGGT	GAAGCAGGAG	ATAACGTTGG	GGTATTGTTA	CGTGGTATCC	550
	AACGTGAAGA	TATCGAACGT	GGACAAGTAA	TCGCAAAACC	AGGTTCAATC	600
	ACACCACATA	CAAAATTCAA	AGCAGAAGTG	TACGTATTGA	CAAAAGAAGA	650
40	AGGTGGACGT	CATACACCA				669

2) INFORMATION FOR SEQ ID NO: 616

45

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 669 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

55

- (A) ORGANISM: *Enterococcus pseudoavium*
- (B) STRAIN: ATCC 49372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 616

60	GGTGCAATTT	TAGTAGTATC	TGCTACTGAT	GGCCCAATGC	CACAAACACG	50
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TGAACATATC TTGTTATCAC GTCAAGTAGG GGTAAACAC TTAATCGTCT 100
TCTTGAACAA AGTTGATTGA GTTGATGATG AAGAATTGAT CGATTTAGTT 150
GAAATGGAAG TTCGGAATT GCTTTCTGAA TATGGTTTCC CAGGCGATGA 200
TATTCCAGTA CTTAAAGGTT CTGCTTTGAA AGCTTTAGAA GGCGATCCTG 250
5 AACAAGAACA AGTAATCCTT GACTTGATGG ATACGGTTGA TGAATACATC 300
CCAACGCCTG AACGTGATAC TGACAAACCA TTCTTGTTAC CAGTCGAAGA 350
TGTCTTCTCA ATCACAGGAC GTGGTACGGT TGCATCTGGT CGTATCGATC 400
GTGGGGAAGT TAAAGTCGGT GATGAAGTTG AAATCATCGG GATCAAACCT 450
GAAGTGCAA AAGCTGTCGT AACTGGACTA GAAATGTTCC GTAAGACATT 500
10 GGATTACGGT GAAGCTGGCG ATAACGTTGG GGTCTATTA CGTGGGATTA 550
CTCGTGATGA AATCGAACGT GGACAAGTAT TAGCTAAACC AGGTTCAATC 600
ACTCCACATA CGAAATTCAG TGCAGAAAGT TATGTATTGA CGAAAGAAGA 650
AGGTGGCCGT CATACGCCA 669

```

15

2) INFORMATION FOR SEQ ID NO: 617

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 668 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Enterococcus dispar*
- (B) STRAIN: ATCC 51266
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 617

```

GGGGCAATTT TAGTTGTATC TGCAACTGAT GGCCCAATGC CACAAACACG 50
TGAACACATT TTGTTAGCTC GTCAAGTAGG GGTAAATAT TTAATCGTCT 100
35 TCTTGAACAA AACAGATTGA GTTGATGATG AAGAATTATT GGAAGTAGTT 150
GAAATGGAAG TTCGTGAATT ATTAAATGAA TACAATTTCC CTGGCGATGA 200
TATTCCTGTT ATTCGCGGAT CTGCTTTAAA AGCATTAGAA GGCGATCCAG 250
AACAAGAAGA AGTAATTATG AACTTGATGG ATACTGTGGA TGAATATATC 300
CCAACCTCAG AACGTGACAA TGATAAACCA TTCTTGTTAC CAGTGGAAGA 350
40 TGTCTTCACA ATTACTGGTC GTGGTACTGT TGCTTCAGGT CGTATCGACC 400
GTGGTAAAGT CAACGTTGGT GATGAAATTG AAATTATCGG AATTAAACCA 450
GAAACACAAA AAGCTGTTGT AACCGGTTTG GAAATGTTCC GTAAACTTTT 500
GGATTATGGT GAAGCTGGTG ATAACGTTGG GGTCTTATTA CGTGGGATTA 550
CTCGTGATGA AGTAGAACGT GGTCAAGTAT TAGCAAAACC AGGTTCCATT 600
45 ACACCGCATA CCAAATTTAA AGGTGAAGTT TATATCTTAA CAAAGAAGA 650
AGGTGGACGT CATACTCC 668

```

50 2) INFORMATION FOR SEQ ID NO: 618

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 673 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:

60

(A) ORGANISM: *Enterococcus avium*

(B) STRAIN: ATCC 14025

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 618

```

5      GGTGCAATCC TAGTAGTATC AGCTACTGAT GGTCCAATGC CGCAAACACG      50
      TGAACATATT TTGCTATCAC GGCAAGTGGG TGTAAACAC TTAATCGTAT      100
      TTTTAAACAA AGTTGATTTA GTCGATGATG AAGAATTGAT CGATCTAGTT      150
      GAAATGGAAG TCCGTGAATT ACTTTCTGAA TATGGTTTCC CAGGTGACGA      200
10     TATTCCAGTT CTCAAAGGTT CAGCTTTGAA AGCATTAGAA GGCGATCCTG      250
      AACAGAACA AGTAATCCTT GATTTAATGG ATACAGTTGA CGAATATATC      300
      CCAACTCCAG AACGTGACAC TGACAAGCCA TTCTTGTTAC CAGTCGAAGA      350
      TGTATTTTCT ATCACTGGTC GTGGGACTGT AGCGTCTGGA CGGATTGATC      400
      GTGGTGAAGT TAAAGTCGGC GATGAAGTTG AAATCATCGG GATCAAACCT      450
15     GAAATTCAAA AAGCAGTCGT AACTGGACTT GAAATGTTCC GTAAAACTTT      500
      AGATTATGGT GAAGCTGGCG ATAACGTTGG GGTCTATTA CGTGGGATTA      550
      CACGTGATGA AATCGAACGT GGTCAAGTCT TAGCTAAACC AGGTTCAATC      600
      ACACCACATA CAAAATTCAG TGCAGAAGTT TACGTATTGA CGAAAGAAGA      650
      AGGTGGACGT CATAACCAT CTT                                673
20

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2) INFORMATION FOR SEQ ID NO: 619

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1713 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*
 (C) ACCESSION NUMBER: K00428

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 619

```

      TTTCATATTT TTAAGGATTT TGTTTTAGCA CCCATCCGAC CTCAGTCAAT      50
40     ATATCCTTTC GCGACCAGGC TTTCTCCCT TTTGCTGCTA ACTGGTTACA      100
      GATTTTCCTA TTTTGGTCA TTTTATCTT TGAAACTGAT TAAGCTGAAA      150
      AAATTTGAGC TTCTTTGTTG TAAACTATTT TGTGCTTTCA GTTTTATTCT      200
      AGCTCGACAA AGGTAACAGA CAAAAATGTC AGCTTTATTA CCAAGATTAC      250
      TCACAAGAAC AGCTTTTAAA GCTTCTGGGA AACTTCTGAG GCTCTCTTCA      300
45     GTAATTTCTA GGACCTTTTC TCAAACACT ACTTCCTATG CAGCTGCTTT      350
      TGATCGTTCC AAACCGCATG TAAATATAGG TACGATCGGC CATGTTGATC      400
      ATGGGAAGAC AACTTTAACC GCAGCCATTA CGAAAACGTT AGCCGCAAAA      450
      GGTGGTGCCA ACTTCTTGGA CTATGCTGCC ATCGATAAGG CTCCGGAAGA      500
      AAGAGCTCGT GGTATTACAA TTTCTACTGC ACACGTGGAA TACGAAACGG      550
50     CCAAGAGACA TTATTCTCAC GTCGACTGTC CAGGCCACGC TGATTACATC      600
      AAGAATATGA TTACCGGTGC TGCTCAAATG GATGGTGCTA TCATTGTTGT      650
      AGCTGCTACC GATGGACAAA TGCCCCAAAC TAGAGAACAT TTACTTTTGG      700
      CCAGACAAGT TGGTGTCCAA CATATTGTCG TTTTGTGTTA CAAGGTTGAT      750
      ACCATTGATG ATCCAGAAAT GTTAGAGTTA GTCGAAATGG AAATGAGAGA      800
55     ACTTTTAAAC GAATATGGGT TTGACGGTGA TAATGCTCCA ATTATCATGG      850
      GTTCTGCCCT TTGCGCTTTG GAAGGTCGCC AACCTGAAAT TGGGGAGCAG      900
      GCCATCATGA AACTTTTGGA TGCAGTGGAT GAGTATATTC CTACACCTGA      950
      AAGAGATTTG AACAAGCCTT TCTTGATGCC CGTTGAAGAT ATCTTCTCTA      1000
      TCTCCGGTAG AGGTACTGTG GTCAGTGGTC GTGTGGAAAG GGGTAATTTA      1050
60     AAGAAAGGTG AGGAATTGGA AATTGTTGGT CACAACTCCA CCCCATTGAA      1100

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AACAAACAGTT ACTGGTATTG AAATGTTTAG AAAGGAATTG GACTCTGCTA 1150
TGGCAGGTGA CAATGCCGGT GTTTTACTTA GAGGTATCAG GAGAGATCAA 1200
TTGAAGAGAG GTATGGTCTT AGCTAAGCCA GGTACCGTTA AAGCCCATAC 1250
AAAGATTCTA GCCTCTTTGT ACATTTTATC CAAAGAGGAA GGTGGTAGAC 1300
5 ATTCTGGGTT TGGTGAAAAC TACAGACCAC AAATGTTTAT AAGAACAGCT 1350
GATGTTACAG TTGTGATGAG ATTTCCCTAAG GAGGTTGAAG ATCATTCTAT 1400
GCAAGTTATG CCAGGTGACA ATGTTGAAAT GGAATGTGAT TTGATCCATC 1450
CTACCCCATT AGAAGTTGGT CAACGTTTCA ATATCAGAGA GGGTGGAAGA 1500
ACTGTTGGTA CCGGTCTAAT CACACGTATT ATTGAATAGA CTTATTGATG 1550
10 CAACTGGAGT ATATTTCTAT ATATTCTGTT CATTTCCCCT CTCATAATAT 1600
ATACTTGTTT CGTTAAAATT TTATACGTGT AAATAAAGTG CCATAAATTT 1650
TTCAGCTTTA CTTTTGGTAG AGTCCTGCTA GCACTAGATT TTACAATTTT 1700
ATGTGCACAC ACC 1713

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15

2) INFORMATION FOR SEQ ID NO: 620

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20 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 18 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Single
    (D) TOPOLOGY: Linear

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25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 620

30 ATTGGTGCAT TGCTACGT

18

2) INFORMATION FOR SEQ ID NO: 621

```

35 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 751 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

```

45 (A) ORGANISM: Enterococcus faecium
    (B) STRAIN: ATCC 19434

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 621

```

TGGTGCAATC TTAGTTGTTT CTGCAACTGA CCGTCCGATG CCTCAAACAC 50
50 GTGAACACAT TTTATTGTCA CGCCAAGTTG GTGTAAAATA CCTGATTGTT 100
TTCTTGAACA AAGTTGATTT AGTCGATGAT GAAGAATTGA TCGATTTGGT 150
AGAAATGGAA GTTCGCGAGT TATTGAGCGA ATATGGTTTC CCAGGCGATG 200
ACACTCCTGT GATCAAAGGT TCCGCATTAA AAGCATTGCA AGGCGATCCA 250
GATGCTGAAG CTGCTATTAT GGAATTGATG GATACAGTAG ATGAATATAT 300
55 CCCAACACCA GAACGTGATA CAGATAAACC ATTACTATTG CCAGTGGAAG 350
ACGTCTTCTC AATTACAGGT CGAGGAAGTG TTGCCTCAGG TCGTATTGAT 400
CGTGGTGCTG TTCGTGTCGG TGATGAGGTA GAGATCGTAG GGATCAAACC 450
TGAAACACAA AAAGCAGTTG TAACAGGTGT AGAAATGTTT CGTAAACGTT 500
TAGATTACGG GGAAGCTGGG GATAACGTAG CCGTGTGTTT ACGGGGGATC 550
60 CAACGTGACG ATATCGAACG TGGACAAGTA CTTGCTAAAC CAGGTTCCAT 600

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TACTCCACAT	ACAAAATTCA	AAGCAGAAGT	GTACGTGTTG	ACAAAAGAAG	650
AAGGTGGACG	TCATACTCCA	TTCTTCAACA	ACTATCGTCC	ACAGTTCTAC	700
TTCCGCACAA	CTGATGTTAC	AGGAACAATC	ACATTGCCAG	AAGATACAGA	750
A					751

5

2) INFORMATION FOR SEQ ID NO: 622

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*
 (B) STRAIN: ATCC 13264

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 622

GTCAAATGGG	ACGAATCCAG	ATTCCAAGAA	ATTGTCAAGG	AAACCTCCAA	50
CTTTATCAAG	AAGGTTGGTT	ACAACCCAAA	GACTGTTCCA	TTCGTCCCAA	100
TCTCTGGTTG	GAACGGTGAC	AACATGATTG	AAGCTACCAC	CAACGCTCCA	150
TGGTACAAGG	GTTGGGAAAA	GGAAACCAAG	GCCGGTGTCTG	TCAAGGGTAA	200
GACTTTGTTG	GAAGCCATTG	ACGCCATTGA	ACAACCATCT	AGACCAACTG	250
ACAAGCCATT	GAGATTGCCA	TTGCAAGATG	TTTACAAGAT	TGGTGGTATT	300
GGTACTGTGC	CAGTCGGTAG	AGTTGAAACC	GGTGTCATCA	AGCCAGGTAT	350
GGTTGTTACT	TTCGCCCCAG	CTGGTGTTAC	CACTGAAGTC	AAGTCCGTTG	400
AAATGCATCA	CGAACAATTG	GAACAAGGTG	TTCCAGGTGA	CAACGTTGGT	450
TTCAACGTCA	AGAACGTTTC	CGTTAAGGAA	ATCAGAAGAG	GTAACGTCTG	500
TGGTGACGCT	AAGAACGATC	CACCAAAGGG	TTGCGCTTCT	TTCAACGCTA	550
CCGTCATTGT	TTTGAACCAT	CCAGGTCAAA	TCTCTGCTGG	TTACTCTCCA	600
GTTTTGGATT	GTCACACTGC	TCACATTGCT	TGTAGATTCTG	ACGAATTGTT	650
GGAAAAGAAC	GACAGAAGAT	CTGGTAAGAA	GTTGGAAGAC	CATCCAAAGT	700
TCTTGAAGTC	CGGTGACGCT	GCTTTGGTCA	AGTTCGTTCC	ATCTAAGCCA	750

40

2) INFORMATION FOR SEQ ID NO: 623

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1269 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptococcus neoformans*
 (B) STRAIN: ATCC 44104

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 623

TCTTGAAAGC	TTAAGGCCGA	GCGAGAGCGA	GGTATCACCA	TCGACATTGC	50
TCTTTGGAAG	TTGAGACCC	CCAGGTACCA	GGTCACCGTC	ATTGACGCCC	100
CCGGTCACCG	AGACTTCATC	AAGAACATGA	TCACCGGTAC	CTCCCAGGCT	150

60

	GACTGTGCCA	TCCTCATCAT	TGCCACCGGT	ATCGGTGAGT	TCGAGGCCGG	200
	TATCTCCAAG	GACGGTCAGA	CCCGAGAGCA	CGCCCTCCTC	GCCTTCACCC	250
	TCGGTGTGAG	GCAGCTCAT	GTTGCTTGCA	ACAAGATGGA	CACCTGCAAG	300
	TGGTCCGAGG	ACCGATTCAA	CGAAATCGTC	AAGGAGACCA	ACGGTTTCAT	350
5	CAAGAAGGTT	GGTTACAACC	CCAAGGCTGT	CCCCTTCGTC	CCCATCTCTG	400
	GTTGGCACGG	TGACAACATG	TTGGAGGAGA	CCACCAAGTC	AGTGAATCCG	450
	CTTCTACGTG	ATGAGATGTT	TTTCTGACTT	TCCGTGCAGC	ATGCCCTGGT	500
	ACAAGGGATG	GACCAAGGAG	ACCAAGTCTG	GTGTTTCCAA	GGGTAAGACC	550
	CTCCTCGAGG	CCATCGACGC	CATCGAGCCC	CCTACCCGAC	CCACCGACAA	600
10	GCCCTCCCGT	CTCCCTCTCC	AGGACGTCTA	CAAGATCGGT	GGTATCGGCA	650
	CAGTCCCTGT	CGGCCGAGTC	GAGACCGGTG	TCATCAAGGC	CGGTATGTTG	700
	TCTCATCTCT	CTTGCTCTCGT	AACATGCGTC	TCGTAACATG	CGCTTACTTC	750
	ATTTTCAGGT	ATGGTCGTCA	AGTTCGCCCC	CACCAACGTC	ACCACTGAAG	800
	TCAAGTCCGT	TGAGATGCAC	CACGAGCAGA	TCCCGGAGGG	TCTTCCCGGA	850
15	GACAACGTTG	GTTTCAACGT	CAAGAACGTT	TCCATCAAGG	ACATCCGACG	900
	AGGTAACGTC	TGTGGTGACT	CCAAGAACGA	CCCCCCTATG	GAGGCTGCTT	950
	CTTTCAACGC	CCAGGTTATC	GTCTTAAC	ACCCTGGTCA	GATCGGTGCC	1000
	GGTTACACCC	CCGTTCTCGA	CTGTCAACT	GCCCGTAAGC	CTGACCCAAT	1050
	ACCTCCAACA	TACCTTTGAA	GCTGACCCTT	TCTAGACATT	GCCTGCAAGT	1100
20	TTGCTGAGTT	GATCGAGAAG	ATTGACCGAC	GAACCGGTAA	GGTCATGGAG	1150
	GCCGCCCCCA	AGTTCGTCAA	GTCTGGTGAC	GCCGCCATTG	TCAAGCTTGT	1200
	TGCCCAGAAG	CCCCTCTGTG	TTGAGACCTA	CGCCGACTAC	CCCCCTCTTG	1250
	GTGCATTGCG	CGTCCGAGA				1269

25

2) INFORMATION FOR SEQ ID NO: 624

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 753
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Candida albicans*
- (B) STRAIN: ATCC 36801
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 624

	TCTGTCAAAT	GGGACAAAAA	CAGATTTGAA	GAAATCATCA	AGGAAACCTC	50
	CAACTTCGTC	AAGAAGGTTG	GTTACAACCC	AAAGACTGTT	CCATTCGTTT	100
45	CAATCTCTGG	TTGGAATGGT	GACAACATGA	TTGAACCATC	CACCAACTGT	150
	CCATGGTACA	AGGGTTGGGA	AAAGGAAACC	AAATCCGGTA	AAGTTACTGG	200
	TAAGACCTTG	TTAGAAGCTA	TTGACGCTAT	TGAACCACCA	ACCAGACCAA	250
	CCGACAAACC	ATTGAGATTG	CCATTGCAAG	ATGTTTACAA	GATCGGTGGT	300
	ATTGGTACTG	TGCCAGTCGG	TAGAGTTGAA	ACTGGTATCA	TCAAAGCCGG	350
50	TATGGTTGTT	ACTTTCGCCC	CAGCTGGTGT	TACCACTGAA	GTCAAATCCG	400
	TTGAAATGCA	TCACGAACAA	TTGGCTGAAG	GTGTTCCAGG	TGACAATGTT	450
	GGTTTCAACG	TTAAGAACGT	TTCCGTAA	GAAATTAGAA	GAGGTAACGT	500
	TTGTGGTGAC	TCCAAGAACG	ATCCACCAA	GGTTGTGAC	TCTTTCAATG	550
	CCCAAGTCAT	TGTTTTGAAC	CATCCAGGTC	AAATCTCTGC	TGGTTACTCT	600
55	CCAGTCTTGG	ATTGTCACCC	TGCCACATT	GCTTGTAAT	TCGACACTTT	650
	GGTTGAAAAG	ATTGACAGAA	GAACGGTAA	GAAATTGGAA	GAAAATCCAA	700
	AATTCGTCAA	ATCCGGTGAT	GCTGCTATCG	TCAAGATGGT	CCCAACCAA	750
	CCA					753

60

2) INFORMATION FOR SEQ ID NO: 625

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 625

CGTTGAAGAC ACGACCCAAA GTATCC

26

2) INFORMATION FOR SEQ ID NO: 626

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 626

TACCACCTTT TAAGTAAGGT GCTAAT

26

2) INFORMATION FOR SEQ ID NO: 627

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 627

ATTGTCTATA AAAATGGCGA TAAGTC

26

2) INFORMATION FOR SEQ ID NO: 628

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus agalactiae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 628

AAAATGGCGA TAAGTCACAA AAAGTA

26

2) INFORMATION FOR SEQ ID NO: 629

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Chlamydia pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 629

AAGTTCCATC TCAACAAGGT CAATA

25

2) INFORMATION FOR SEQ ID NO: 630

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Chlamydia pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 630

CGGAGCTATC CTAGTCGTTT CA

22

2) INFORMATION FOR SEQ ID NO: 631

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 631

CAGACCAACY GAIAARCCAT TRAGAT

26

2) INFORMATION FOR SEQ ID NO: 632

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 632

CCCTTTGGTG GRTCSTKCTT GGA

23

2) INFORMATION FOR SEQ ID NO: 633

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 633

CAGACCAACY GAIAARCCIT TRAGAT

26

2) INFORMATION FOR SEQ ID NO: 634

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 634

AACACYGTCA GRRCIATTGC YATGGA

26

2) INFORMATION FOR SEQ ID NO: 635

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 635
AAACCRGTIA RRGCRCTCT IGCTCT 26

2) INFORMATION FOR SEQ ID NO: 636

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 636
ACTGGYGTTG AIATGTTCCG YAA 23

2) INFORMATION FOR SEQ ID NO: 637

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 637
ACGTCAGTIG TACGGAARTA GAA 23

2) INFORMATION FOR SEQ ID NO: 638

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 638
CCAATGCCAC AAACICGTGA RCACAT 26

2) INFORMATION FOR SEQ ID NO: 639

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 639

TTTACGGAAC ATTCWACAC CWGTIACA

28

2) INFORMATION FOR SEQ ID NO: 640

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 640

TCCATGGTIT WYGGICARAT GAA

23

2) INFORMATION FOR SEQ ID NO: 641

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 641

TGATAACCWA CIGCIGAIGG CATACG

26

2) INFORMATION FOR SEQ ID NO: 642

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 642

GGCGTIGGIG ARCGIACICG TGA

23

2) INFORMATION FOR SEQ ID NO: 643

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 643

ACTGGIGTIG ARATGTTCCG YAA

23

2) INFORMATION FOR SEQ ID NO: 644

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 644

ACGTCIGTIG TICKGAARTA GAA

23

2) INFORMATION FOR SEQ ID NO: 645

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 645

ACGTCIGTIG TICKGAARTA RAA

23

2) INFORMATION FOR SEQ ID NO: 646

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 646

ATCGACAAGC CITTCTTIAT GSC

23

2) INFORMATION FOR SEQ ID NO: 647

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 647

ACGTCCGTSG TRCGGAAGTA GAACTG

26

2) INFORMATION FOR SEQ ID NO: 648

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 648

ACGTCSGTSG TRCGGAAGTA GAACTG

26

2) INFORMATION FOR SEQ ID NO: 649

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 649

GTCCTATGCC TCARACWCGI GAGCAC

26

2) INFORMATION FOR SEQ ID NO: 650

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
5 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 650
TTACGGAACA TYTCAACACC IGT 23

15 2) INFORMATION FOR SEQ ID NO: 651

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 bases
20 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 651
TGACGACCAC CITCYTCYTT YTTCA 25

30 2) INFORMATION FOR SEQ ID NO: 652

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 bases
35 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 652
CCWAYAGTIY KICCICCYTC YCTIATA 27

45 2) INFORMATION FOR SEQ ID NO: 653

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 653

60 GAYTTTATIA ARAAYATGAT 20

2) INFORMATION FOR SEQ ID NO: 654

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 654

TACAARATYK GIGGTATYGG

20

2) INFORMATION FOR SEQ ID NO: 655

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 655

CCRATACCIC MRATYTTGTA

20

2) INFORMATION FOR SEQ ID NO: 656

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 656

AATTAATGGC TGCAGTTGAY GA

22

2) INFORMATION FOR SEQ ID NO: 657

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 657

TTGTCCACGT TCGATRTCTT CA

22

5

2) INFORMATION FOR SEQ ID NO: 658

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

10

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 658

GATYTAGTCG ATGATGAAGA ATT

23

2) INFORMATION FOR SEQ ID NO: 659

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

25

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 659

35

GCTTTTGTGIG TTTCWGGTTT RAT

23

2) INFORMATION FOR SEQ ID NO: 660

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

40

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 660

50

GTAGAATTGA GGACGGTAGT TAG

23

2) INFORMATION FOR SEQ ID NO: 661

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid

55

60

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 661

GTAGAAATGT GGWCGATART TRT

23

2) INFORMATION FOR SEQ ID NO: 662

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 832 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Corynebacterium diphtheriae*
(B) STRAIN: ATCC 27010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 662

	CGGCGCAATC	CTCGTTGTTG	CTGCCACCGA	CGGCCCAATG	CCTCAGACCC	50
	GTGAGCACGT	TCTGCTCGCT	CGCCAGGTCG	GCGTTCCTTA	CATCCTCGTT	100
30	GCTCTGAACA	AGTGCGACAT	GGTTGATGAT	GAGGAAATCA	TCGAGCTCGT	150
	CGAGATGGAG	ATCCRTGAGC	TGCTCGCTGA	GCAGGATTAC	GACGAAGAGG	200
	CTCCAATCAT	CCACATCTCC	GCACTGAAGG	CTCTTGAGGG	CGACGAGAAG	250
	TGGACCCAGT	CCATCATCGA	CCTCATGCAG	GCTTGCKATG	ATTCCATCCC	300
	AGACCCAGAG	CGTGAGACCG	ACAAGCCATT	CCTCATGCCT	ATCGAGGACA	350
35	TCTTCAACAT	CACCGGCCGC	GGTACCGTTG	TTACCGGCCG	TGTTGAGCGT	400
	GGCTCCCTGA	AGGTCAACGA	GGACGTCGAG	ATCATCGGTA	TCCGCGAGAA	450
	KGCTACCACC	ACCACCGTTA	CCGGTATCGA	GATGTTCCGT	AAGCTTCTCG	500
	ACTACACCGA	GGCTGGCGAC	AACTGTGGTC	TGCTTCTCCG	TGGCGTTAAG	550
	CGCGAAGACG	TTGAGCGTGG	CCAGGTTGTT	GTTAAGCCAG	GCGCTTACAC	600
40	CCCTCACACC	GAGTTCGAGG	GCTCTGTCTA	CGTTCTGTCC	AAGGACGAGG	650
	GTGGCCGCCA	CACCCCATTC	TTCGACAAC	ACCGCCACA	GTTCTACTTC	700
	CGCACCACCG	ACGTTACCGG	TGTTGTGAAG	CTTCCTGAGG	GCACCGAGAT	750
	GGTCATGCCT	GGCGACAACG	TCGACATGTC	CGTCACCCTG	ATCCAGCCTG	800
45	TCGCTATGGA	TGAGGGCCTG	CGCTTCGCTA	TC		832

2) INFORMATION FOR SEQ ID NO: 663

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1192 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida catenulata*
(B) STRAIN: ATCC 10565

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 663

```

AACGCGCAGC AAGACTTGGT GTTGGAGGTT TCTCAGCACT TGGGTGAGAA      50
5  CACCGTGCGT ACCATTGCCA TGGACGGTAC CGAGGGTTTG GTGAGAGGTA      100
   CCGCTGTCAC TGACACCGGT GCTCCCATCT CGGTCCCCGT TGGTCAGGGT      150
   ACCTTGGGCC GGATCATCAA CGTTGTCGGT GAGCCCATCG ACGAGCGTGG      200
   TCCCATCCAG TGCAAGCAGA GAAACCCCAT TCACGCCGAG CCCCCGTCTT      250
   TCACCGAGCA GTCCGTCGAG GCTGAGGTGT TGGAGACCGG TATCAAGGTT      300
10  TGGTGCCGGT GTCGGTAAGA CCGTGTTTCAT CCAGGAGTTG ATTAACAACA      350
   TTGCCAAGGC CCACGGTGGT TTCTCCGTGT TCACTGGTGT CGGTGAGCGT      450
   ACTCGTGAGG GTAACGACTT GTACCGTGAA ATGAAGGAGA CCGGTGTCAT      500
   CAACTTGGAG GGCGACTCCA AGGTGGCCTT GGTGTTTCGGT CAGATGAACG      550
15  AGCCCCCGGG GGCTCGTGCC CGTGTCGCCT TGACCGGTTT GACCATTGCC      600
   GAGTACTTCC GTGACGAGGA AGGCCAGGAC GTGTTGTTGT TCGTTGACAA      650
   CATTTTCAGA TTCACCCAGG CCGGTTCCGA GGTGTCGGCG TTGTTGGGTC      700
   GTATCCCCTC CGCCGTCGGT TACCAGCCCA CTTTGGCCAC CGACATGGGT      750
   TTGTTGCAGG AGAGAATTAC CACCACCAAG AAGGGTTCCG TCACCTCTGT      800
20  GCAGGCCGTG TACGTCCCTG CCGATGACTT GACTGACCCT GCCCCGCCA      850
   CCACTTTCGC TCACTTGAGC GCCACCACCG TGTTGTCGCG TGGTATCTCC      900
   GAGTTGGGTA TCTACCCCGC CGTCGACCCC TTGGACTCCA AGTCGAGATT      950
   GTTGAGCGTC GAGGTTGTTG GCCAGGAGCA CTACGACGTC GCCACCGGTG     1000
   TCCAGGAGTG CTTGCAGGCC TACAAGTCGT TGCAGGACAT CATTGCCATT     1050
25  TTGGGTATGG ACGAGTTGTC CGAGCAGGAC AAGTTGACCG TCGAGAGAGC     1100
   CCGTAAGATC CAGCGTTTCT TGTCGCAGCC CTTCGCTGTC GCCGAGGTTT     1150
   TCACTGGTAT CCCCGGTAGA TTGGTGAGAT TGCAGGACAC CG              1192

```

30

2) INFORMATION FOR SEQ ID NO: 664

(i) SEQUENCE CHARACTERISTICS:

```

(A) LENGTH: 29 bases
35 (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Single
   (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: DNA

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 664

AAAYATGATIA CIGGIGCIGC ICARATGGA

29

45

2) INFORMATION FOR SEQ ID NO: 665

(i) SEQUENCE CHARACTERISTICS:

```

50 (A) LENGTH: 1377 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: Saccharomyces cerevisiae
60 (C) ACCESSION NUMBER: extracted from X00779

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 665

	ATGGGTAAAG	AGAAGTCTCA	CATTAACGTT	GTCGTTATCG	GTCATGTCGA	50
	TTCTGGTAAG	TCTACCACTA	CCGGTCATTT	GATTTACAAG	TGTGGTGGTA	100
5	TTGACAAGAG	AACCATCGAA	AAGTTCGAAA	AGGAAGCCGC	TGAATTAGGT	150
	AAGGGTTCTT	TCAAGTACGC	TTGGGTTTTG	GACAAGTTAA	AGGCTGAAAG	200
	AGAAAGAGGT	ATCACTATCG	ATATTGCTTT	GTGGAAGTTC	GAAACTCCAA	250
	AGTACCAAGT	TACCGTTATT	GATGCTCCAG	GTCACAGAGA	TTTCATCAAG	300
	AACATGATTA	CTGGTACTTC	TCAAGCTGAC	TGTGCTATCT	TGATTATTGC	350
10	TGGTGGTGTC	GGTGAATTCG	AAGCCGGTAT	CTCTAAGGAT	GGTCAAACCA	400
	GAGAACACGC	TTTGTGGCT	TTACCTTGG	GTGTTAGACA	ATTGATTGTT	450
	GCTGTCAACA	AGATGGACTC	CGTCAAATGG	GACGAATCCA	GATTCCAAGA	500
	AATTGTCAAG	GAAACCTCCA	ACTTTATCAA	GAAGGTTGGT	TACAACCCAA	550
	AGACTGTTCC	ATTTCGTCCA	ATCTCTGGTT	GGAACGGTGA	CAACATGATT	600
15	GAAGCTACCA	CCAACGCTCC	ATGGTACAAG	GGTTGGGAAA	AGGAAACCAA	650
	GGCCGGTGTC	GTCAAGGGTA	AGACTTTGTT	GGAAGCCATT	GACGCCATTG	700
	AACAACCATC	TAGACCAACT	GACAAGCCAT	TGAGATTGCC	ATTGCAAGAT	750
	GTTTACAAGA	TGGTGCTAT	TGGTACTGTG	CCAGTCGGTA	GAGTTGAAAC	800
	CGGTGTCATC	AAGCCAGGTA	TGGTTGTTAC	TTTTGCCCCA	GCTGGTGTTA	850
20	CCACTGAAGT	CAAGTCCGTT	GAAATGCATC	ACGAACAATT	GGAACAAGGT	900
	GTTCCAGGTG	ACAACGTTGG	TTTCAACGTC	AAGAACGTTT	CCGTTAAGGA	950
	AATCAGAAGA	GGTAACGTCT	GTGGTGACGC	TAAGAACGAT	CCACCAAAGG	1000
	GTTGCGCTTC	TTTCAACGCT	ACCGTCATTG	TTTTGAACCA	TCCAGGTCAA	1050
	ATCTCTGCTG	GTTACTCTCC	AGTTTGGAT	TGTCACACTG	CTCACATTGC	1100
25	TTGTAGATTG	GACGAATTGT	TGGAAAAGAA	CGACAGAAGA	TCTGGTAAGA	1150
	AGTTGGAAGA	CCATCCAAAG	TTCTTGAAGT	CCGGTGACGC	TGCTTTGGTC	1200
	AAGTTCGTTT	CATCTAAGCC	AATGTGTGTT	GAAGCTTTCA	GTGAATACCC	1250
	ACCATTAGGT	AGATTGCTG	TCAGAGACAT	GAGACAAACT	GTCGCTGTCG	1300
	GTGTTATCAA	GTCTGTTGAC	AAGACTGAAA	AGGCCGCTAA	GGTTACCAAG	1350
30	GCTGCTCAAA	AGGCTGCTAA	GAAATAA			1377

2) INFORMATION FOR SEQ ID NO: 666

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1536 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

45

- (A) ORGANISM: *Saccharomyces cerevisiae*
 (C) ACCESSION NUMBER: extracted from M12082

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 666

50	ATGGTTTTGC	CAAGACTATA	TACTGCTACA	TCCCGTGCTG	CTTTTAAAGC	50
	AGCCAAACAA	TCCGCTCCGC	TTCTATCCAC	TTCGTGGAAA	AGATGTATGG	100
	CCTCAGCTGC	TCAATCTACT	CCAATCACCG	GTAAAGTTAC	CGCTGTCATT	150
	GGTGCCATTG	TTGACGTTCA	TTTGAACAA	TCAGAGTTGC	CCGCTATTTT	200
	GAACGCTTTA	GAAATTAAAA	CACCTCAAGG	TAAGTTGGTT	TTGGAAGTTG	250
55	CTCAACATTT	GGGTGAAAAC	ACTGTCAGAA	CCATTGCTAT	GGATGGTACC	300
	GAAGGTTTGG	TCCGTGGTGA	AAAGGTTCTT	GACACTGGTG	GCCCTATCTC	350
	CGTCCCAGTT	GGGAGAGAAA	CTTTAGGGAG	AATCATCAAC	GTTATCGGTG	400
	AACCTATTGA	TGAAAGAGGT	CCAATTAAAT	CCAAATAAG	AAAGCCAATT	450
	CACGCAGACC	CTCCTAGTTT	TGCAGAACAA	CTACTTCGG	CTGAAATTTT	500
60	GGAAACAGGT	ATCAAAGTCG	TCGATCTATT	AGTCTCTTAT	GCCAGAGGTG	550

	GTAAGATTGG	TCTTTTCGGT	GGTGCAGGTG	TCCGTAAGAC	TGTGTTTCATT	600
	CAAGAATTGA	TTAACAATAT	CGCCAAGGCC	CATGGTGGTT	TTTCCGTTTT	650
	CGCCGGTGTT	GGTGAAAGGA	CCAGAGAGGG	TAATGACTTG	TACCGTGAAA	700
	TGAAGGAAAC	TGGAGTCATT	AAC TTGGAAG	GTGAATCCAA	GGTCGCCTTA	750
5	GTTTTTCGGT	AAATGAACGA	ACCTCCAGGA	GCCAGAGCCA	GAGTCGCTTT	800
	AACTGGTTTG	ACGATCGCTG	AATATTTTCTG	AGATGAAGAA	GGTCAAGACG	850
	TCTTGTGTT	TATCGACAAT	ATCTTTTAGAT	TTACTCAAGC	TGGTTCAGAA	900
	GTCTCTGCCC	TTTTGGGGTCG	TATTCCATCT	GCCGTCGGTT	ATCAACCAAC	950
	TTTGGCCACT	GATATGGGTC	TCTTACAAGA	AAGAATTACC	ACCACAAAGA	1000
10	AGGGTTCTGT	CAC TTCTGTG	CAAGCCGTTT	ATGTTCCAGC	CGATGATTTA	1050
	ACAGATCCGT	CTCCGTCCAC	ATCTTTTGCC	CATTTGGACG	CATCATCCGT	1100
	CTTGTCAGA	GGTATTTTCTG	AATTAGGTAT	TTACCCCTGCA	GTGGATCCAT	1150
	TGGATTCTAA	ATCAAGGTTA	TTGGATGCCG	CCGTTGTCGG	TCAAGAACAT	1200
	TATGACGTCG	CCTCCAAGGT	TCAAGAAACT	TTACAGACCT	ATAAATCTTT	1250
15	ACAAGATATC	ATTGCTATTT	TGGGTATGGA	TGAATTGTCC	GAACAAGATA	1300
	AACTAACTGT	CGAAAGGGCA	AGAAAGATTC	AAAGATTCTT	ATCTCAACCA	1350
	TTTGCTGTCTG	CCGAAGTCTT	TACTGGTATC	CCAGGTAAAT	TAGTGAGATT	1400
	AAAGGACACC	GTTCCTCTGT	TCAAAGCCGT	TTTGGAAGGT	AAATACGATA	1450
	ATATACCAGA	ACATGCTTTC	TATATGGTTG	GTGGTATTGA	AGATGTTGTT	1500
20	CGTAAAGCTG	AAAAGTTAGC	CCGTGAAGCC	AACTAG		1536

2) INFORMATION FOR SEQ ID NO: 667

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1293 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma cruzi*
 (B) STRAIN: Y

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 667

40	CGGAAGGCGT	GCCGCCGGTG	TTAACTGCTT	TGGATGTGGT	GGAAAACTT	50
	GGCCGTGACG	AGCCCTTGAC	ACTTGAAATT	GTACAGCACT	TGGACGCCCCA	100
	CACCGGCCGT	TGCATTGCGA	TGCAGACGAC	AGATCTGCTT	AAGCTGAAAT	150
	CGAAGGTAGT	CTCGAGTGGC	GGGAACATTT	CTGTGCCTGT	GGGTCGGGAG	200
	ACACTTGGCA	GAATCTTCAA	TGTGCTGGGC	GATGCCATTG	ACCAGCGCGG	250
45	CCATGTTGGA	GAGAAGCAAC	GCATGCCTAT	TCACGCTGTG	GCACCAAAGT	300
	TGGCGGATCA	GGCGGCAGAG	GACACCATTC	TCACAACGGG	TATCAAGGTG	350
	ATTGATCTGA	TTTTGCCCTA	CTGCAAGGGT	GGGAAGATTG	GTCTTTTGTG	400
	TGGTGCTGGC	GTGGGCAAGA	CGGTTATTAT	CATGGAACCT	ATTAACAACG	450
	TTGCCAAGGG	CCATGGTGGG	TTCTCCGTCT	TTGCGGGTGT	TGGTGAACGC	500
50	ACGCGTGAGG	GGACGGATCT	TTACCTGGAG	ATGATGCAAT	CCAAAGTTAT	550
	TGACCTGAAG	GGTGACTCGA	AGTGTGTGTT	GGTGTATGGT	CAGATGAACG	600
	AGCCTCCGGG	TGCCCCTGCT	CGTGTGGCGC	AGTCTGCCTT	GACAATGGCC	650
	GAGTACTTCC	GTGATGTGGA	AGGGCAAGAC	GTGTTGCTTT	TTATCGACAA	700
	CATTTTCCGC	TTTACGCAGG	CAAACCTGTA	GGTGTACGCG	CTGTTGGGTC	750
55	GTATTCCCGC	TGCCGTCGGC	TACCAGCCTA	CCCTTGCTGA	GGATCTTGGG	800
	CAGTTGCAGG	AGCGCATTAC	GTCCACGACA	AAAGGTTCCA	TTACCTCTGT	850
	GCAGGCTGTG	TACGTGCCAG	CCGATGATAT	TACCGACCCT	GCGCCAGCAA	900
	CGACCTTTTC	CCACCTCGAT	GCCACGACGG	TGCTGGACCG	TGCCGTTGCC	950
	GAATCCGGCA	TTTACCCCGC	TGTCAACCCA	CTGGAGTGTG	CCTCGCGTAT	1000
60	CATGGACCCG	GATGTAATCA	GCGTTGACCA	CTACAACGTG	GCGCAGGATG	1050

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TGGTGCAGAT GCTTACCAAG TACAAGGAGC TGCAGGATAT CATTGCGGTG 1100
CTTGGCATTG ATGAGCTCAG TGAGGAGGAT AAACCTTATCG TGGACCGTGC 1150
GCGTAAGGTG ACAAAGTTTC TCTCCCAGCC TTTCAGGTG GCGGAGGTGT 1200
TTACTGGCAT GACAGGCCAC TACGTGCAGC TGGAGGAGAC CATTGAGTCT 1250
5 TTTTCCGGCC TGTGATGGG CACATATGAT CAGGTGCCCG AGA 1293

```

2) INFORMATION FOR SEQ ID NO: 668

10

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 1191 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
15 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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20 (A) ORGANISM: Corynebacterium glutamicum
(C) ACCESSION NUMBER: X77034

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 668

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25 GTGGCAAAGG CGAAGTTCGA GCGTACCAAG CCCACGTAA ACATCGGCAC 50
CATCGGTCAC GTTGACCACG GTAAGACCAC CACCACCGCG GCTATCACCA 100
AGGTTCTGGC TGACACTTAC CCTGAGCTCA ACGAGGCTTT CGCCTTCGAC 150
TCCATCGATA AGGCTCCTGA GGAGAAGGAG CGTGGCATCA CGATCAACAT 200
CTCCCACGTT GAGTACCAGA CTGAAAAGCG CCACTACGCA CACGTTGACG 250
30 CTCCAGGCCA CGCCGACTAC ATCAAGAACA TGATTACCGG CGCTGCTCAG 300
ATGGACGGCG CAATCCTCGT TGTGCTGCT ACCGACGGCC CAATGCCTCA 350
GACCCGTGAG CACGTTCTTC TTGCTCGCCA GGTGCGCGTT CCTTACATCC 400
TCGTTGCTCT TAACAAGTGC GACATGGTTG AGGATGAGGA AATCATCGAG 450
CTCGTCGAGA TGAAGTTTCG TGAATCTCTT GCTGAGCAGG ACTACGACGA 500
35 AGAGGCTCCA ATTGTTTACA TCTCCGCTCT GAAGGCTCTT GAGGGCGACG 550
AGAAGTGGGG CAAGCAGATC CTTGAGCTCA TGCAGGCTTG CGATGACAAC 600
ATCCCTGACC CAGTTCGTGA GACCGACAAG CCATTCCTCA TGCCTATCGA 650
GGACATCTTC ACCATCACCG GTCGTGGCAC CGTTGTTACC GGTCGTGTTG 700
AGCGCGGTAC CCTGAACGTG AACGATGATG TTGACATCAT CCGCATCAAG 750
40 GAGAAGTCCA CCTCCACCAC CGTTACCGGT ATCGAGATGT TCCGTAAGCT 800
TCTTGACTCC GCTGAGGCTG GCGACAAC TGCTGCTGCTT CTCCGTGGTA 850
TCAAGCGCGA AGATGTTGAG CGTGGCCAGG TTATCGTTAA GCCAGGCGCT 900
TACACCCCTC ACACCGAGTT CGAGGGCTCT GTCTACGTTT TGTCCAAGGA 950
TGAAGGTGGC CGCCACACCC CATTCTTCGA CAACTACCGT CCTCAGTTCT 1000
45 ACTTCCGCAC CACCGACGTT ACCGGTGTG TGAAGCTTCC AGAGGGCACC 1050
GAGATGGTCA TGCCTGGCGA CAACGTCGAC ATGTCCGTCA CCCTGATCCA 1100
GCCTGTCGCT ATGGACGAGG GCCTGCGTTT CGCTATCCGC GAAGGCTCCC 1150
GCACCGTTGG CGCTGGTCGT GTCACCAAGA TCATCAAGTA A 1191

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50

2) INFORMATION FOR SEQ ID NO: 669

(i) SEQUENCE CHARACTERISTICS:

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55 (A) LENGTH: 1383 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*

(C) ACCESSION NUMBER: extracted from V00267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 669

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5      ATGGGCTACTG GAAAGATTGT CCAGGTAATC GGCGCCGTAG TTGACGTCGA      50
      ATTCCCTCAG GATGCCGTAC CGCGCGTGTA CGATGCTCTT GAGGTGCAAA      100
10     ATGGTAATGA GCGTCTGGTG CTGGAAGTTC AGCAGCAGCT CGGCGGCGGT      150
      ATCGTACGTA CCATCGCAAT GGGTTCCTCC GACGGTCTGC GTCGCGGTCT      200
      GGATGTAAAA GACCTCGAAC ACCCGATTGA AGTCCCGGTA GGTAAGCGA      250
      CTCTGGGCCG TATCATGAAC GTACTGGGTG AACC GGTCGA CATGAAAGGC      300
      GAGATCGGTG AAGAAGAGCG TTGGGCGATT CACCGCGCAG CACCTTCCTA      350
15     CGAAGAGCTG TCAAACCTCT AGGAAC TGCTG GAAACCGGT ATCAAAGTTA      400
      TCGACCTGAT GTGTCCGTTC GCTAAGGGCG GTAAAGTTGG TCTGTTCCGT      450
      GGTGCGGGTG TAGGTAAAAC CGTAAACATG ATGGAGCTCA TTCGTAACAT      500
      CGCGATCGAG CACTCCGGTT ACTCTGTGTT TCGGGGCGTA GGTGAACGTA      550
      CTCGTGAGGG TAACGACTTC TACCACGAAA TGACCGACTC CAACGTTATC      600
20     GACAAAGTAT CCCTGGTGTA TGGCCAGATG AACGAGCCGC CGGGAAACCG      650
      TCTGCGCGTT GCTCTGACCG GTCTGACCAT GGCTGAGAAA TTCCGTGACG      700
      AAGGTCGTGA CGTTCTGCTG TTCGTTGACA ACATCTATCG TTACACCCTG      750
      GCCGGTACGG AAGTATCCGC ACTGCTGGGC CGTATGCCTT CAGCGGTAGG      800
      TTATCAGCCG ACCCTGGCGG AAGAGATGGG CGTTCGTCAG GAACGTATCA      850
25     CCTCCACCAA AACTGGTTCT ATCACCTCCG TACAGGCAGT ATACGTACCT      900
      GCGGATGACT TGACTGACCC GTCTCCGGCA ACCACCTTTG CGCACCTTGA      950
      CGCAACCGTG GTACTGAGCC GTCAGATCGC GTCTCTGGGT ATCTACCCGG      1000
      CCGTTGACCC GCTGGACTCC ACCAGCCGTC AGCTGGACCC GCTGGTGGTT      1050
      GGTCAGGAAC ACTACGACAC CGCGCGTGGC GTTCAGTCCA TCCTGCAACG      1100
30     TTATCAGGAA CTGAAAGACA TCATCGCCAT CCTGGGTATG GATGAACTGT      1150
      CTGAAGAAGA CAAACTGGTG GTAGCGCGTG CTCGTAAGAT CCAGCGCTTC      1200
      CTGTCCCAGC CGTTCTTCGT GGCAGAAGTA TTCACCGGTT CTCCGGGTAA      1250
      ATACGTCTCC CTGAAAGACA CCATCCGTGG CTTTAAAGGC ATCATGGAAG      1300
      GCGAATACGA TCACCTGCCG GAGCAGGCGT TCTACATGGT CGGTTCCATC      1350
35     GAAGAAGCTG TGGAAAAAGC CAAAAA ACTT TAA      1383

```

2) INFORMATION FOR SEQ ID NO: 670

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1410 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(B) STRAIN: NCTC 11638

(C) ACCESSION NUMBER: extracted from AF004014

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 670

```

55     ATGAAAGCGA TGGAAGGTAA AATCATTCAG GTTTTAGGCC CGGTGGTAGA      50
      TGTGGAGTTT GAATCCTATC TGCCGCGCAT TTTTGAAGCA CTAGACATTA      100
      ATTTTGAAGT TAATGGCGTT CAAAAATCTT TAGTTTTAGA GGTGGCAGCC      150
      CATTGCGGTG GTAATCGGGT GCGAGCGATT GCTATGGATA TGACAGAAGG      200
60     CTTAGTGCGT AACCAAGCCG TCAAAGCTCG TGGCAAATG ATTGAAGTGC      250

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CTGTGGGCGA AGAAGTGTTA GGGCGTATTT TTAATGTTGT GGGCGAGAGC 300
ATTGATAATT TAGAGCCGCT TAAGCCGTCC TTAACCTGGC CCATTCACAG 350
AAAAGCCCCCT AGTTTTTGAGC AGCAAAGCAC TAAAACAGAA ATGTTTGAAA 400
CCGGTATTAA AGTCATTGAC TTGCTCGCGC CTTATTCTAA GGGCGGTAAA 450
5 GTAGGCTTGT TTGGTGGGGC TGGCGTAGGC AAAACGGTGA TCATTATGGA 500
GCTTATCCAC AATGTGGCTT ATAAGCATAA CGGGTATTCTG GTGTTTGCAG 550
GTGTGGGGGA GCGCACCAGA GAAGGGAACG ATCTGTATTT TGAGATGAAA 600
GAAGGGGGCG TTTTAGACAA AGTTGCGTTG TGCTATGGGC AAATGAATGA 650
GCCACCAGGT GCAAGGAATC GCATCGCATT CACCGGCTTG ACGATGGCGG 700
10 AGTATTTCCG TGATGAAAAG GGCTTAGATG TGTGATGTT TATTGATAAC 750
ATCTTTAGAT ACGCTCAAAG CGGTGCGGAA ATGAGCGCGC TATTAGGCCG 800
TATCCCTTCA GCGGTGGGGT ATCAGCCCAC GCTAGCCGGG GAAATGGGGA 850
AACTTCAAGA GCGTTCGCT TCCACTAAAA ATGGCTCTAT CACTTCGGTT 900
CAAGCGGTGT ATGTGCCAGC AGAGGACTTG ACTGACCCAG CCCCTGCTTC 950
15 GGTGTTTGCG CATTAGATG CGACTACGGT GTTGAATAGA AAGATCGCTG 1000
AAAAAGGGAT TTATCCGGCG GTGGATCCTT TGGATTCCAC TTCAAGGATT 1050
TTAAGCCCTC AAATGATTGG CGAGAAGCAC TATGAAATCG CCACCGGTAT 1100
CCAGCAAGTT TTGCAAAAAAT ACAAGGATTT GCAAGATATT ATTGCGATTT 1150
TGGGATTGGA CGAATTGAGC GAAGAGGATA AAAAAACGGT TGAAAGGGCC 1200
20 AGAAAAATTG AGAAGTTTTT ATCCCAGCCG TTTTTGTGG CTGAAGTGTT 1250
TACAGGAAGT CCCGGTAAAT ATGTGACTCT CCAAGAGACT TTAGAGGGCT 1300
TTGGAGGGAT TTTAGAGGGC AAATACGATC ACATTCTCTG AAACGCGTTT 1350
TACATGGTGG GCAGCATTCA AGAGGTTTTA GAAAAAGCTA AAAACATGAA 1400
AAATTCCTAA 1410
25

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2) INFORMATION FOR SEQ ID NO: 671

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30 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 1401 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
35 (ii) MOLECULE TYPE: Genomic DNA
    (vi) ORIGINAL SOURCE:
    (A) ORGANISM: Clostridium acetobutylicum
    (B) STRAIN: DSM 792
    (C) ACCESSION NUMBER: extracted from AF101055
40

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 671

```

45 ATGCCAGAAC ATGTAGGTAA AATTGTTTCTG GTAATAGGAC CTGTTGTGGA 50
TATTAAATTT GATGCAGAGA ACCTTCCTGA CATCTATAAT TCCATAGAAA 100
TAGATATGGG AGATAATAAA AAATCATTG CTGAAGTTGA ACAACATGTA 150
GGAGATGACA TAGTAAGAAC AATAGCAATG GAAGGTACTG ACGGATTAAA 200
AAGAGGAATG GAAGCAGTTA AACTGTTTAA ACCAATATCT GTACCAGTTG 250
50 GAGAAAAATG TTTAGGACGT CTTTTTAATG TTTTAGGTCA GACAATAGAT 300
GAAGCAGGAG ACATGAATGC TGATAAGTAT TATCCAATTC ATAGACCAGC 350
TCCAACCTTT GAAGAACAAT CAGTTCAACC AGAAATGTTT GAAACAGGTA 400
TTAAGGTTAT AGATTTACTT GCTCCATATC AAAAGGGTGG AAAAAATCGGT 450
TTGTTTCGGTG GTGCCGGTGT TGGTAAAACA GTTCTTATTC AGGAACTTAT 500
55 AAATAATATA GCAAAAAGAAC ACGGTGGATT ATCAGTATTC ACAGGTGTTG 550
GAGAAAGAAC AAGAGAAGGT AATGACCTTT ATTATGAAAT GAAAGATTCA 600
GGAGTTATAA ATAAAACAGC TCTAGTATTT GGTGAGATGA ATGAACCACC 650
TGGCGCTAGA ATGAGAGTTG CTTTAAACAGG ACTTACAATG GCTGAATATT 700
TTAGAGACAA AGGTCAAGAT GTGCTTCTAT TTATAGATAA TATATTCAGA 750
60 TTTACACAAG CTGGTTCAGA GGTTCAGCT TACTTGGTA GAATACCTAG 800

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	TGCCGTTGGT	TATCAGCCAA	CACTTGCAAA	TGAAATGGGT	GCTCTTCAAG	850
	AGAGAATAAC	ATCAACAAA	CAGGGTTCAA	TCACATCCGT	TCAGGCTGTA	900
	TATGTTCTCT	CTGATGACCT	TACAGACCCA	GCTCCAGCAA	CAACATTTAC	950
	GCATCTTGAT	GCAACAACAG	TTCTTTCAAG	AGAAATATCA	AACTTAGGAA	1000
5	TATATCCTGC	AGTTAGTCCT	CTTGAATCAA	CTTCAAGAAT	ACTTGATCCA	1050
	AGAATTGTTG	GAGAAGAGCA	TTATGAAGTT	GCTAACAAGG	TTAAACATAT	1100
	ACTTGAAAGA	TATCAAGAAC	TTCAAGATAT	CATAGCTATA	CTTGGTGTTG	1150
	ATGAACTTTC	AGATGAGGAT	AGATTGTTAG	TTGGAAGAGC	AAGAAGAGTA	1200
	CAGAGATTCT	TATCTCAAGC	TTTTAGTGTT	GCTGAACAAT	TTACAGGAAT	1250
10	GAAAGGTCAG	TTTGTACCTG	TAAAAGATAC	TATAAGAAGT	TTTAAAGAAA	1300
	TATTAGATGG	TAAGTGTGAT	GATCTTCCAG	AAGCTGCATT	TTTATTTGCA	1350
	GGAACAATAG	AAGATGTAAA	AGAAAAAGCT	AAAAAATGA	TGGAAAGCTA	1400
	A					1401

15

2) INFORMATION FOR SEQ ID NO: 672

	(i) SEQUENCE CHARACTERISTICS:
20	(A) LENGTH: 1509 bases
	(B) TYPE: Nucleic acid
	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear
25	(ii) MOLECULE TYPE: Genomic DNA
	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: <i>Cytophaga lytica</i>
	(B) STRAIN: DSM 2039
30	(C) ACCESSION NUMBER: M22535

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 672

	ATGTCTAAAG	TTACAGGTAA	AGTTTCCCAA	ATTATTGGCC	CAGTTATAGA	50
35	TGTGGAGTTC	CAAGCAGGGG	TAGATCTTCC	AAAAATTTAT	GATTCATTAG	100
	AAATTAAAAA	AGCAGATGGA	TCAATTTTGG	TTTTGGAAGT	ACAATCACAC	150
	ATTGGTGAGA	ACACAGTAAG	AACTATATCT	ATGGATTCTT	CTGATGGTTT	200
	AAGTCGTGGA	GCAGAGGTTA	ATGCAACAGG	AAGCGCTATA	CAAATGCCAG	250
	TTGGAGATGA	CGTTTACGGA	CGTTTATTTA	ACGTAATTGG	AGACGCTATT	300
40	GATGGTCTTG	GGAATTTACC	AAAATCTGGT	AAAGATGGTT	TGCCAATACA	350
	CAGAGAGGCA	CCAAAATTTG	AAGACTTATC	TACTTCTACA	GAAGTATTAT	400
	TTACAGGTAT	TAAAGTAATT	GACCTTATTG	AGCCTTATGC	AAAAGGTGGT	450
	AAGATTGGTT	TATTTGGAGG	TGCCGGAGTA	GGTAAAACAG	TATTAATTCA	500
	GGAATTAATT	AACAACATTG	CAAAAGGTCA	CGGTGGACTT	TCTGTATTTG	550
45	CTGGTGTAGG	TGAGCGTACT	CGTGAGGGTA	ACGATTTACT	ACGTGAGATG	600
	TTAGAGTCTG	GTATTATTAA	ATACGGAGAT	GACTTTATGC	ACTCTATGGA	650
	AGAAGGTGGT	TGGGATTTAT	CTAAAGTTGA	TAAATCTGTA	ATGAAAGATT	700
	CTAAAGCAAC	CTTTGTATTT	GGACAAATGA	ATGAGCCACC	AGGAGCACGT	750
	GCACGTGTTG	CATTATCTGG	TTTAACTATT	GCAGAATATT	TCCGTGATGG	800
50	AGCAGGTGAA	GGTCAAGGTA	AAGATGTACT	TTTCTTTGTG	GATAACATTT	850
	TCCGTTTTAC	ACAAGCTGGT	TCTGAGGTAT	CTGCATTACT	TGGTCGTATG	900
	CCATCTGCGG	TAGGTTACCA	ACCAACATTA	GCAACAGAAA	TGGGTGCTAT	950
	GCAAGAGCGT	ATTACATCAA	CAAAAAGAGG	TTCTATTACA	TCTGTACAGG	1000
	CGGTTTACGT	ACCTGCGGAT	GATTTAACGG	ATCCAGCACC	GGCAACTACC	1050
55	TTTGCTCACT	TAGATGCAAC	AACGGTATTG	TCTCGTAAAA	TTGCAGAGTT	1100
	AGGTATTTAC	CCAGCGGTAG	ATCCATTAGA	TTCTACTTCT	AGAATCTTAG	1150
	CTCCAGAAAT	TTTAGGAAAA	GATCACTACT	CTTGTGCACA	ACGTGTAAAA	1200
	GAGTTGTTAC	AACGTTATAA	AGAATTACAA	GATATTATTG	CTATCCTTGG	1250
	TATGGAAGAA	TTATCTGAGG	AAGATAAAAT	GGCAGTTGGT	AGAGCAAGAC	1300
60	GTGTACAACG	TTTCTTATCT	CAGCCTTTCC	ACGTAGCAGA	GCAATTTACA	1350

GGTCTTAAAG	GTGTTTTAGT	AGATATCAAG	GATACTATTA	AAGGATTTAA	1400
TATGATTATG	GATGGTGAAT	TAGATCACTT	ACCAGAATCT	GCATTTAACC	1450
TTAAAGGTAC	TATTGAAGAA	GCTATAGAAG	CAGGAGAAAA	AATGCTTGCT	1500
GAAGCATAA					1509

5

2) INFORMATION FOR SEQ ID NO: 673

- 10 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 819 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

- 15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 20 (A) ORGANISM: *Ehrlichia risticii*
- (B) STRAIN: HRC-IL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 673

	CCTAAAATAT	ATGATGCATT	ATATGTAAAA	CTAGATAATG	AAAATTTGTG	50
25	TTTAGAAGTT	TCACAAATTA	TTGGAGATAA	TGTTGTTAGA	TGTATTGCAA	100
	TGGGAGCTAC	TTATGGATTA	AATCGTGGTT	TAGAAGTAGT	TTGTTTCAGGA	150
	AATCCAATTC	AGGTTCCCTGT	AGGTGAACAA	GTTTTAGGTA	GAATGTTTAA	200
	TGTTGTTGGT	AAAACAATTG	ACAATCTTGA	ATCTTTAGAT	GATAAAAATA	250
	TAAAAATGAT	GCCAATTCAT	CGAAATCCAC	CATCATTTGA	AGAGCAATCC	300
30	AATGAAATTG	AAATTTTGA	AACAGGCATT	AAAGTTATTG	ATTTATTAAT	350
	TCCATATGCT	AAAGGTGGTA	AGATTGGATT	ATTTGGTGGA	GCAGGGGTTG	400
	GGAAAACGGT	TCTTGTTCAA	GAATTAATTC	ACAATATCGC	AAAAGGTCAT	450
	GGTGGTCTAT	CTGTTTTTGC	TGGAGTTGGT	GAAAGAACTC	GTGAAGGTAA	500
	TGACTTGTAT	TATGAAATGA	TTGAAGGTGG	AGTTATAGAT	AAAACAGCCT	550
35	TAGTGTTTGG	GCAAATGAAT	GAACCTCCTG	GCGCAAGAAT	GCGCGTAGCA	600
	TTAACTGCTT	TAACAATGGC	TGAATATTTT	CGTGATGTTT	AAAACCAAGA	650
	TGTTTTGTTA	TTTATTGATA	ATATCTTTAG	ATTTACACAA	GCTGGTAGTG	700
	AAGTTTCAGC	ATTATTAGGA	AGAATGCCAT	CTGCTGTTGG	TTATCAACCA	750
	ACTTTGGCAT	ATGAAATGGG	ATTGTTACAA	GAAAGAATCA	CTTCCACTAA	800
40	AAGTGGTTCT	ATAACATCT				819

2) INFORMATION FOR SEQ ID NO: 674

- 45 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 840 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - 50 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 55 (A) ORGANISM: *Vibrio cholerae*
- (B) STRAIN: ATCC 25870

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 674

60	AGAGCGAAGT	ACCAAGTGTT	TACGATGCTC	TGAATGTTGT	GGATTCCAAA	50
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	GAACGTCTGG	TTCTGGAAGT	TCAACAGCAG	CTAGGCGGTG	GCGTGATTCTG	100
	CGCTATCGTT	ATGGGTAGCT	CGGATGGTTT	ACGTCGTGGA	ATGACAGTAC	150
	AAAACACTGG	CGCTCCAATT	TCAGTACCAG	TAGGTACTAA	AACCCTAGGT	200
	CGTATCATGA	ACGTGCTTGG	TGATGCGATT	GACGAACGTG	GCGACATTGG	250
5	CGCAGAAGAG	GTGTACTCGA	TTCACCGTCC	TGCTCCAAGC	TACGAAGAAC	300
	AGTCTAGTGC	AACTGAACTT	TTGGAAACGG	GTGTTAAGGT	TATCGACCTG	350
	ATCTGTCCGT	TTGCGAAAGG	CGGTAAAATC	GGTCTGTTTC	GTGGTGCGGG	400
	TGTAGGTAAG	ACCGTTAACA	TGATGGAACT	TATCAACAAC	ATCGCGCTAC	450
	AGCACTCAGG	TTTGTCTAGT	TTTGCTGGGG	TAGGTGAGCG	TACTCGTGAG	500
10	GGTAACGACT	TCTACCACGA	AATGCAGGAA	GCGGGCGTTG	TAAACGTTGA	550
	ACAACCAGAA	CTGTCTGAAAG	TAGCGATGGT	TTACGGTCAG	ATGAACGAGC	600
	CACCAAGCAA	CCGTCTGCGT	GTAGCACTGA	CTGGTCTGAC	TATGGCGGAA	650
	AAGTTCCGTG	ATGAAGGCCG	TGACGTACTG	CTGTTTATCG	ACAACATCTA	700
	CCGTTACACC	CTAGCGGGAA	CGGAAGTATC	TGCTCTGCTT	GGCCGTATGC	750
15	CTTCAGCGGT	AGGTTACCAA	CCAACACTGG	CTGAAGAGAT	GGGTGTTCTG	800
	CAAGAACGTA	TCACGTCAAC	CAAAAAGGT	TCTATCACCT		840

20 2) INFORMATION FOR SEQ ID NO: 675

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 828 bases
	(B)	TYPE: Nucleic acid
25	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Vibrio cholerae</i>
	(B)	STRAIN: ATCC 25870

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 675

35	CGGCGGTATC	CTAGTTGTAG	CGGCAACTGA	CGGTCCAATG	CCACAAACTC	50
	GTGAGCACAT	CCTGCTGGGT	CGCCAAGTAG	GTATTCCTTA	CATCATCGTA	100
	TTCATGAACA	AGTGTGACAT	GGTTGACGAT	GAAGAGCTTC	TAGAGCTGGT	150
	AGAGATGGAA	GTTCGTGAGC	TGCTGTCTGA	GTACGATTTC	CCAGGTGATG	200
40	ACCTGCCAGT	AATCCAAGGT	TCAGCACTAG	GCGCGCTAAA	CGGCGAAGCA	250
	CAGTGGGAAG	CGAAGATTGT	TGAGCTAGCA	GAAGCACTGG	ATACTTAYAT	300
	TCCAGAGCCA	GAGCGTGCAG	TAGACATGGC	ATTCTTGATG	CCAATCGAAG	350
	ACGTATTCTC	AATCCAAGGT	CGTGGTACAG	TAGTAACTGG	CCGTATCGAG	400
	CGCGGCATCC	TGAAAGTGGG	TGACGAAGTA	GCGATCGTTG	GTATCAAAGA	450
45	GACAGTAAAA	ACGACCTGTA	CAGGTGTAGA	GATGTTCCGT	AAGCTGCTTG	500
	ACGAAGGTCG	TGCAGGTGAG	AACGTAGGTG	CACTRCTACG	TGGTACTAAG	550
	CGTGAAGAAG	TAGAGCGTGG	TCAAGTACTG	GCGAAGCCAG	GTTCAATCAC	600
	ACCACACACT	AAGTTCGAAT	CAGAAGTATA	CGTACTGTCA	AAAGATGAAG	650
	GTGGCCGTCA	TACTCCATTC	TTCAAAGGTT	ACCGTCCACA	GTTCTACTTC	700
50	CGTACAACCTG	ACGTAACAGG	CAGCATTGAG	CTACCAGARG	GCGTAGAAAT	750
	GGTAATGCCA	GGCGACAACG	TGAAGATGGT	TGTAGACCTG	ATTGCACCAA	800
	TCGCGATGGA	CGAAGGTCTA	CGCTTCGC			828

55

2) INFORMATION FOR SEQ ID NO: 676

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 1298 bases
60	(B)	TYPE: Nucleic acid

- (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania enriettii*
(B) STRAIN: ATCC 50120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 676

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10      CTTCTCGGAT GGCCTGCCGC CGGTGCTGAC GCGCTGGAC GTGACGGAGG      50
      AACTCGGGCG CGACGAGCCG CTGACGCTAG AGATCGTGCA ACACTTGGAC      100
      GCGCACACCG GCCGCTGCAT TCGCATGCAG ACGACGGACC TACTGAAGCT      150
15      GAAGTCGAAG GTCGTGTCTG CCGCGGGGAA CATCTCTGTG CCTGTGGGCC      200
      GCGAGACGCT TGGCCGCATC TTCAACGTAC TGGGCGACGC GATTGACCAG      250
      CGCGGCCCCG TGGGCGAGAA GATGCGCATG GCGATCCACG CGGAGGCGCC      300
      GAAGCTGGCG GACCAGGCGG CGGAGGACAC GATCCTGACG ACCGGCATCA      350
      AAGTGATCGA TCTGATCCTG CCGTACTGCA AGGGCGGCAA GATCGGTCTG      400
20      TTCGGCGGTG CCGGTGTGGG GAAGACTGTG ATCATCATGG AGCTGATCAA      450
      CAACGTCGCG AAGGGCCACG GTGGCTTCTC CGTGTTCCGC GCGTTGGGG      500
      AGCGCACCCG CGAGGGGACG GATCTGTACC TGGAGATGAT GCAATCGAAG      550
      GTGATCGACC TGAAAGGTGA GTCGAAGTGT GTGCTTGTGT ACGGGCAGAT      600
      GAACGAGCCC CCGGGTGCAG GCGCGCGCGT TCGCGAGTCT GCGCTGACGA      650
25      TGGCCGAGTA CTTCCGCGAC GTGGAGGGCC AGAACGTGCT GCTGTTCATC      700
      GACAACATCT TCCGCTTCAC GCAGGCGAAC TCCGAGGTGT CAGCGCTGCT      750
      GGGCCGCATC CCCGCCGCTG TGGGCTACCA ACCGACGCTT GCGGAGGATC      800
      TCGGCATGTT GCAGGAGCGC ATCAGCTCGA CGACGAAGGG GTCGATCACG      850
      TCTGTGCAGG CCGTGTACGT GCCTGCGGAT GATATCACGG ATCCCGCGCC      900
30      GCGCAGACA TTCTCGCACC TGGACGCGAC GACGGTGCTG GACCGCGCGG      950
      TGGCGGAGTC TGGCATCTAC CCCGCGGTCA ACCCACTGGA GTGCGCGTGC      1000
      CGTATCATGG ACCCTGATGT GATCGACGTG GATCACTACA ACGTTGCGCA      1050
      GGACATTGTT CAGATGCTGA CCAAGTACAA GGAGCTGCAG GATATCATTG      1100
      CCGTGCTTGG TATCGACGAG CTGAGCGAGG AGGACAAGGT TGTGGTGGAC      1150
35      CGTGCGCGCA AGGTGACCCG GTTCCTGTCA CAGCCGTTCC AGGTTGCGGA      1200
      GGTGTTTACT GGCATGACAG GCCATTACGT ACAGCTGAGC GACACGGTGG      1250
      AGTCGTTCTC CGGTTTGCTG ATGGGGTCGT ACGACCAGAT TCCGGAGA      1298

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2) INFORMATION FOR SEQ ID NO: 677

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1083 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Babesia microtti*
(B) STRAIN: Persing-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 677

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60      CAAGCTCAAG TCTGAGCGTG AGAGAGGTAT TACTATTGAC ATTACTCTCT      50
      GGAAATTTGA GACCCAGAAA TACGAGTACA CTGTCATAGA CGCACCTGGT      100
      CATCGTGACT TTATCAAAAA TATGATTACT GGGACTTCAC AAGCCGACGT      150
      TGCTATGCTT GTCGTTCTCT CTGAATCTGG CGGATTCGAG GCTGCTTTTT      200

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	CCAAAGAAGG	TCAGACCCGT	GAACACGCCT	TACTAGCCTT	CACACTTGGC	250
	GTCAAACAGA	TGATTGTTGC	TATTAACAAA	ATGGATTCTT	GTCAGTACAA	300
	GGAGGATCGT	TATATGGAAA	TTTTCAAGGA	AGTACAGCAG	TACTTGAAGA	350
	AGGTGGGTTA	CAAAGTTGAA	AGCGTGCCGT	TTGTTGCTAT	TTCAGGATTC	400
5	CACGGTGACA	ACATGGTTGA	AAAATCTACT	AACATGCCTT	GGTATAAGGG	450
	TAAGACCCTC	GTAGAGGCAC	TTGATCAAAT	GGAGCCTCCA	AAACGTCCGG	500
	TCGAAAAACC	TCTTAGATTG	CCCCTGCAGT	CAGTCTATAA	AATTGGAGGT	550
	ATTGGTACGG	TACCAGTCGG	AAGGGTCGAA	ACAGGACAAC	TGAAAGCAGG	600
	AATGATCATT	ACTTTTGCCC	CCACTGGTTT	GACCACTGAA	TGTAAATCTG	650
10	TTGAAATGCA	TCACGAGGTT	GTGGAAGTGG	CTAGCCCCGG	TGATAACGTT	700
	GGATTTAATG	TCAAGAATGT	GTCTGTTAAG	GATATTAAGA	GAGGAAATGT	750
	GGCTTCGGAT	TCGAAAAATG	ACCCAGCCAA	GGAAGCTACC	TCTTTCTCTG	800
	CACAAGTCAT	TGTACTCAAT	CACCCTGGTA	CCATCAAGGC	CGGTTACTCA	850
	CCTGTGGTTG	ATTGCCATAC	TGCCCACATT	GCTTGCAAAT	TCGAATCTCT	900
15	AGACACTAGG	ATTGACAAGC	GTA CTGGCAA	GACTTTGGAA	GAAAATCCTA	950
	AGACTATTAA	GAATGGTGAC	GCTGCCATGG	TGACTATGAA	ACCAAATAAA	1000
	CCCATGGTTG	TGGAAACTTT	CACCGACTAC	GCCCCGTTGG	GCCGGTTCGC	1050
	CGTGCGTGAT	ATGCGCCAAA	CCGTTGCCGT	CGG		1083

20

2) INFORMATION FOR SEQ ID NO: 678

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 551 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Cryptococcus neoformans*
- (B) STRAIN: Lev-12

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 678

	TGTGCTCATT	CAGGAGCTCA	TTAACAACAT	TGCCAAGGCT	CACGGTGGTT	50
	ACTCTGTCTT	CACTGGTGTC	GGTGAGCGAA	CTCGTGAGGG	TAACGACTTG	100
40	TACCACGAAA	TGAGGGAGAC	TGGTGTTATC	AACCTTGAGG	GTGACTCCAA	150
	GGTCGCTCTT	GGTGAGTTCT	TTTTTTTCTT	CAGGCTAATT	AGTCGATGAC	200
	GTGGGGCCCTG	ACTAAACTG	TTTCTTCCAG	TCTTCGGTCA	GATGAACGAG	250
	CCCCCTGGAG	CCCGTGCCCG	AGTTGCCCTT	ACTGGTTTGA	CCATTGCCGA	300
	GTA CTCCGT	GACGAGGAAG	GCCAGGATGT	GTTGCTTTTC	ATTGACAACA	350
45	TTTTCCGATT	CACCCAGGCC	GGTTCCGAGG	TGTCTGCCTT	GCTCGGTCGT	400
	ATCCCCCTCTG	CCGTCGGTTA	CCAGCCCACT	CTTTCCACCG	ACATGGGTGG	450
	TATGCAGGAG	CGAATGTAGG	TTGCATTCTC	TGTGATTTTA	CGGCAAGCCT	500
	TGACTTTTTT	TTTCTAGTAC	CACCACCAAG	AAGGGTTCCA	TTACCTCCGT	550
	C					551

50

2) INFORMATION FOR SEQ ID NO: 679

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 552 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cryptococcus neoformans*

(B) STRAIN: ATCC 44104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 679

	TGTGCTCATT	CAGGAGCTCA	TTAACAACAT	TGCCAAGGCC	CACGGTGGTT	50
10	ACTCCGTCTT	CACCGGTGTC	GGTGAGCGAA	CTCGTGAGGG	TAACGACTTG	100
	TACCACGAAA	TGAGGGAGAC	TGGTGTTATC	AACCTTGAGG	GTGACTCCAA	150
	GGTCGCTCTT	GGTGAGTTCT	TTTTTTTGGG	AGCTAATTAG	TCGATGACGT	200
	GGGCCCTGAC	CAAAACCGTT	TCTTTCAGTC	TTCGGTCAGA	TGAACGAGCC	250
	CCCTGGAGCC	CGTGCCCGAG	TTGCTCTTAC	TGGTTTGACC	ATTGCCGAGT	300
15	ACTTCCGTGA	CGAGGAAGGC	CAGGATGTGT	TGCTTTTCAT	TGACAACATT	350
	TTCCGATTCA	CCCAGGCCGG	TTCCGAGGTG	TCTGCCTTGC	TCGGTCGTAT	400
	CCCCTCTGCC	GTCGGTTACC	AGCCCACTCT	TTCCACCGAT	ATGGGTGGTA	450
	TGCAAGAGCG	AATGTAAGTT	GCATTTTTTG	TGATTTTACG	GCAAGTCTTG	500
	ACTTACATTT	TTTTCTAGCA	CCACCACCAA	GAAGGGTTCC	ATTACCTCCG	550
20	TC					552

2) INFORMATION FOR SEQ ID NO: 680

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1018 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cunninghamella bertholletiae*

(B) STRAIN: ATCC 42115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 680

40	TCTCCCTGCT	ATTTTAAACG	CTCTTGAAGT	TAAGGATCAT	GCTGGTGGTC	50
	GTCTTGTTCT	TGAAGTTGCT	CAACACTTGG	GTGAAAACAC	TGTACGTACT	100
	ATTGCTATGG	ATGGTACTGA	AGGTAAGTTT	ATTTTTAGAT	GATCATAAAT	150
	AATTGATCAT	AATGATAAAA	AAAAAAGAAG	AAGAAGAACA	GGATGTATAT	200
	AATGGTTAAT	AAATAATATT	TTCATATTGK	ATATAACTAT	TTAATCTGTT	250
45	TTTTTTTCTT	CATGATTATA	TATATATATG	TMCTAATATC	TAATATGAAC	300
	CTTTTTTATA	AAATTAATCA	GGTCTTGTC	GTGGTCAAAA	GGTTGTTGAT	350
	ACTGGTGCTC	CTATTACCAT	TCCTGTTGGT	AAGGAAGTTC	TTGGTCGTAT	400
	CATCAACGTT	ATTGGTGAAC	CCATTGATGA	ACGTGGTCCT	ATTAAGGCCA	450
	AGTCTCACCG	TGCTATTAC	GCTGAAGCTC	CAGAATTCGT	TGATCAATCT	500
50	CCTACTCCCG	AAATTCTTGA	AACTGGTATT	AAGGTTGTCG	ATTTATTAGC	550
	TCCTTATGCT	CGTGGTGGTA	AGATTGGTCT	TTTCGGTGGT	GCTGGTGTAG	600
	GTAAAACTGT	CTTGATTCAA	GAACCTATTA	ACAACATTGC	TAAAGCCCAT	650
	GGTGGTTACT	CTATTTTCTG	TGGTGTGGT	GAACGTACTC	GTGAAGGTAA	700
	CGATTTATAC	CACGAAATGA	TGGAAACTGG	TGTCATTAAA	CTTGAAGGTG	750
55	ACTCCAAGTG	TGCTCTTGTA	TTCCGGTCAA	TGAACGAACC	TCCTGGTGCT	800
	CGTGCCCGTG	TTGCTTTAAC	TGGTTTAAAC	ATTGCTGAAT	ACTTCCGTGA	850
	TGAAGAAGGT	CAAGATGTGT	TACTTTTCAT	TGATAACATT	TTCCGTTTCA	900
	CTCAAGCTGG	TTCTGAAGTA	TCTGCCCTTT	TAGGTCGTAT	TCCATCTGCT	950
	GTAGGTTACC	AACCCACTTT	ATCTACTGAT	ATGGGTGGTA	TGCAAGAACG	1000
60	TATTACTACT	ACCAAGAA				1018

2) INFORMATION FOR SEQ ID NO: 681

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 681

GGISSITTYG GIISIGGIAA RAC

23

2) INFORMATION FOR SEQ ID NO: 682

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 682

GTIACIGGYT CYTCRAARTT ICCICC

26

2) INFORMATION FOR SEQ ID NO: 683

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 683

GTIACIGGIT CISWIAWRTC ICCICC

26

2) INFORMATION FOR SEQ ID NO: 684

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3267 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Candida tropicalis*

(C) ACCESSION NUMBER: M64984

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 684

	ATGGCTGGTG	CTTTAGAAAA	CGCAAGAAAA	GAAATTAAAC	GTCTTTCATT	50
	AGATGACACC	AATGAATCCC	AATATGGTCA	AATCTATTCT	GTTTCCGGTC	100
10	CGGTTGTTAT	TGCCGAAAAC	ATGATTGGAT	GTGCCATGTA	CGAATTGGTT	150
	AAAGTTGGTC	ATGATAATTT	AGTTGGGGAA	GTTATTAGAA	TTAATGGTGA	200
	TAAAGCAACC	ATTCAAGTTT	ATGAAGAAAC	TGCAGGGGTC	ACTGTTGGTG	250
	ATCCAGTTTT	AAGAACTGGT	AAACCATTAT	CTGTTGAATT	AGGTCCTGGT	300
	TTAATGGAAA	CTATTTATGA	TGGTATTCAA	AGACCTTTAA	AAGCCATTAA	350
15	AGATGAATCC	CAATCTATTT	ATATCCCAAG	AGGTATTGAT	GTTCTGCTT	400
	TATCAAGAAC	TGTTCAATAT	GATTTCACTC	CAGGTCAATT	GAAAGTTGGT	450
	GATCATATCA	CTGGTGGGGA	CATTTTTGGT	TCTATTTATG	AAAACCTCTT	500
	ATTGGATGAC	CATAAGATTT	TGTTACCTCC	AAGAGCAAGA	GGTACTATTA	550
	CTTCTATTGC	TGAAGCCGGT	TCTTATAATG	TTGAAGAACC	AGTTTTGGAA	600
20	GTTGAATTTG	ATGGTAAGAA	ACATAAATAC	TCTATGATGC	ATACATGGCC	650
	AGTTAGAGTT	CCAAGACCAG	TTGCTGAAAA	ATTGACTGCT	GATCATCCAT	700
	TGTTGACCGG	TCAAAGAGTC	TTGGATTCTT	TATTCCTATG	TGTTCAAGGT	750
	GGTACTACTT	GTATCCCAGG	GGCTTTTGGT	TGTGGTAAAA	CTGTTATTTT	800
	TCAATCTTTG	TCCAAATTCT	CCAACCTCTG	TGTTATTATC	TATGTTGGTT	850
25	GTTTCACTAA	AGGTACTCAA	GTCATGATGG	CTGATGGTGC	CGACAAATCT	900
	ATTGAATCTA	TTGAAGTTGG	TGACAAAGTC	ATGGGTAAAG	ATGGTATGCC	950
	AAGAGAAGTT	GTTGGCTTAC	CAAGAGGTTA	TGATGATATG	TACAAGGTTT	1000
	GTCAACTTTT	TAGTACTAGA	CGTAATGCTA	AATCCGAAGG	CTTGATGGAT	1050
	TTCACCTGTT	CTGCTGATCA	TAAACTTATC	TTGAAAACTA	AACAAGATGT	1100
30	CAAGATTGCT	ACACGTAAAA	TTGGTGGCAA	CACCTATACT	GGTGTACTTT	1150
	TCTATGTTTT	GGAAAAGACT	AAGACTGGTA	TTGAATTAGT	TAAAGCCAAG	1200
	ACTAAAGTTT	TCGGTCATCA	TATCCATGGT	CAAAATGGCG	CTGAAGAAAA	1250
	AGCTGCTACT	TTTGCTGCTG	GCATTGACTC	TAAAGAATAC	ATTGATTGGA	1300
	TCATTGAAGC	TAGAGATTAT	GTACAAGTTG	ATGAAATTGT	CAAGACCAGC	1350
35	ACCACTCAAA	TGATCAACCC	AGTTCATTTT	GAATCTGGTA	AACTCGGTAA	1400
	CTGGTTACAC	GAACACAAGC	AAAACAAATC	ACTTGCTCCA	CAATTGGGTT	1450
	ACTTGTGGGG	TACTTGGGCT	GGTATTGGAA	ATGTTAAATC	TTCTGCTTTT	1500
	ACCATGAACT	CCAAAGATGA	TGTTAAATTA	GCTACAAGAA	TTATGAACTA	1550
	CTCTTCAAAA	TTGGGCATGA	CTTGTTCTTC	TACTGAATCC	GGTGAATCA	1600
40	ATGTCGCTGA	AAACGAAGAA	GAATTTTCTA	ATAACCTTGG	TGCTGAAAAG	1650
	GATGAAGCTG	GTGATTTTCA	TTTTGATGAA	TTTACCGATG	CTATGGATGA	1700
	ATTGACTATC	AATGTTTCATG	GTGCAGCTGC	AAGCAAGAAG	AACAATTTGT	1750
	TGTGGAATGC	TTTGAAATCT	CTTGGTTTCA	GAGCCAAGTC	TACTGATATT	1800
	GTCAAGAGTA	TTCCTCAACA	TATTGCTGTT	GATGATATTG	TTGTCAGAGA	1850
45	ATCTTTGATT	GCCGGTTTAT	TTGATGCTGC	TGGTAATGTT	GAAACCAAAT	1900
	CCAATGGTTC	TATTGAAGCT	GTTGTTAGAA	CTTCTTTCAG	ACATGTCGCT	1950
	AGAGGTCTTG	TCAAGATTGC	TCAATCTTTG	GGTATTGAAT	CATCTATTAA	2000
	TATTAAAGAT	ACTCACATTG	ATGCTGCTGG	TGTTAGACAA	GAATTTGCTT	2050
	GTATTGTCAA	TTTGACTGGT	GCTCCACTTG	CTGGTGTTCT	TTCTAAATGT	2100
50	GCACTTGCAA	GAAACCAAAC	TCCAGTTGTC	AAATTTACCA	GAGACCCAGT	2150
	TTTGTTCAAC	TTTGATTGTA	TCAAATCTGC	AAAAGAAAAC	TATTATGGTA	2200
	TTACTTTGGC	TGAAGAAACT	GATCATCAAT	TCCTTTTATC	CAACATGGCC	2250
	TTGGTGCACA	ACTGTGGTGA	ACGTGGTAAT	GAGATGGCTG	AAGTTTTGAT	2300
	GGAATTTCCA	GAATTGTTTA	CTGAAATTTT	TGGTAGAAAA	GAACCAATTA	2350
55	TGAAACGTAC	CACCTTGGTT	GCCAATACTT	CTAATATGCC	AGTCGCTGCC	2400
	AGAGAAGCTT	CTATTTATAC	TGGTATTACA	TTGGCTGAAT	ATTTTCAGAGA	2450
	TCAAGGTAAG	AATGTTTCTA	TGATTGCTGA	TTCTTCTTCA	CGTTGGGCTG	2500
	AAGCTTTGAG	AGAAATTTCT	GGTAGATTGG	GTGAAATGCC	TGCTGATCAA	2550
	GGTTTCCCAG	CTTATTTGGG	TGCTAAATTG	GCTTCTTTCT	ATGAGCGTGC	2600
60	CGGTAAAGCC	ACTGCTTTGG	GTTTACCAGA	TAGAGTTGGT	TCAGTTTCTA	2650

	TTGTTGCTGC	TGTTTCTCCA	GCTGGTGGTG	ATTTCTCTGA	TCCAGTTACT	2700
	ACTTCTACTT	TGGGTATTAC	TCAAGTTTTC	TGGGGGTTGG	ATAAGAAATT	2750
	GGCCCAAAGA	AAACATTTCC	CATCTATTAA	CACCAGTGTT	TCTTATTCTA	2800
	AATACACCAA	TGTTTTGAAC	AAATACTATG	ATTCCAATA	TCCAGAATTC	2850
5	CCACAATTGA	GAGACAAAAT	TAGAGAAATT	TTATCTAATG	CTGAAGAATT	2900
	GGAACAAGTT	GTTCAATTAG	TTGGTAAATC	TGCATTGTCT	GATTCTGATA	2950
	AGATTACTTT	AGATGTTGCT	ACCTTGATTA	AAGAAGATTT	CTTGCAACAA	3000
	AATGGTTATT	CTTCATATGA	TGCATTCTGT	CCAATTTGGA	AGACTTTTGA	3050
	TATGATGAGA	GCATTTATTT	CATATTATGA	TGAAGCACAA	AAAGCAATTG	3100
10	CCAATGGTGC	TCAATGGTCT	AAATTAGCTG	AAAGTACTAG	TGATGTTAAA	3150
	CATGCTGTTT	CTTCAGCTAA	ATTCTTTGAA	CCATCAAGAG	GTCAAAAAGA	3200
	AGGTGAAAAA	GAATTTGGAG	ATTTATTAAC	CACTATCTCC	GAAAGATTTG	3250
	CTGAAGCTTC	AGAATAA				3267

15

2) INFORMATION FOR SEQ ID NO: 685

	(i) SEQUENCE CHARACTERISTICS:
20	(A) LENGTH: 1782 bases
	(B) TYPE: Nucleic acid
	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear
25	(ii) MOLECULE TYPE: Genomic DNA
	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: <i>Enterococcus hirae</i>
	(B) STRAIN: ATCC 9790
30	(C) ACCESSION NUMBER: D17462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 685

	TTGCAAATTG	GAAAAATCAT	AAAAGTCTCC	GGTCCTCTCG	TTATGGCAGA	50
35	AAATATGTCA	GAAGCAAGTA	TTCAAGACAT	GTGTTTAGTG	GGAGATTTAG	100
	GAGTCATCGG	CGAAATCATT	GAGATGCGTC	AAGATGTGGC	GTCTATTCAA	150
	GTATATGAAG	AAACTTCAGG	AATTGGTCCC	GGAGAACCTG	TTCGTTCCAC	200
	TGGGGAAGCA	CTATCTGTTG	AGCTAGGACC	AGGAATCATT	TCACAAATGT	250
	TTGACGGGAT	TCAAAGACCA	CTGGATACAT	TTATGGAAGT	GACTCAAAGT	300
40	AACTTCTTAG	GACGTGGGGT	CCAATTACCA	GCTTTAGATC	ATGAGAAACA	350
	ATGGTGGTTT	GAAGCGACAA	TCAAGAAGG	AACAGAAGTA	AGTGCTGGAG	400
	ACATCATTGG	GTACGTGGAT	GAAACGAAGA	TCATTCAGCA	CAAAATCATG	450
	GTCCCTAATG	GTATCAAAGG	AACTGTACAA	AAAATTGAAT	CTGGATCATT	500
	TACGATCGAT	GATCCGATTT	GTGTGATCGA	AACGGAACAA	GGCTTAAAAG	550
45	AGCTGACGAT	GATGCAAAAA	TGGCCAGTAC	GTCGTGGTCG	ACCAATCAAA	600
	CAAAAATTAA	ATCCAGATGT	ACCGATGATC	ACCGGTCAAA	GGGTCATTGA	650
	CACGTTTTTC	CCAGTAACTA	AAGGAGGAGC	GGCAGCCGTT	CCAGGTCCGT	700
	TTGGTGCAGG	GAAGACAGTT	GTGCAACACC	AGATTGCTAA	GTGGTCGGAC	750
	GTAGATCTAG	TGTTTACGT	TGTTTGTGGG	GAACGAGGAA	ATGAAATGAC	800
50	GGATGTCGTC	AATGAATTTT	CTGAAC TGAT	CGATCCAAAT	ACAGGCGAGT	850
	CTTTGATGGA	ACGAACTGTG	TTGATCGCTA	ATACATCGAA	CATGCCAGTA	900
	GCTGCTCGAG	AAGCTTCTAT	TTATACGGGA	ATCAGATTG	CCGAGTACTT	950
	CCGTGACATG	GGGTATGATG	TAGCAATCAT	GGCAGATTCC	ACTTCTCGTT	1000
	GGGCAGAAGC	ACTGCGTGAA	ATGAGCGGAC	GTTTAGAAGA	AATGCCTGGT	1050
55	GATGAAGGTT	ATCCCGCTTA	TCTGGGCTCT	CGTCTAGCTG	AATACTATGA	1100
	ACGTTTCAGG	CGTGTCAATT	CTCTAGGCTC	TGACCAACGT	GAGGGCAGTA	1150
	TCACTGCCAT	CAGTGCGGTT	TCTCCTCTG	GTGGAGATAT	CTCTGAACCA	1200
	GTGACTCAAA	ATACCTTACG	TGTGGTGAAG	GTTTTCTGGG	GATTAGATTC	1250
	TAGTCTTGCT	CAAAAAGAC	ATTTTCCATC	GATTAAGTGG	ATCCAAAGTT	1300
60	ACTCATTATA	TTCAACAGAA	GTTGGCAGAT	ATATGGATCA	AATCTTACAA	1350

CAGGATTGGT CTGATATGGT AACTGAAGGC ATGCGGATCT TGCAAGAAGA 1400
 AGAACAATTA AATGAAATCG TGCGCTTGGT AGGGATCGAT TCGCTTTCTG 1450
 ATAACGATCG CTTGACCCTT GAAGTAGCAA AATCGATTCTG AGAAGACTAT 1500
 TTACAACAAA ATGCTTTTGA TGATGTAGAT ACGTTTACTT CAAGAGAAAA 1550
 5 ACAATTCAAC ATGTTGAAAG TTATTTTGAC TTTTGGGAAA GAAGCTCGAA 1600
 AAGCCTTATC GTTGGGAGCG TACTTCAATG AAATCATGGA AGGTACAGTA 1650
 GCGGTCAGAG AACGCATTAG TCGGAGCAAG TATATTCCAG AAGAAGAGTT 1700
 AGCCAAAATT AGTAGTATAA ATGAAGAAAT CAAAGAAACG ATCCAATTGA 1750
 TTGTTTCAGA AGGAGGGATG ACCGATGATT AA 1782
 10

2) INFORMATION FOR SEQ ID NO: 686

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1781 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Chlamydia pneumoniae*
 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 686

CAGGGACATG TTATAGAAGC TTATGGAAAC TTGTTACGTG TACGCTTTGA 50
 CGGATATGTT AGACAAGGTG AAGTTGCATA TGTCACGTA GATAATACCT 100
 30 GGTAAAAGC AGAAGTGATT GAAGTTGCTG ATCAAGAAGT CAAGGTTTCAG 150
 GTATTTGAAG ATACACAAGG CGCGTGTCGA GGAGCTCTTG TTACGTTTTT 200
 AGGACATCTT TTAGAAGCCG AGTTAGGGCC TGGCTTGCTT CAGGGCATT 250
 TCGATGGACT TCAAAATCGT CTTGAGGTGC TAGCTGAAGA TAGTCTTTC 300
 TTGCAGAGAG GCAAGCATGT TAATGCTATT TCTGATCATA ATTTATGGAA 350
 35 TTATACTCCC GTAGCTTCTG TTGGGGATAC TTTAAGACGA GGAGATCTTC 400
 TAGGAACAGT ACCTGAAGGA CGATTTACTC ATAAGATTAT GTTCCTTTT 450
 TCTTGCTTTC AAGAGGTTAC CCTGACTTGG GTAATTTCTG AAGGAACCTA 500
 TAATGCTCAT ACTGTGGTCG CAAAAGCTCG AGATGCTCAG GGTAAAGAAT 550
 GTGCCTTTAC TATGGTGCAA AGATGGCCGA TCAAACAAGC TTTTATTGAA 600
 40 GGAGAGAAGA TCCCTGCGCA TAAGATTATG GATGTGGGTT TGCGAATCTT 650
 AGATACGCAA ATTCCAGTAT TGAAGGGGGG AACTTTCTGT ACCCCAGGAC 700
 CTTTTGGTGC AGGGAAAACA GTCTTACAAC ACCATCTTTC TAAGTACGCT 750
 GCTGTAGATA TTGTGATTTT GTGTGCGTGC GGAGAGCGTG CTGGTGAAAGT 800
 TGTTGAGGTA TTACAAGAGT TCCCTCATCT TATCGACCCC CATACCGGAA 850
 45 AGTCTTTAAT GCACAGAACA TGTATTATTT GTAACACATC ATCCATGCCT 900
 GTGGCTGCCC GAGAGTCTTC GATCTATTTA GGAGTGACGA TTGCAGAATA 950
 CTATCGCCAG ATGGGACTAG ATATTCTGCT TTTAGCTGAT TCTACATCCC 1000
 GATGGGCACA AGCCCTTAGA GAGATTTCCG GACGTCTTGA AGAAATCCCT 1050
 GGAGAGGAAG CATTTCCTGC ATACCTGTCT TCTAGAATAG CTGCTTTTAA 1100
 50 TGAGCGAGGA GGAGCTATCA CCACGAAAGA TGGTTCTGAA GGATCTTTAA 1150
 CTATATGTGG TGCGGTGTCT C'TGCAGGAG GAACTTTTGA AGAACCAGTC 1200
 ACTCAATCTA CATTAGCTGT AGTCGGAGCG TTCTGTGGTC TTTCAAAGC 1250
 ACGAGCTGAC GCACGTAGGT ATCCTTCAAT AGACCCTTTG ATTTCTTGGT 1300
 CAAAATATTT GAACCAAGTA GGACAAATTT TAGAAGAGAA GGTTTCAGGC 1350
 55 TGGGGTGGTG CTGTGAAAAA AGCAGCACAG TTTCTAGAGA AAGGTTTCAGA 1400
 AATCGGCAAG CGTATGGAAG TTGTCAGTGA AGAAGGGGTT TCTATGGAAG 1450
 ACATGGAAAT CTACTTAAAG GCAGAACTTT ATGATTTTTG TkATCTCCAG 1500
 CAGAACGCAT TCGATCCTGT GGACTGTTAT TGTCCTTTTG AGAGACAGAT 1550
 AGAGTTATTT TCATTAATCA GTCGTATTTT TGATGCTAAA TTTGTTTTTG 1600
 60 ATAGTCCTGA TGATGCAAGA AGCTTTTTTC TTGAGCTGCA GAGCAAGATT 1650

AAGACATTAA	ATGGCCTGAA	ATTTCTTTCA	GAGGAATATC	ATGAGAGTAA	1700
AGAGGTCATA	GTTAGACTGT	TGGAAAAAAC	AATGGTACAA	ATGGCGTAAG	1750
GATATGCAAA	CAATCTACAC	AAAAATAACT	G		1781

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2) INFORMATION FOR SEQ ID NO: 687

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1758 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Halobacterium salinarum*
 (C) ACCESSION NUMBER: S56356

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 687

ATGAGTCAAG	CTGAAGCAAT	CACTGACACC	GGCGAAATCG	AGAGCGTGAG	50
CGGTCCGGTC	GTGACCGCCA	CGGGCCTCGA	CGCGCAGATG	AACGACGTCG	100
25 TCTACGTGGG	CGACGAGGGT	CTGATGGGCG	AGGTCATCGA	GATCGAAGGC	150
GACGTAACCA	CCATCCAGGT	CTACGAGGAG	ACGTCCGGCA	TCGGGCCGGG	200
CCAGCCCGTC	GACAACACGG	GCGAACCCTG	CACCGTGGAC	CTGGGCCCGG	250
GGATGCTGGA	CTCCATCTAC	GATGGTGTGC	AGCGTCCACT	GGACGTCCTC	300
GAAGACGAGA	TGGGGGCGTT	CCTCGATCGC	GGTGTTGACG	CACCCGGCAT	350
30 CGACCTCGAC	ACCGACTGGG	AGTTCGAGCC	CACCGTCGAG	GCGGGCGACG	400
AGGTCGCGGC	CGGCGATGTC	GTGCGCACCG	TGCACGAAAC	GGTCAGCATC	450
GAACACAAGG	TTCTGGTGCC	CCCCCGCAGT	GACGGCGGCG	AAGTCGTCGC	500
CGTCGAATCC	GGCACGTTCA	CCGTCGACGA	CACGGTCGTC	GAGTTGGACA	550
CCGGCGAGGA	GATCCAGATG	CACCAGGAGT	GGCCGGTCCG	CCGCCAGCGC	600
35 CCCACCGTCG	ACAAGCAGAC	GCCGACGGAG	CCGCTGGTGT	CCGGCCAGCG	650
CATCCTCGAC	GGCCTGTTCC	CGATCGCGAA	AGGCGGGACG	GCCGCGATCC	700
CTGGGGCCGTT	CGGGTCCGGG	AAGACGGTCA	CCCAGCAGTC	CCTCGCGAAG	750
TTGCCCAGCG	CGGAGTCGT	TGTCTACATC	GGCTGTGGTG	AGCGCGGCAA	800
CGAGATGACG	GAAGTCATCG	AGGACTTCCC	GGAGCTGCCC	GACCCCCAGA	850
40 CCGGGAACCC	GCTGATGGCC	CGCACCACGC	TCATCGCGAA	CACGTCGAAC	900
ATGCCGGTTG	CCGGGCGTGA	GTCCTGCATT	TACACGGGAA	TCACCATCGC	950
GGAGTACTAC	CGCGACATGG	GCTACGACGT	GGCGCTGATG	GCCGACTCCA	1000
CCTCGCGGTG	GGCGGAGGCC	ATGCGGGAGA	TCTCCTCGCG	ACTCGAGGAG	1050
ATGCCCCGGC	AGGAGGGGTA	TCCCCGCTAC	CTGGCCGCCC	GCCTCTCGGA	1100
45 GTTCTACGAG	CGCGCCGGCT	ACTTCGAGAA	CTTCAACGGG	ACCGAGGGCT	1150
CCATCTCGGT	CATCGGTGCG	GTGTGCGCCG	CCGGCGGGGA	CTTCTCCGAG	1200
CCGGTCACCC	AGAACACGCT	GCGCATCGTG	AAGACGTTCT	GGGCGCTTGA	1250
CTCGGACCTC	GCCGAGCGCC	GGCACTTCCC	GGCGATCAAC	TGGGACGAGT	1300
CCTACAGCCT	CTACAAGGAC	CAACTCGACC	CGTGGTTTAC	GGACAACGTC	1350
50 GTCGACGACT	GGGCCGAGCA	GCGCCAGTCG	GCGGTCGACA	TCCTCGACGA	1400
GGAATCCGAA	CTCGAAGAGA	TCGTGCAGCT	CGTCGGGAAG	GACGCGCTGC	1450
CCGAGGACCA	GCAGCTCACG	CTGGAAGTCG	CGCGGTACAT	CCGCGAGGCG	1500
TGGCTCCAGC	AGAACGCGCT	CCACGACGTG	GATCGCTACT	GCCCGCCCGA	1550
GAAGACGTAC	GCCATCCTCT	CCGGCATCAA	GACGCTTTCAC	GAGGAGTCCT	1600
55 TTGAGGCGTT	GGACGCCGGT	GTGCCAGTCG	AGGAGATCAC	GTGATCGAC	1650
GCCGCGCCGC	GCCTGAATCG	TCTCGGCACG	ACGCCCCGAC	ACGAGCACGA	1700
GGCGGAGGTC	GCGGAGATCA	AACAGCAGAT	TACCGAGCAG	CTTCGGGAGC	1750
TCTACTGA					1758

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2) INFORMATION FOR SEQ ID NO: 688

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3118 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Human
 (C) ACCESSION NUMBER: L09234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 688

	GAATTCCGGC	AGCTGACTAG	TCTTGTGATT	GGGGTCCTGG	GCTGATAAAA	50
	TCATTCCAAA	TGACGAGCAC	ATTGATAAAG	ACGTCCGATG	AGGACCGGGA	100
20	GTCCAAATTC	GGCTTTGT	TTGCCGTATC	TGGACCTGTG	GTGACAGCTG	150
	AACGAATGGC	CGGTTCTGCT	ATGTACGAAC	TGGTGCGTGT	CGGTTATTAT	200
	GAACTGGTCG	GAGAGATCAT	CCGGTTGGAG	GGTGACATGG	CAACAATCCA	250
	AGTATACGAA	GACACCTCAG	GTGTGACAGT	AGGCGATCCC	GTGCTGCGCA	300
	CAGGCAAGCC	GCTGTCCGTG	GAAGTGGGAC	CCGGAATCAT	GGGCAGCATC	350
25	TTCGACGGTA	TCCAGCGACC	GCTGAAGGAT	ATCAATGAAC	TGTCAAATAG	400
	TATCTACATC	CCGAAAGGTG	TCAATGTGCC	TGCCCTGAGT	CGCACTGCAC	450
	AGTGGGACTT	CAGTCCCCTG	AGTGTCAAAG	TTGGAAGCCA	CATTACTGGT	500
	GGTGACCTGT	ACGGTTTGGT	CCACGAAAAT	ACTCTGGTGA	AACACAAGTT	550
	GCTGCTGCCG	CCCCGTGCCA	AGGGAAGTGT	CACGTACATT	GCAGAACCTG	600
30	GAAACTACAC	AGTTGATGAT	GTTGTCTCTG	AGACAGAATT	TGACGCGCAG	650
	CGATCAAAGT	TCACCATGCT	GCAAGTGTGG	CCTGTACGTC	AGCCAGGCC	700
	TGTTACAGAA	AAGTTGCCAG	CTAACTACCC	CCTCCTTACT	GGCCAGCGTG	750
	TGCTCGACTC	CCTATTCCCG	TGTGTCCAGG	GTGGAACAAC	AGCTATTCTT	800
	GGGGCCTTCG	GATGTGGCAA	GATGTGTAATA	TCACAGTCTT	TGTCAAATA	850
35	CTCAAATCC	GATGTAATTA	TCTATGTAGG	TTGTGGTGAG	CGAGGTAATG	900
	AAATGTCAGA	AGTACTCAGG	GATTTCCCGC	AGTTGTCTGT	GGAGATTGAT	950
	GGTGTGACTG	AATCAATCAT	GAAGAGAACA	GCCCTGGTCT	CAAACACATC	1000
	AAACATGCCT	GTGGCTGCTC	GAGAAGCATC	TATCTACACA	GGTATTACAC	1050
	TGTCAGAATA	CTTCAGGGAC	ATGGGTTACA	ATGTATCCAT	GATGGCTGAC	1100
40	TCAACTTCAC	GATGGGCCGA	AGCTCTTCGA	GAAATCTCAG	GTCGATTGGC	1150
	TGAAATGCCT	GCCGACAGCG	GTTATCCCGC	CTACCTAGGT	GCACGACTTG	1200
	CCAGTTTCTA	CGAGCGTGCC	GGCCGTGTGA	AGTGCTTGGG	TAACCCAGAC	1250
	AGGGAGGGCT	CCGTGAGTAT	AGTGGGCGCC	GTGTCGCCGC	CCGGTGGAGA	1300
	CTTCTCAGAT	CCCGTGACGA	CGGCCACACT	AGGTATCGTC	CAGGTGTTCT	1350
45	GGGGTCTCGA	CAAGAACTT	GCCCAGCGAA	AGCACTTCCC	ATCCATCAAC	1400
	TGGCTCATCT	CGTACAGTAA	ATACATGCGT	GCTCTGGATG	ACTTCTACGA	1450
	CAAGAATTTT	CCAGAGTTTG	TCCCCTGCG	TACAAAGGTG	AAGGAGATTT	1500
	TGCAGGAGGA	AGAAGACCTG	TCTGAAATTG	TGCAGTTGGT	CGGTAAAGCT	1550
	TCATTGGCAG	AAACTGACAA	GATCACACTT	GAGGTTGCCA	AACTATTAAA	1600
50	GGATGATTTT	CTGCAACAGA	ACAGCTATTG	ACCATATGAC	CGTTTCTGCC	1650
	CATTCTACAA	GACAGTAGGA	ATGCTGAAAA	ATATGATTGC	TTTCTACGAT	1700
	ATGTCTCGGC	ATGCAGTTGA	ATCTACTGCT	CAGAGCGAGA	ACAAGATCAC	1750
	TTGGAATGTT	ATTAGAGATT	CTATGGGCAA	TATTCTGTAT	CAGCTTTCCT	1800
	CCATGAAATT	CAAGGATCCA	GTCAAGGATG	GAGAAGCGAA	GATCAAGGCA	1850
55	GACTTTTGAGC	AGCTTCATGA	AGACATTGAG	CAAGCCTTCA	GGAACCTGGA	1900
	GGATTAAAGT	GGTAGCTGCC	AGTGGTTCTC	TCGGTGACAGT	TGTCACATTT	1950
	GGCAAGCTCT	GTAGGGTTGC	CGAGTGGCAT	CGGTGCTAGA	CACCTGAGCA	2000
	TTCCTTTGCC	ACATAAAGAC	TAAAGCAGGT	GGAATTTTCA	TTGTAAAAAG	2050
	CTGGTTCCAT	TGGTGCTAAG	ATTATGTTGT	GCCCTTTTCT	GCTTCTCACA	2100
60	TTCCAACAGA	GGAATTTACT	TCCAGTTTTC	TTCCATTTTC	CTCCTCATTT	2150

	TAAGTGTCGG	TACAGAGGCA	ATAATCTGAT	AACTCTGTAC	CGTCACTTAC	2200
	AAGCAGGGAG	AATTTGTAAT	TATTACAAAT	CCCATTATCT	CTGTGCACCA	2250
	CAGCCTTGTA	AATTCATTTG	TCCCAGGACT	CCCTCTTG TG	TGTACGTGAG	2300
	ATTGCCGTCT	GTATGTATGT	ACACACCGTA	CTGCAGTATT	TGAAGTCAGT	2350
5	CAGAAAGTGA	ATTACACCAC	TTACTCATTG	TGTCACGTAG	CAAGTGTGCA	2400
	AACTGCCATC	CATTGTCCTA	TTTATTTCACA	TAAC TAGTTT	TCTTTGCATT	2450
	TCCAGTGTTG	CAAATTGTGT	TTAGAAAATT	ATGCCATCGA	GACTGGTCGA	2500
	ACCTCACATT	GTAAC TCAGT	ATTTACACAC	ACGTTTACTT	GCTACAGAAA	2550
	TGTAGAAAAA	ATAATTGTTG	TATATTGAAA	GTACAAGTGA	CAAAGTTGCA	2600
10	TTTAAAAATGG	TGAATGTATT	TTATATTTCT	TTTGTAGACA	CAAGAGTTAA	2650
	TGCATTTTGC	TTAATGGAGA	TGTATGTAAA	CCTAAAAATAG	CAGTTTGTGC	2700
	ACAAATTATG	TATATGTGAA	ATGGAGATGG	TTTCTAATTT	GCTGATTGAT	2750
	TGCCAGTATT	AATTTAAACA	ACTGTAGTTG	TGGGATGTAG	TGGGAAGATT	2800
	TTTTTTTTTCC	TATAAAATTG	GTGGATGTAT	GTGTCGGAGA	TTTTGATTGT	2850
15	ATGTGTAAAA	TAGTGATCCC	AGTAACTGTA	AAGCTTTAGA	ATACAGTTAC	2900
	TGACTGTATA	GTTGTACAGG	TGTTGTTACT	TTTAAGAATT	TATTGACACA	2950
	AAGGTGAAAG	TCTATTATTG	TATTGTAATG	TTTAAAGCAT	TTAAGGTTTA	3000
	AAAATCCTAC	TTCTGTGTAT	AAATGTTACC	ATTCCTCATA	TAACATAACT	3050
	GTGTAGAAAT	ACAGTCAACT	TCATGTTTCAT	TAGCATTTC A	CTGTTGTCA C	3100
20	ATAAATTATG	CCCGGAAT				3118

2) INFORMATION FOR SEQ ID NO: 689

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1836 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Plasmodium falciparum*
 (B) STRAIN: 3D7
 (C) ACCESSION NUMBER: L08200

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 689

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	ATGACAAAAG	TTGCTGTTGA	AAAAGAGGAA	CCAGGAGTTG	TTTATAAGGT	50
	GGCTGGTTCA	TTAGTTATTG	CTGAGAATAT	GAGTGGA ACT	CGTATGTACG	100
	AGTTAGCTAA	AGTAGGATGG	AATAAATTGG	TTGGAGAAAT	TATTAGATTA	150
	GAAGGGAATT	ATGCATATAT	ACAAGTTTAT	GAAGATACTT	CAGGTTTATC	200
45	TGTAGGAGAC	CCTGTTATAA	AAACAGGAAA	TGCTTTATCA	GTCGAATTGG	250
	GTCCTGGTAT	TTTAGATAAT	ATTTATGATG	GTATTCAAAG	ACCATTAGAA	300
	AGAATAGCAA	ATGTGTGTGG	TGATGTATAT	ATATATAAAG	GTATTGATAT	350
	GACATCTTTA	GATCATGATA	AACAATGGCA	ATTTTATGCT	GATAAGAAAT	400
	TAAAATTAAA	TGATATTGTT	ACTGGTGGAG	ATATCTTTGG	ATTTGTTGAT	450
50	GAAAATAAAT	TATTTAAAGA	ACACAAAATT	ATGGCTCCAC	CTAATGCTAA	500
	AGGGAGGCTT	ACATATATTG	CTCCAGATGG	ATCATATACT	TTAAAAGATA	550
	AAATATTTGC	ATTAGAATAT	CAAGGAAAAA	AATATACATA	TGGTTTATCT	600
	CATTTATGGC	CTGTTTCGTG	TCCTAGACCT	GTTT TAGAAA	AGGTAACAGG	650
	GGATACTTTA	TTATTAACAG	GGCAAAGAGT	TTTAGATTCC	TTATTTCCAA	700
55	CAGTTCAAGG	AGGTACTTGT	GCTATTCCTG	GTGCATTTGG	TTGTGGAAAA	750
	ACTTGTGTTT	CTCAGGCCTT	ATCAAAATAT	TCTAATAGTG	AAGTTATTAT	800
	ATATGTAGGA	TGTGGTGAAA	GAGGTAATGA	AATGGCTGAA	ATTTTATCCG	850
	ACTTTCCTGA	ATTA ACTACT	AAAGTAGATA	ATGAAGATGT	AGGTATTATG	900
	CAAAGAACGT	GTTTAGTTGC	TAATACTTCT	AACATGCCTG	TCGCTGCAAG	950
60	AGAAGCTAGT	ATTTATACAG	GTATTACTTT	ATGTGAATAT	TTCCGTGATA	1000

	TGGGTTATAA	TGCTACCATG	ATGGCTGATA	GTACAAGTAG	ATGGGCAGAA	1050
	GCCTTAAGAG	AAATTTTCAGG	ACGTTTTCAGT	GAAATGCCTG	CAGATAGTGG	1100
	TTATCCAGCT	TATTTAGGTG	CTAGATTAGC	TTCCTTTTAT	GAACGTGCAG	1150
	GAAAAGTCAA	ATGTATTGGT	TCTCCATCTC	GTATAGGATC	CATTACAATT	1200
5	GTGGGTGCTG	TGTCTCCACC	AGGTGGTGAT	TTCTCTGACC	CTGTAACTAC	1250
	AGCAACCATG	TCTATTGTTT	AAGCATTTTG	GGGGTTAGAT	AAAAAACTAG	1300
	CTCAAAGAAA	ACATTTCCCT	TCTGTTAATT	GGTCTACATC	CTTTTCAAAG	1350
	TATGTCAGAC	AATTAGAACA	ATACTTTGAT	AATTTTGATC	AAGATTTCTT	1400
	ATCTTTAAGA	CAAAAAATTA	GTGATATTTT	ACAACAAGAA	AGTGACTTGA	1450
10	ATGATATTGT	TCAACTAGTA	GGAAAGGATT	CATTATCAGA	AGACCAAAAA	1500
	GTTGTTATGG	AAGTAGCCAA	AATTATTAGA	GAAGATTTTC	TTCAACAAAA	1550
	TGCATTTAGC	GATTATGATT	ATATGTGCCC	ATTACAAAAA	ACAGTTGGTA	1600
	TGATGAGAAT	TATTTGCCAC	TTTTATGCTG	AATGCTTAAG	AACATTACAA	1650
	GAATATGACT	CAAGAGAAAG	AAAAATTGGT	TGGGGATCTA	TATATAATAC	1700
15	ATTAAGACCA	ACTATAAATA	AAATTACACA	TATGAAATTT	GAAAACCCAA	1750
	AAAATTCAGA	TGAATATTTT	AAAAAGTATT	TTAAGGCACT	TGAAGAAGAA	1800
	ATAACAGTAG	GTTTAAGAAA	CTTGATGGAA	AAATGA		1836

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2) INFORMATION FOR SEQ ID NO: 690

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 3216 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*
- (B) STRAIN: X2180-1A
- (C) ACCESSION NUMBER: J05409

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 690

	ATGGCTGGTG	CAATTGAAAA	CGCTCGTAAG	GAAATAAAAA	GAATCTCATT	50
	AGAAGACCAT	GCTGAATCTG	AATATGGTGC	CATCTATTCT	GTCTCTGGTC	100
40	CGGTCGTCAT	TGCTGAAAAA	ATGATTGGTT	GTGCCATGTA	CGAATTGGTC	150
	AAGGTCGGTC	ACGATAACCT	GGTGGGTGAA	GTCATTAGAA	TTGACGGTGA	200
	CAAGGCCACC	ATCCAAGTTT	ACGAAGAAAC	TGCAGGCCTT	ACGGTCGGTG	250
	ACCCTGTTTT	GAGAACAGGT	AAGCCTCTGT	CGGTAGAATT	GGGTCCTGGT	300
	CTGATGGAAA	CCATTTACGA	TGGTATTCAA	AGACCTTTGA	AAGCCATTAA	350
45	GGAAGAATCG	CAATCGATTT	ATATCCCAAG	AGGTATTGAC	ACTCCAGCTT	400
	TGGATAGGAC	TATCAAGTGG	CAATTTACTC	CGGGAAAGTT	TCAAGTCGGC	450
	GATCATATTT	CCGGTGGTGA	TATTTACGGT	TCCGTTTTTG	AGAATTCGCT	500
	AATTTCAAGC	CATAAGATTC	TTTTGCCACC	AAGATCAAGA	GGTACAATCA	550
	CTTGGAATTGC	TCCAGCTGGT	GAGTACACTT	TGGATGAGAA	GATTTTGGAA	600
50	GTTGAATTTG	ATGGCAAGAA	GTCTGATTTT	ACTCTTTACC	ATACTTGGCC	650
	TGTTTCGTGTT	CCAAGACCAG	TTACTGAAAA	GTTATCTGCT	GACTATCCTT	700
	TGTTAACAGG	TCAAAGAGTT	TTGGATGCTT	TGTTTCCTTG	TGTTCAAGGT	750
	GGTACGACAT	GTATTCAGG	TGCTTTTGGT	TGTGGTAAGA	CCGTTATCTC	800
	TCAATCTTTG	TCCAAGTACT	CCAATTCTGA	CGCCATTATC	TATGTCGGGT	850
55	GCTTTGCCAA	GGGTACCAAT	GTTTTAATGG	CGGATGGGTC	TATTGAATGT	900
	ATTGAAAACA	TTGAGGTTGG	TAATAAGGTC	ATGGGTAAAG	ATGGCAGACC	950
	TCGTGAGGTA	ATTAAATTGC	CCAGAGGAAG	AGAAACTATG	TACAGCGTCG	1000
	TGCAGAAAAG	TCAGCACAGA	GCCCCAAAAA	GTGACTCAAG	TCGTGAAGTG	1050
	CCAGAATTAC	TCAAGTTTAC	GTGTAATGCG	ACCCATGAGT	TGGTTGTTAG	1100
60	AACACCTCGT	AGTGTCCGCC	GTTTGTCTCG	TACCATTAAAG	GGTGTCGAAT	1150

	ATTTTGAAGT	TATTACTTTT	GAGATGGGCC	AAAAGAAAGC	CCCCGACGGT	1200
	AGAATTGTTG	AGCTTGTCAA	GGAAGTTTCA	AAGAGCTACC	CAATATCTGA	1250
	GGGGCCTGAG	AGAGCCAACG	AATTAGTAGA	ATCCTATAGA	AAGGCTTCAA	1300
	ATAAAGCTTA	TTTTGAGTGG	ACTATTGAGG	CCAGAGATCT	TTCTCTGTTG	1350
5	GGTTCCCATG	TTCGTAAAGC	TACCTACCAG	ACTTACGCTC	CAATTCTTTA	1400
	TGAGAATGAC	CACTTTTTTCG	ACTACATGCA	AAAAAGTAAG	TTTCATCTCA	1450
	CCATTGAAGG	TCCAAAAGTA	CTTGCTTATT	TACTTGTTTT	ATGGATTGGT	1500
	GATGGATTGT	CTGACAGGGC	AACTTTTTTCG	GTTGATTCCA	GAGATACTTC	1550
	TTTGATGGAA	CGTGTTACTG	AATATGCTGA	AAAGTTGAAT	TTGTGCGCCG	1600
10	AGTATAAGGA	CAGAAAAGAA	CCACAAGTTG	CCAAAACGTG	TAATTTGTAC	1650
	TCTAAAGTTG	TCAGAGGTAA	TGGTATTTCG	ATAAATCTTA	ATACTGAGAA	1700
	TCCATTATGG	GACGCTATTG	TTGGCTTAGG	ATTCTTGAAG	GACGGTGTCA	1750
	AAAATATTCC	TTCTTTCTTG	TCTACGGACA	ATATCGGTAC	TCGTGAAACA	1800
	TTTCTTGCTG	GTCTAATTGA	TTCTGATGGC	TATGTTACTG	ATGAGCATGG	1850
15	TATTAAAGCA	ACAATAAAGA	CAATTCATAC	TTCTGTCAGA	GATGGTTTGG	1900
	TTTCCCTTGC	TCGTTCTTTA	GGCTTAGTAG	TCTCGGTTAA	CGCAGAACCT	1950
	GCTAAGGTTG	ACATGAATGG	CACCAAACAT	AAAATTAGTT	ATGCTATTTA	2000
	TATGTCTGGT	GGAGATGTTT	TGCTTAACGT	TCTTTCGAAG	TGTGCCGGCT	2050
	CTAAAAAATT	CAGGCCTGCT	CCCGCCGCTG	CTTTTGCACG	TGAGTGCCGC	2100
20	GGATTTTATT	TCGAGTTACA	AGAATTGAAG	GAAGACGATT	ATTATGGGAT	2150
	TACTTTATCT	GATGATTCTG	ATCATCAGTT	TTTGCTTGCC	AACCAGGTTG	2200
	TCGTCCATAA	TTGCGGAGAA	AGAGGTAATG	AAATGGCAGA	AGTCTTGATG	2250
	GAATTCCCAG	AGTTATATAC	TGAAATGAGC	GGTACTAAAG	AACCAATTAT	2300
	GAAGCGTACT	ACTTTGGTCG	CTAATACATC	TAACATGCCG	GTTGCAGCCA	2350
25	GAGAAGCTTC	TATTTACACT	GGTATCACTC	TTGCAGAATA	CTTCAGAGAT	2400
	CAAGGTAAAA	ATGTTTCTAT	GATTGCAGAC	TCTTCTTCAA	GATGGGCTGA	2450
	AGCTTTGAGA	GAAATTTCTG	GTCGTTTGGG	TGAGATGCCT	GCTGATCAAG	2500
	GTTTCCCAGC	TTATTTGGGT	GCTAAGTTGG	CCTCCTTTTA	CGAAAGAGCC	2550
	GGTAAAGCTG	TTGCTTTAGG	TTCCCCAGAT	CGTACTGGTT	CCGTTTCCAT	2600
30	CGTTGCTGCC	GTTTCGCCAG	CCGGTGGTGA	TTTCTCAGAT	CCTGTTACTA	2650
	CTGCTACATT	GGGTATCACT	CAAGTCTTTT	GGGGTTTAGA	CAAGAAATTG	2700
	GCTCAAAGAA	AGCATTTCCC	ATCTATCAAC	ACATCTGTTT	CTTACTCCAA	2750
	ATACACTAAT	GTCTTGAACA	AGTTTATGA	TTCCAATTAC	CCTGAATTTT	2800
	CTGTTTTAAG	AGATCGTATG	AAGGAAATTC	TATCAAACGC	TGAAGAATTA	2850
35	GAACAAGTTG	TTCAATTAGT	TGGTAAATCG	GCCTTGCTCTG	ATAGTGATAA	2900
	GATTACTTTG	GATGTTGCCA	CTTTAATCAA	GGAAGATTTT	TTGCAACAAA	2950
	ATGGTTACTC	CACTTATGAT	GCTTTCGTGC	CAATTTGGAA	GACATTTGAT	3000
	ATGATGAGAG	CCTTCATCTC	GTATCATGAC	GAAGCTCAAA	AAGCTGTTGC	3050
	TAATGGTGCC	AACTGGTCAA	AACTAGCTGA	CTCTACTGGT	GACGTTAAGC	3100
40	ATGCCGTTTC	TTCATCTAAA	TTTTTTGAAC	CAAGCAGGGG	TGAAAAGGAA	3150
	GTCCATGGCG	AATTCGAAAA	ATTGTTGAGC	ACTATGCAAG	AAAGATTTCG	3200
	TGAATCTACC	GATTAA				3216

45

2) INFORMATION FOR SEQ ID NO: 691

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1860 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55

(vi) ORIGINAL SOURCE:

60

- (A) ORGANISM: *Schizosaccharomyces pombe*
- (B) STRAIN: 972 h-
- (C) ACCESSION NUMBER: S47814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 691

	ATGGCGGGAG	GAATTGAACT	GGCCAAGAAG	GCTATCAGGA	GCCTCAAAAA	50
	TTACGACGAG	CATGAAAACC	GATATGGATC	TATTTTCAGC	GTTTCTGGTC	100
5	CTGTCGTTGT	TGCAGCCAAT	ATGCTTGGAT	GTTTCGATGA	CGAACTCGTT	150
	CGCGTTGGTC	ATGAAGAACT	AGTTGGTGAA	GTAATTCGTA	TCCATCAAGA	200
	TAAATGTACT	ATTCAAGTAT	ACGAAGAGAC	GTCCGGTCTC	ACTGTTGGTG	250
	ATCCTGTCCA	ACGCACTGGA	AAGCCATTAT	CTGTTGAATT	AGGTCCTGGT	300
	TTAGCTGAGA	CTATTTATGA	TGGTATCCAA	CGTCCGTAA	AGCAAATTTT	350
10	CGACAAATCT	CAAAGTATTT	ATATTCCTAG	AGGTATTAAT	ACAGAATCAC	400
	TTAATCGTGA	GCATAAGTGG	GATTTACACAC	CAAATAAGGA	TTTACGCATT	450
	GGCGATCATG	TATCCGGTGG	TGATGTTTTT	GGTTCGTAT	TTGAAAACCTC	500
	TCTTTTCAAT	GATCATAAAA	TTATGTTACC	CCCTAGAGCC	CGTGGTACCG	550
	TCACATATAT	TGCTGAAGCT	GGATCATACC	ATGTTGATGA	AAAACCTTCTT	600
15	GAAGTCGAGT	TTAATGGCAA	GAAACATTCT	TTTAGTATGT	TGCATACTTG	650
	GCCTGTCCGT	GCTGCTCGTC	CAGTTGCGGA	CAACTTAACT	GCTAATCAAC	700
	CTTTATTGAC	TGGTCAACGT	GTTTTGGATG	CGTTATACCC	CTGTGTTCAA	750
	GGTGGCACTA	CTGCTATCCC	CGGTGCCTTT	GGTTGTGGTA	AAACAGTTAT	800
	TTCACAATCT	CTTCTAAGT	ACTCTAATTC	TGATTTGATT	GTTTACGTCG	850
20	GTTGTGGTGA	ACGTGGAAAC	GAAATGGCAG	AAGTGTTAAT	GGATTTCCCA	900
	GAACATAACAA	TTGATATTAA	TGGTAAACCA	GAGCCCATTA	TGAAGCGTAC	950
	TACATTGGTA	GCCAACACTT	CTAACATGCC	TGTCGCTGCT	CGTGAAGCTT	1000
	CCATTTATAC	CGGTATTACA	CTTGCTGAAT	ATTATCGTGA	TCAAGGTAAG	1050
	AACGTTTCAA	TGATGGCTGA	TTCTACATCT	CGTTGGGCTG	AAGCTTTGCG	1100
25	TGAAATTTCT	GGTCGTTTGG	CTGAGATGCC	TGCCGATTCT	GGTTATCCCG	1150
	CTTATTTGGG	TGCCAAATTG	GCTTCTTTTT	ACGAACGTGC	TGGTCGTGCT	1200
	CGTTGCTTGG	GAAGTCCTGA	CCGTGAAGGA	ACAGTTTCAA	TTGTTGGAGC	1250
	TGTTTCTCCT	CCGGGTGGTG	ATTTTTCTGA	TCCTGTTACT	AGTGCAACCT	1300
	TGGGAATTGT	TCAAGTCTTC	TGGGGTTTGG	ACAAGAAATT	GGCCCAACGT	1350
30	AAACACTTTC	CCTCAATCAA	CACCTCTCTT	TCCTATTCTA	AATACATCAA	1400
	TGCTTTGCAA	CCTTGGTATG	AGGAAAGAGT	TCCAGGCTTT	AATACTCTTC	1450
	GTGATCAAAT	CAAACAGATC	ATTCAACAAG	AAGATTCCAT	GTTGGAAATT	1500
	ATTCAGTTGG	TTGGTAAGTC	GGCTCTTTCT	GAAACGGATA	AAGTTACTTT	1550
	GGACATAGCC	GGTATTATTA	AGAATGACTT	CTTACAACAA	AACGGTTATT	1600
35	CTGATTACGA	TCGCTGTTGC	CCTCTTTACA	AGACTTATCA	TATGATGCGA	1650
	AACATGATTG	CTTACTACAC	AAAGGCTAAA	AGTGCCGTTG	AAACTGGTAG	1700
	CGTTCCTTGG	TCAAAGATTA	AAGAAAGTAC	TTCAGATATC	TTTTATGAGT	1750
	TAACCTCGAT	GAAATTCGAA	AACCCTAATG	AAGGCGAGAA	GGAAATAGTC	1800
	GAACACTATG	AAACTCTGCA	CAAGAAGATT	GAGGACAAGT	TTCACACTCT	1850
40	GACTGAGTAA					1860

2) INFORMATION FOR SEQ ID NO: 692

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1833 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma congolense*
- (B) STRAIN: IL3000
- (C) ACCESSION NUMBER: Z25814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 692


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ATGACGAGCG ATAAAAACCC TTACAAAACA GAGCAGCGCA TGGGGGCCGT      50
GAAGGCCGTC TCCGGGCCAG TTGTCATTGC TGAAAACATG GGCGGTAGCG      100
CTATGTATGA GCTTGTGCAG GTAGGTTCCCT TCCGGTTAGT GGGCGAGATC      150
ATTCGTCTAG AGGGCGATAC CGCCACTATT CAGGTCTATG AGGAAACAGG      200
5  TGGCCTCACT GTCGGAGACC CGGTGTACTG TACGGGTAAG CCTCTTTCGC      250
TTGAGCTTGG ACCTGGAATC ATGTCTGAAA TATTTGACGG TATCCAGCGG      300
CCTCTTGACA CCATCTACCG CATGGTGGA AACGTGTTTA TCCCCAGGGG      350
CGTTCAGGTG AAGTCACTCA ATGACCAGAA ACAGTGGGAC TTTAAGCCAT      400
GCCTGAAGGT TGGAGATCTT GTGTCTGGTG GTGATATCAT TGGCTCAGTG      450
10 GTGGAGAACT CTCTCATGTA CAATCACAGC ATTATGATTC CGCCCAATGT      500
GCGGGGCCGT GTTACTTCCA TTGTTCCCTT AGGAAATTAC ACCCTCCAAG      550
ATGACATTAT TGAATTGGA TATAATGGG CAGTGAAATC ACTAAAACCT      600
ATGCATCGTC GGCACGTACG GACCCCGCGT CCTGTGGCGT CAAAAGAATC      650
CGGCAATCAT CCGCTTCTCA CCGGACAGCG TGTGCTCGAT GCTCTCTTTC      700
15 CATCCGTCCA GGGTGGAACA TGCGCCATCC CTGGCGCGTT TGGATGCGGA      750
AAGACGGTTA TCAGTCAGGC TCTTTCGAAG TTCTCCAACA GCGACGCTGT      800
TATCTATGTC GGCTGCGGCG AGCGTGGGAA TGAGATGGCA GAGGTGCTCA      850
TGGACTTCCC CACACTCACC ACCGTTATTG ATGGTCGTGA GGAGTCCATC      900
ATGAAGCGTA CCTGCCTGGT GGCAAACACC TCAAATATGC CTGTCGCTGC      950
20 TCGTGAGGCG TCTATTTACA CTGGCATCAC TTTAGCTGAG TATTATCGTG      1000
ATATGGGCAA GCACATTGCT ATGATGGCCG ACTCTACCTC TCGATGGGCT      1050
GAGGCTCTCC GTGAGATCTC TGGGCGTCTC GCTGAAATGC CCGCTGATGG      1100
TGGTTACCCT GCGTACCTCA GTGCGCGTCT TGCTTCCTTC TACGAGCGTG      1150
CGGGGCGCGT GACATGCATC GGTGGGCCAA AACCGGAGGG CTCAGTAACC      1200
25 ATCGTTGGTG CCGTTTCTCC TCCTGGAGGT GACTTTTCTG ACCCAGTGAC      1250
GTCCGCTACG CTTGGTATTG TGCAAGTCTT TTGGGGTCTT GAGAAGCGTC      1300
TTGCGCAACG TAAACACTTT CCTTCTGTTA ATTGGCTCAT TTCCTATTCA      1350
AAATACCTTA ATGCTTTTGA GCCCTTCTTC AACACGCTTG ACCCTGACTA      1400
CATGCGCCTG CGGTCAGTTG CTGCGGAGAT CCTTCAGCGT GAGGAAGAGT      1450
30 TGCAAGAAAT TGTTCAACTT GTCGGTAAGG ACTCACTTTC GGAGTCTGAC      1500
AAAATTATTC TAGAAACGGC TAAGGTTATT CGTGAAGAGT TTCTCCAGCA      1550
GAATGCCTTT ACGCCGTACG ACAAGTATTG CCCGCCGTAC AAGACCTGCT      1600
GGATGCTACG TAACATTGTC GCGTTCTACG AGGAGAGCCA GCGCGTTGTA      1650
GCTGAGTCCG CTGGGGAAC TAAAGATTAC TGGAACTACA TTCGTGAAAT      1700
35 GATTCCCTCAT ATTTACACGG GTTTAACTGA GATGAAGTTC CGTGATCCTC      1750
AGGAGGGTGA GGAGGCCAAC GTAGAATTCT ACAGAAAACA AAATGAGGAA      1800
ATTGTCAGCG CATTCGCCTC GCTGCTGCAA TAA      1833

```

40 2) INFORMATION FOR SEQ ID NO: 693

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 1758 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

50

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Thermus thermophilus*
 (B) STRAIN: HB8
 (C) ACCESSION NUMBER: D63799

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 693

```

ATGATCCAAG GGGTGATCCA GAAGATCGCG GGCCCGGCGG TGATCGCCAA      50
GGGCATGCTC GGGGCCCGCA TGTACGACAT CTGCAAGGTG GGCGAAGAGG      100
60 GCCTCGTGGG CGAGATCATC CGCCTGGACG GGGACACGGC CTTCGTCCAG      150

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GTCTACGAGG ACACCTCGGG CCTAAAGGTG GGGGAGCCCC TGGTCTCCAC 200
 GGGCCTTCCC TTGGCGGTGG AGCTCGGCCC CGGGATGCTG AACGGCATCT 250
 ACGACGGCAT CCAGCGCCCC CTGGAGCGCA TCCGGGAGAA GACGGGGATC 300
 TACATCACCC GGGGCGTGGT GGTCCACGCC CTGGACCGGG AGAAGAAGTG 350
 5 GGCCTGGACG CCCATGGTCA AGCCCAGGGA CGAGGTGCGG GGGGGTATGG 400
 TCCTGGGCAC GGTGCCCCGAG TTCGGCTTCA CCCACAAGAT CCTGGTACCC 450
 CCGGACGTGC GGGGCCGGGT CAAGGAGGTG AAGCCCGCCG GGGAGTACAC 500
 CGTGGAGGAG CCGGTGGTGG TCCTCGAGGA CGGCACCGAG CTCAAGATGT 550
 ACCACACCTG GCCCGTTTCG CGGGCGAGGC CCGTGCAAAG GAAGCTTGAC 600
 10 CCCAACACCC CTTTCTCAC GGGGATGCGC ATCCTGGACG TCCTCTTCCC 650
 CGTGGCCATG GGGGGCACCG CCGCCATCCC TGGGCCCTTC GGCAGCGGCA 700
 AGACCGTGAC CCAGCAGTCC CTGGCCAAGT GGTCCAACGC CGACGTGGTG 750
 GTCTACGTGG GCTGCGGGGA GCGGGGGAAG GAGATGACCG ACGTGCTCGT 800
 GGAGTTCCCC GAGCTCACCG ACCCCAAGAC GGGTGGGCCC TTGATGCACC 850
 15 GCACCGTCTC CATCGCCAAC ACCTCCAACA TGCCCGTGGC CGCCCGCGAG 900
 GCCAGCATCT ACGTGGGCGT GACCATCGCC GAGTACTTCC GCGACCAGGG 950
 CTTCTCCGTG GCCCTCATGG CCGACTCCAC GAGCCGCTGG GCCGAGGCTT 1000
 TGCGCGAGAT CTCTAGCCGC CTCGAGGAGA TGCCCGCCGA GGAGGGCTAC 1050
 CCGCCCTACC TCGCCGCCAG GCTCGCCGCC TTCTACGAGC GGGCGGGCAA 1100
 20 GGTCAACACC CTGGGCGGCG AGGAGGGGAG GGTGACCATC GTGGGGGCCG 1150
 TCTCCCCGCG GGGCGGCGAC ATGTCCGAGC CCGTGACCCA GTCCACCTTG 1200
 AGGATCGTGG GGGCCTTCTG GCGGCTTGAC GCCTCCCTGG CCTTCCGCCG 1250
 CCACTTCCCC GCCATCAACT GGAACGGCTC CTACAGCCTC TTCACCTCCG 1300
 CCCTTGACCC CTGGTACCGG GAGAACGTGG CCGAGGACTA CCCCAGGCTC 1350
 25 CGCGACGCCA TCTCCGAGCT TTTGCAGCGG GAGGCGGGCC TCCAGGAGAT 1400
 CGTCCAGCTC GTGGGGCCCG ACGCCCTCCA GGACGCCGAG CGCCTCGTCA 1450
 TTGAGGTGGG CCGGATCATC CGCGAGGACT TCCTGCAGCA GAACGCCTAC 1500
 CACGAGGTGG ACGCCTACTG CTCCATGAAG AAGGCCTACG GGATCATGAA 1550
 GATGATCCTC GCCTTCTACA AGGAGGCGGA GCGGGCCATC AAGCGGGGGG 1600
 30 TTTCCATAGA CGAGATCCTG CAGCTCCCCG TTCTGGAGCG CATCGGCCCG 1650
 GCCCGCTACG TGAGCGAGGA GGAGTTCCCC GCCTACTTTG AGGAGGCCAT 1700
 GAAGGAGATC CAGGGGGCCT TCAAGGCTGG CCTAAAGGGG GAGAGATGGA 1750
 CTTTCTGA

35

2) INFORMATION FOR SEQ ID NO: 694

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 694

50 CGGCGCIATC YTS GTTGTG C

21

2) INFORMATION FOR SEQ ID NO: 695

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 695

5 GTTTCACGTG ATGACGTACA

20

2) INFORMATION FOR SEQ ID NO: 696

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 696

ATIGGICAYR TIGAYCAYGG IAARAC

26

2) INFORMATION FOR SEQ ID NO: 697

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 697

CCIACIGTIC KICCRCCYTC RCG

23

2) INFORMATION FOR SEQ ID NO: 698

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1185 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*

(C) ACCESSION NUMBER: extracted from J01690

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 698

GTGTCTAAAG	AAAAATTTGA	ACGTACAAAA	CCGCACGTTA	ACGTTGGTAC	50
TATCGGCCAC	GTTGACCACG	GTA AAACTAC	TCTGACCGCT	GCAATCACCA	100
CCGTACTGGC	TAA AACCTAC	GGCGGTGCTG	CTCGTGCATT	CGACCAGATC	150
GATAACGCGC	CGGAAGAAAA	AGCTCGTGGT	ATCACCATCA	ACACTTCTCA	200

	CGTTGAATAC	GACACCCCGA	CCCGTCACTA	CGCACACGTA	GACTGCCCCG	250
	GGCACGCCGA	CTATGTTAAA	AACATGATCA	CCGGTGCTGC	TCAGATGGAC	300
	GGCGCGATCC	TGGTAGTTGC	TGCGACTGAC	GGCCCCGATC	CGCAGACTCG	350
	TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	400
5	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTT	450
	GAAATGGAAG	TTCGTGAACT	TCTGTCTCAG	TACGACTTCC	CGGGCGACGA	500
	CACTCCGATC	GTTTCGTGGT	CTGCTCTGAA	AGCGCTGGAA	GGCGACGCAG	550
	AGTGGGAAGC	GAAAATCCTG	GAACTGGCTG	GCTTCCTGGA	TTCTTATATT	600
	CCGGAACCAG	AGCGTGCGAT	TGACAAGCCG	TTCCTGCTGC	CGATCGAAGA	650
10	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAAGAC	700
	GCGGTATCAT	CAAAGTTGGT	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAG	750
	ACTCAGAAGT	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	800
	CGAAGGCCGT	GCTGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAAC	850
	GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CACCATCAAG	900
15	CCGCACACCA	AGTTCGAATC	TGAAGTGTAC	ATTCTGTCCA	AAGATGAAGG	950
	CGGCCGTTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	1000
	GTACTACTGA	CGTGACTGGT	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	1050
	GTAATGCCGG	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TCCACCCGAT	1100
	CGCGATGGAC	GACGGTCTGC	GTTTCGCAAT	CCGTGAAGGC	GGCCGTACCG	1150
20	TTGGCGCGGG	CGTTGTTGCT	AAAGTTCTGG	GCTAA		1185

2) INFORMATION FOR SEQ ID NO: 699

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 26 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 699

GTIACIGGYT CYTYRARRTT ICCICC

26

2) INFORMATION FOR SEQ ID NO: 700

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 700

TIRTIGAYGT CGARTTCCCT CARG

24

2) INFORMATION FOR SEQ ID NO: 701

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 bases
 - (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 701

GTGTTACGA TCATCGATGC G

21

2) INFORMATION FOR SEQ ID NO: 702

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 702

CTCTCGATAT CCGCGAAGCG

20

2) INFORMATION FOR SEQ ID NO: 703

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 703

TATGGAAATT CGAAACATCT

20

2) INFORMATION FOR SEQ ID NO: 704

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 704

AGTGCTCAA TTAATGTTGG

20

2) INFORMATION FOR SEQ ID NO: 705

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 705
GTACAGTTCC AATACCTGAA

2) INFORMATION FOR SEQ ID NO: 706

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 706
TGAAATCTTC ACATCCAACA

2) INFORMATION FOR SEQ ID NO: 707

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 707
TWACCATTTTC AGTACCTTCT GGTA

2) INFORMATION FOR SEQ ID NO: 708

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 708
TCRTCCATIC CIARIATIGC IATAT

2) INFORMATION FOR SEQ ID NO: 709

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1656 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Borrelia burgdorferi*
 (C) ACCESSION NUMBER: extracted from AE00783

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 709

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20  ATGAATGAAG TTTTATTTGT AAAGACTGCT GGTAGGAATT TAAAAGCAGA      50
    AGTAATTCGT ATTAGGGGCA ATGAAGTTGA TGCACAGGTT TTTGAATTGA      100
    CAAAAGGGAT ATCTGTTGGA GACCTAGTTG AATTTACAGA CAAACTTTTA      150
    ACAGTTGAAC TCGGACCAGG GCTTTTAACT CAAGTATATG ATGGGCTTCA      200
    AAATCCTTTG CCTGAATTGG CTATTCAATG TGGATTTTTT TTAGAAAGGG      250
25  GAGTATATTT AAGGCCCTTG AATAAAGATA AAAAGTGGAA TTTTAAAAAA      300
    ACCTCCAAAG TTGGAGATAT CGTTATTGCA GGAGATTTTT TAGGTTTTGT      350
    AATTGAGGGA ACTGTTCAAC ATCAAATAAT GATTCCATTT TATAAAAGGG      400
    ATTCTTATAA AATTGTGGAG ATTGTAAGTG ATGGCGACTA TTCGATTGAT      450
    GAGCAAATTG CTGTAATTGA AGATGATTCT GGTATGAGGC ATAATATTAC      500
30  AATGTCTTTT CATTGGCCTG TTAAAGTTCC TATTACTAAT TATAAGGAAC      550
    GCCTTATTC TAGTGAACCT ATGTTGACTC AAAGTAGAAT TATAGATACA      600
    TTTTTCCCAG TTGCCAAAGG TGGAACTTTT TGCATTCCGG GTCCTTTTGG      650
    AGCAGGAAAA ACGGTTCTTC AGCAGGTTAC AAGTCGAAAT GCTGATGTTG      700
    ATGTAGTGAT TATTGCAGCT TGTGGTGAGC GAGCAGGAGA AGTGGTAGAA      750
35  ACTCTTAAAG AATTTCCCGA ATTAATGGAT CCAAAAACCG GCAAATCTTT      800
    AATGGACAGG ACTTGTATTA TTTGTAATAC ATCTTCAATG CCAGTTGCAG      850
    CTAGAGAAGC TTCTGTTTAT ACTGCTATTA CTATTGGTGA GTATTACAGG      900
    CAAATGGGCC TTGATATTCT TCTTTTGGCA GATTCAACTT CAAGATGGGC      950
    TCAAGCAATG AGAGAAATGT CTGGACGCCT TGAGGAAATT CCTGGCGAGG      1000
40  AGGCTTTTCC GGCATATCTT GAGTCTGTTA TTGCTTCCTT TTATGAAAGG      1050
    GCAGGTATTG TAGTTCTTAA TAATGGGGAT ATTGGATCTG TAACAGTTGG      1100
    TGGCTCTGTA AGTCCTGCTG GTGGTAATTT TGAAGAGCCA GTTACTCAAG      1150
    CAACTTTAAA AGTTGTAGGA GCATTTACAG GGCTTACAAG AGAAAGGTCT      1200
    GATGCTAGGA AATTTCCAGC TATTAGTCCT CTTGAATCTT GGAGTAAATA      1250
45  TAAAGGCGTT ATTGATCAAA AAAAGACTGA ATATGCAAGA TCTTTTTTGG      1300
    TGAAAGGTAA TGAAATTAAT CAAATGATGA AAGTTGTTGG AGAAGAAGGC      1350
    ATAAGTAACG ATGATTTTTT AATTTATTTA AAATCCGAGC TACTTGATTG      1400
    GTGCTATTTG CAGCAAATTT CATTTGATTG TATTGATGCT GCTGTTAGTT      1450
    CAGAGCGTCA AAATTATATG TTTGATATAG TTTATAACAT TCTTAAAACT      1500
50  AACTTTGAGT TTTCTGATAA ACTTCAAGCA AGAGATTTTA TAAATGAGTT      1550
    AAGGCAAAAT CTTTLAGACA TGAATCTTTC TTCTTTTAAG GATCATAAGT      1600
    TTAATAAATT GGAGCATGCT TTGGGTGAAT TGATAAATTT TAAAAGGTA      1650
    ATTTAG
  
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2) INFORMATION FOR SEQ ID NO: 710

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1818 bases

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Treponema pallidum*
 (B) STRAIN: Nichols
 10 (C) ACCESSION NUMBER: extracted from AE000520

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 710

	GTGATCAAAG	ACGATGTGGT	TACAGGCCGT	GTAGTGAGGG	TGTCTGGTCC	50
15	CATTGTGTAT	GCCGAGGGCC	TCTCTGCGTG	CAGCGTATAC	GATGTTGTCG	100
	ACGTAGGGGA	AGCATCGCTC	ATCGGAGAAA	TTATCCGGTT	GGATGAGAGC	150
	AAGGCGGTCTG	TGCAAGTATA	CGAGGATGAC	ACAGGTATGC	GAGTCGGGGA	200
	GAAGGTGACA	AGCTTGCGTC	GACCACTCTC	AGTCCGCTTA	GGGCCTGGAT	250
	TAATCGGCAC	CATTTATGAC	GGTATTCAGC	GCCCACTTGA	GCGCCTCTTC	300
20	CAAGAAGACG	GCGCCTTCTT	GCGTCCTGGT	GCGCGTTTAC	AACCGCTTGA	350
	TGGCTCCGTA	CGCTGGGATT	TTCGTCCTCA	TTGTAACGAG	CGCGGTGAGG	400
	CCCTGTGCGC	GGGGATTCCG	ATTGCACCTG	GGTCAGTGTT	AGGGACCGTG	450
	CAGGAGACTC	CTTCTGTTGT	GCACACTATC	ATGGTTCCTC	CTGACATCCG	500
	GGGGAGCGTG	CTATCTTCGT	TCAAGGGCGC	AGGTGCTTAC	ACAATAGATG	550
25	AAGAAATTGG	ACGCACTGAT	CTTGGTGAGC	CGCTTTTCTT	ATCCCAGTAC	600
	TGGCCAGTGC	GTCGTGCGCG	TCCTTTCAGC	AAAAAACTTG	CAGTGTGTGA	650
	GCCACTAGTT	ACTGGACAGC	GGGCGATTGA	TGTTTTCTTC	CCCCATACAA	700
	AGGGAGGAAC	GGCGGCTATT	CCAGGGGGAT	TTGGAAGTGG	GAAGACAATG	750
	ACGCAGCATG	CCGTTGCCAA	GTGGTGTGAT	GCAGATATTA	TCGTGTACAT	800
30	CGGCTGCGGA	GAGCGGGGCA	ACGAGATGAC	AGACGTGCTC	TCTGAATTTT	850
	CCAAACTCAT	CGATCCGCGC	ACAGGACGCT	CTCTTATGGA	GCGGACGATT	900
	TTGATCGCAA	ATACGTCCAA	TATGCCTGTG	TCCGCACGCG	AGGTGTGCGT	950
	GTATTACAGG	ATTACCCTTG	CGGAATACTA	CCGTGATATG	GGTATGCATG	1000
	TGGCCATCAT	GGCTGATTCT	ACCAGCCGCT	GGGCGGAGGC	GCTGCGTGAA	1050
35	TTGTCTGGGC	GCATGGAAGA	AATGCCTGCG	GAGGAGGGAT	TCCCTGCGTA	1100
	CCTTCCGACG	CGTCTTGACG	AATTTTATGA	GCGCGCAGGA	CGCGTGGAAG	1150
	CCTGTGTGGC	GCGCGAGGGC	TCTGTGAGCA	TCATTGGTGC	TGTTTTCTCC	1200
	CTGGGTGGAG	ATTTCTCTGA	GCCGGTGACG	CAGCACACAA	AGCGCTTCAT	1250
	CCGTTGCTTT	TGGGCCTTGG	ATCGTGAAGT	TGCACACGCG	CGTCATTACC	1300
40	CTGCCATTGG	GTGGATAGAT	TCATACTCTG	AATATGCGCA	GGAAGTAAGT	1350
	GCATGGTGGA	GTAAGTATGA	CCCGCGCGCA	GGCGCGTTGC	GCGCCGCGAG	1400
	CTTGGAATTT	CTGAGAAAGG	AACAGCGGTT	ACAGCAAATT	GTCAGGCTTG	1450
	TCCGTCCTGA	TGCGCTGCCT	GGAGAAGATC	GTCTGGTGCT	AATGGTGTGT	1500
	GAAATGATCA	AAGGTGGCTT	TCTGCAGCAG	AACGCTTTTG	ATCCGACGGA	1550
45	TGTGTTCTCC	TGTCCCGAAA	AGCAGGTGCA	GATCTTGCGT	ACCATAGTGG	1600
	ATTTTCACGA	ACGTGCCGTG	GTGCTGCTGC	GTGCAGGTAT	TTCGCTTTCT	1650
	GCGCTGTCCC	AGCTTTTCGT	CCGGGAGCTC	ATCGTACGTA	TGAAAACTAC	1700
	GTACGGGAAT	GAGGATGTAC	ACAAGATGCA	GAAAGTGTAC	GACACGATGT	1750
	GCACTGAGTT	TGACCAACTG	AGTGTGTGTG	CTGCCGCGCG	CACACAAGGG	1800
50	GGGGAGAAAG	TCGAATGA				1818

2) INFORMATION FOR SEQ ID NO: 711

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1779 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Chlamydia trachomatis*
 (B) STRAIN: MoPn

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 711

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10 CAGGGCTATG TCGTAGAAGC TTACGGAAAT TTATTGCGGG TGCATTTTGA 50
   TGGGCATGTG CGTCAAGGAG AAGTGGCCTA TGTCAGCGTG GATGATACTT 100
   GGTTGAAAGC GGAAATTATA GAAGTTGTGG GAGATGAGGT TAAAGTCCAA 150
   GTTTTGTGAGG AAACCTCAAGG AATTTCTCGA GGCGCTTTGG TAACTTTTTC 200
   CGGGCATTTA TTAGAAGCGG AACTTGGGCC CGGTCTATTG CAAGGTATTT 250
15 TTGACGGACT TCAGAATCGC TTAGAGGTAT TGGCAGATAC AAGCTTGTTT 300
   TTGAAAAGAG GGGAGTATGT TAATGCCATT TGTCGGGAAA CTGTATGGGC 350
   TTATACGCAA AAGGCTTCTG TCGGGGATGT TCTATCTCGG GGAGATGTGC 400
   TTGGTACAGT AAAGGAAGGG CGGTTTGATC ATAAAATCAT GGTTCCTTTC 450
   TCTTGTTTTG AGGAAGTGAC TATCACTTGG GTCATTTCTT CAGGAGATTA 500
20 CACTGTTGAT ACCGTTATTG CTAAAGGACG TACTGCTTCA GGAGCCGAGC 550
   TTGAATTTTAC AATGGTTCAG AAATGGCCCA TTAAACAGGC TTTTTTAGAA 600
   GGGGAAAAGG TACCGTCTCA TGAAATTATG GATGTTGGGT TACGAGTATT 650
   AGATACTCAG ATCCCCGTCT TAAAGGGAGG AACTTTTTGT ACTCCAGGGC 700
   CTTTTGGTGC AGGAAAGACC GTTTTACAGC ACCATTTATC TAAGTATGCA 750
25 GCTGTAGATA TCGTAGTTTT GTGTGCTTGT GGAGAGCGAG CTGGAGAGGT 800
   TGTAGAAATT CTTCAGGAGT TCCCGCATTT GACAGATCCT CATACGGGGC 850
   AGTCTTTGAT GCATAGGACC TGTATTATTT GTAATACATC TTCCATGCCT 900
   GTAGCAGCTA GAGAGTCCTC CATTTATTTG GGTATTACTA TAGCAGAATA 950
   TTACCGTCAA ATGGGGTTGC ATGTTTTGTT ATTGGCTGAC TCGACATCTA 1000
30 GATGGGCTCA AGCTTTAAGG GAAATTTTCAG GCGATTAGA AGAAATCCCT 1050
   GGAGAAGAAG CTTTCCAGC CTATTTGGCG TCTCGAATAG CAGCTTTTGA 1100
   TGAGCGAGGC GGGGCTGTGA AAATGAAAGA TGGATCGGAA GGCTCCTTGA 1150
   CTATCTGTGG AGCGGTTTCT CCCGCAGGAG GAAATTTTGA AGAGCCTGTT 1200
   ACACAAGCAA CTTTATCTGT TGTGTTGGCT TTCTGTGGGC TTTCTAAGGC 1250
35 TAGAGCAGAT GCTAGACGGT ATCCTTCTAT TGATCCGATG ATTTTCATGGT 1300
   CTAAGTACTT GGATTCTGTG GCGGAGATTT TAGAGAAAAA AGTTCCAGGA 1350
   TGGGGAGATT CCGTTAAAAA AGCTTCTCGT TTCTTAGAAG AAGGAGCAGA 1400
   AATTGGTAAG CGAATAGAAG TTGTTGGGGA AGAAGGGATT TCTATGGAAG 1450
   ATATAGAAAT CTTTTTGAAT TCAGAGTTGT ATGATTTCCTG TTACTTACAG 1500
40 CAAAACGCTT TCGATGCAGA GGACTGTTAT TGTCTTTTG ATCGTCAAAT 1550
   AGAGCTTTTT TCTTTAATGA GTCATATTTT TAGCTCTAGA TTCTGTTTTG 1600
   ATTGTCCAGA TAATGCTCGG AGTTTCTTTT TAGAGCTTCA AAGTAAAATT 1650
   AAAACGCTGA ATGGTCAAAA ATTCTTTTCT GAAGACTATC AGAAGGGGCT 1700
   AGAAGTGATC TATAAACTAT TAGAAAGCAA AATGGTGCAG ACGGCGTAGG 1750
45 TATGCAAACA ATATATACAA GAATTACGG 1779

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2) INFORMATION FOR SEQ ID NO: 712

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 965 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*

(B) STRAIN: V583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 712

5	GTGCAAATTG	GAAAAATTGT	CAAAGTTTCA	GGTCCTTTGA	TTTtagCTGA	50
	AAACATGTCA	GATGCTAGTA	TCCAAGACAT	TTGTCATGTA	GGAGATTTAG	100
	GCGTTATCGG	AGAGATTATT	GAAATGCGAG	GCGACGTCGC	TTCGATTCAA	150
	GTATATGAAG	AAACAACAGG	CATTGGACCA	GGAGAACCAG	TTATTTC AAC	200
	AGGAGAACCA	TTATCTGTTG	AATTAGCCCC	AGGTTTAATT	GGCGAAATGT	250
	TTGATGGTAT	TCAACGACCA	TTGGATAACAT	TTCAAGAAGT	AACCCACAGT	300
10	AACTTTT TAG	GCCGTGGCGT	TAAAATTGAT	GCGTTAGATC	GTGAGAAAAA	350
	ATGGACGTTT	GAACCAACTG	TGGCAGTTGG	TGAAGAAGTG	TCGGCAGGTG	400
	ACATCGTCGG	TGTGGTTCAA	GAAACACCGA	TTATTCAACA	TAAAATTATG	450
	GTGCCCTTTCG	GCGTTTCAGG	AACGATTGCC	GAAATTAAAG	CAGGTGACTT	500
15	TGCCATTGAT	GAAACAGTTT	ACTCAGTGGA	AACGGCTAAA	GGAACGGAAA	550
	GTTTTAGCAT	GATGCAAAAA	TGGCCCCGTT	GCGGGGACG	TCCCATTTTA	600
	GAAAACTAA	GTCCCAAAGT	ACCGATGGTG	ACCGGACAAC	GCGTAATTGA	650
	TACCTTTTTTC	CCAATTACGA	AAGGCGGAGC	GCGAGCAGTT	CCAGGACCAT	700
	TTGGCGCTGG	AAAAACAGTC	GTTCAGCACC	AAATTGCTAA	GTGGGCCGAT	750
20	GTGCACTTAG	TCGTTTACGT	TGGTTGTGGG	GAACGCGGGA	ATGAAATGAC	800
	AGATGTTTTTA	AATGAATTTT	CAGAATTAAT	TGACCCAACA	ACTGGTGAGT	850
	CTTTGATGAA	TCGGACGATT	TTAATTGCGA	ATACGTCAAA	TATGCCGGTA	900
	GCGGCACGGG	AAGCCTCGAT	TTATACAGGG	ATTACCATTG	CAGAATATTT	950
	CCGTGATATG	GGTTA				965
25						

2) INFORMATION FOR SEQ ID NO: 713

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1737 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Methanosarcina barkeri*
 (C) ACCESSION NUMBER: J04836

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 713

45	GTGGAAGTAA	AAGGTGAAAT	TTATCGTGTG	TCTGGGCCTG	TCGTCACCGC	50
	CATCGGCTTG	CAGGCAAAAA	TGTATGACCT	GGTCAAAGTC	GGTAATGAAG	100
	GTTTAATGGG	TGAAGTCATT	CAGATATTAG	GGCCCAAGAC	CATCATCCAG	150
	GTATATGAAG	AGACCGCAGG	TATCAAGCCA	GGGGAACCCCT	GTGTATCTAC	200
	AGGGTCGTCT	CTGTCCGTAG	AACTTGGTCC	GGGTCTTCTT	TCCAGTATTT	250
	ATGACGGGGT	TCAAAGGCCT	CTGCACGTCC	TGCTTGAAAA	AATGGGTAGC	300
50	TTCATCCAGA	GAGGTGTCAG	CGCAGATGGG	CTTGATCATA	AGAAACTCTG	350
	GGATTTCAAA	CCCATTGTCA	AGAAGGGCGA	TTCCGTAAAA	GGTGGAGACG	400
	TAATTGGTGT	TGTACAGGAA	ACCGTGAATA	TTGAACATAA	GATCATGGTG	450
	CCTCCTGATA	TCTCAGGTAC	AATTTCCGAC	ATAAAGAGCG	GAAACTTTAC	500
	GGTAGTAGAC	ACAATCTGTA	CTCTGACTGA	TGGGACCGAA	TTGCAGATGA	550
55	TGCAGAGGTG	GCCTGTTTCA	AGACCCAGAC	CTGTGAAGGC	AAAACCTTACT	600
	CCAACCAGGC	CTCTGGTTAC	AGGAATGAGA	ATCCTTGATG	GGCTTTTCCC	650
	TGTGGCAAAA	GGCGGAACAG	CTGCAATCCC	CGGACCTTTC	GGATCGGGAA	700
	AGACCGTAAC	TCAGCAGTCG	CTTGCAAAAT	GGAGTGATAC	CGAAATTGTG	750
	GTCTACATCG	GTTGTGGTGA	GCGTGGAAC	GAAATGGCAG	ATGTTCTGAG	800
60	CGAATTCCCT	GAACCTCGAAG	ATCCGCGAGC	CGGGCGCCCA	CTTATGGAGC	850

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GTACTGTTCT TATCGCTAAC ACTTCAAACA TGCCTGTGGC CGCAAGAGAA 900
GCATCTGTGT ATACCGGAAT CACCATTGCA GAATACTACC GTGACATGGG 950
ATTAGATGTA TCCCTTATGG CAGACTCCAC CTCAAGGTGG GCAGAAGCCA 1000
TGAGAGAAAT CTCTTCCCGT CTGGAAGAAA TGCCTGGTGA AGAAGGTTAC 1050
5 CCAGCATACC TGTCTGCAAG ACTGGCCGAA TTCTACGAGC GTGCCGGGGT 1100
TGCGGAGAGT CTTTGC GGCG AAACAGGTTT CATTACTGTT ATTGGAGCAG 1150
TATCTCCACC TGGCGGTGAC TTCTCAGAGC CTGTTACACA GAATACCCTG 1200
CGTATCGTAA AAGTGTTCTG GGCTCTCGAT GCCAACTAT CTCAGAGGCG 1250
TCACTTCCCG GCCATCAACT GGCTGAACAG TTACAGTCTG TATAAGGACA 1300
10 GTCTTAATGA CTGGTTTGCA GATAATGTGG CTCCTGATTA TGTGCCTTTG 1350
AGGGAAAGAG CAATGGAAAT GCTCCAGACA GAATCTGAAC TGCAGGAAAT 1400
CGTGCAGCTT GTAGGTTCCG ATGCTCTGCC AGACGACCAG CAGCTTCTGC 1450
TTGAAATCAC CCGTATGCTT AGGGAAATTT TCCTGCAGCA GAATGCATTG 1500
CACCCAGTAG ATGCATACAG CCCGTTTCGAT CAGCAGTACA AGATCCTTAA 1550
15 GGCAATCATG AAATGGGGAG ACGCTGCGAT GGATGCCTTG AAATCAGGTG 1600
TTCCCGTAAC TGAAATTATC AAGCTTGAAT CCAAAAATGT GCTTGCTAAG 1650
GTCAAGTACG AAGAGAAGTT TGATGAGTCT ATGAATGCTG TCCTGGCACA 1700
GATGGATAAA GAGTTTGCAT CCCTGAGAGG TAGGTAA 1737

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2) INFORMATION FOR SEQ ID NO: 714

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25 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 1785 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Methanosarcina jannaschii
        (C) ACCESSION NUMBER: U67477

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 714

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ATGAAAAGAG AGGTTGAGAA TATGCCAGTT GTTGGTAAGA TTATTAAAT 50
CGCAGGGCCT GTTGTAGTTG CAGAGGGAAT GAAAGGAGCT CAGATGTATG 100
40 AGGTCGTTAA AGTAGGAGAA GAGAAATTGA CTGGAGAAAT CATTCAAGTTG 150
CAGCATGATA AAGCAGTTAT TCAGGTTTAT GAAGAAACAT CTGGAATTAA 200
ACCAGGAGAG CCAGTTGTTG GTACTGGAGC TCCATTGTCT GTTGAATTAG 250
GGCCAGGGAT GTTAAGAGCT ATGTATGATG GTATTCAGAG GCCTTTAACA 300
GCAATTGAAG AGAAAACAGG TTCAATCTTT ATCCCAAGAG GAGTTGATGT 350
45 CCCTGCATTA CCAAGAGATA TAAAATGGGA ATTTAAACCA GTGGTAAATG 400
AAGGAGATTA TGTGAAGAA GGAGACATAA TTGGAAGTGT TGATGAAACT 450
CCTTCAATAG TTCATAAAAT CTTAGTTCCA ATTGGTGTTA AAGGAAAAAT 500
TGTTGAAATA AAAGAGGGTA AATTTACAGT TGAAGAGACA GTTGCAGTTG 550
TAGAAACAGA AAATGGAGAA AGGAAAGAAA TTACAATGAT GCAAAAATGG 600
50 CCAAGTAAGAA AACCAAGACC ATATAAGAGG AAACCTACCTC CAGAAAATTC 650
ATTAATTACA GGGCAAAGAG TTGAAGACAC TTTCTTTACA TTAGCAAAAG 700
GAGGAACAGC AGCAATTCCA GGTCCATTCTG GTTCAGGAAA AACGGTTACT 750
CAGCATCAGT TGGCAAAGTG GTCTGACGCT GATGTCGTTG TTTATATCGG 800
ATGTGGAGAA AGAGGAAACG AGATGACAGA GGTATTGAA GAGTTCCAC 850
55 ACTTAGAAGA TATTAGAACT GGAAACAAAT TAATGGATAG AACTGTATTA 900
ATAGCCAACA CATCAAACAT GCCTGTCGCT GCAAGGGAAG CATCTGTCTA 950
TACAGGAATT ACAATTGCAG AGTACTTCAG AGATATGGGT TATGGAGTTT 1000
TATTAACAGC AGATTCAACA TCAAGATGGG CAGAGGCAAT GAGAGAAATT 1050
TCAGGTAGAT TGGAAGAAAT GCCAGGGGAA GAAGGGTATC CAGCATACTT 1100
60 AGCTTCAAGA TTGGCTCAGT TCTATGAAAG AGCTGGAAGA GTTATAACCT 1150

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	TAGGGAAAGA	TAACAGACAA	GGATTCGTTT	GTATCGTTGG	AGCTGTTTCA	1200
	CCACCAGGAG	GGGACTTCTC	AGAACCAGTT	ACATCAAACA	CACTAAGGAT	1250
	AGTTAAGGTA	TTCTGGGCGT	TAGATGCAAA	CTTGGCAAGA	AGAAGACACT	1300
	TCCCAGCTAT	CAACTGGTTG	CAGAGTTATT	CATTATACAT	TGATGATGTT	1350
5	ACAGAGTGGT	GGAACACAAA	TACTGGTCCA	GATTGGAGAC	AATTAAGAGA	1400
	TGAAGCAATG	AGCTTATTAC	AAAAAGAGGC	AGAGTTGCAA	GAGATTGTTC	1450
	AGTTAGTTGG	GCCTGATGCA	TTGCCAGATA	GGGAGAGAGT	TATTTTAGAA	1500
	GTTGCAAGAA	TGTTGAGGGA	GGATTTCTTA	CAGCAAGATG	CGTTTGATGA	1550
	GGTAGATACC	TACTGTCCTC	CAATGAAACA	GTACTTAATG	TTAAAGATAA	1600
10	TTATGACATT	CTACCAAGAA	GCATTGAAGG	CAGTTGAAAG	AGGAGTTGAA	1650
	CCAGCTAAGA	TTTTAGGAGT	TTCAGTTAAG	CAAGATATTG	CAAGAATGAA	1700
	ATACATCCCA	CACGATGAGT	TTATAAATGT	TAAATCAAAA	GAAATAATGG	1750
	AGAAAATTAA	GAATGAATTA	GGTTCATTAA	ACTAA		1785

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2) INFORMATION FOR SEQ ID NO: 715

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1354 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Porphyromonas gingivalis*
- (B) STRAIN: W83

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 715

	TGAGCGAGGT	GATCAAGGTG	ATCGGCAAAA	ATGCTTATGT	GCAGGTTTTTC	50
	GAAAGTACTC	GCGGTATGCA	CGTAGGAGAT	GAGGCAGAGT	TTACCGGCAG	100
35	TATGCTTGAG	GTAACGCTCG	GCCCCGGTAT	GCTTTCGAAG	AACTACGACG	150
	GTCTGCAACA	CGACTTGGAC	AAGATGGACG	GGATCTTCCT	CAAACGAGGC	200
	GATTATACTC	CCGCTCTCGA	TGACGACAAG	CTGTGGGACT	TCAAGCCTTT	250
	GGCCAATGTG	AACGACAATG	TGATCGCAGG	CTCATGGCTC	GGAGAGGTGA	300
	CGGAAAATTT	CCAACCGCAC	AAGATCATGG	TACCTTTCGT	TTTCGAAGGC	350
40	AATTACAAGG	TGAAGAGTCT	GGCCAAAGCC	GGTTCGTACA	AAGTGAACGA	400
	TGTGATCGCT	GTGGTAACGG	ATCAGGACGG	GAAAGACCAC	AATGTAACCA	450
	TGGTGACAGAA	ATGGCCGGTG	AAACGTGCTA	TCACTTGCTA	TCGCGAGAAG	500
	CCGCGTCCTT	TCAAACGTCT	CGAAACGGGT	ATCCGTATCA	TCGACACTTT	550
	CAACCCCATC	GTAAGAGGGT	GTACGGGATT	TATCCCCGGT	CCTTTCGGTA	600
45	CGGGAAAGAC	GGTGCTCCAG	CATGCTATCT	CGAAGCAGGC	GGAAGCCGAT	650
	ATCGTGATCA	TTGCAGCCTG	TGGCGAGCGT	GCAAACGAGG	TTGTGGAGAT	700
	CTTTGCGGAA	TTCCCCCACC	TGAATGACCC	CCACACGGGA	CGTAAATTGA	750
	TGGAACGTAC	CATTATTATT	GCTAATACGT	CGAATATGCC	TGTGGCTTCG	800
	CGTGAGGCAT	CCGTATATAC	GGCCATGACG	ATAGCCGAGT	ACTATCGCTC	850
50	CATGGGCCTT	CGCGTGCTGA	TGATGGCAGA	CTCCACTTCG	CGTTGGGCAC	900
	AGGCTCTGCG	TGAGATGTCT	AACCGTCTGG	AAGAGCTTCC	CGGACCGGAT	950
	GCTTTCCCGA	TGGACTTGTC	AGCTATCGTA	GCCAACTTCT	ACGCTCGTGC	1000
	AGGATACGTT	TACCTGAACA	ACGGTTCGGC	CGGTTTCGGTA	ACGTTTCATCG	1050
	GTACGGTATC	TCCCGCCGGT	GGTAACCTCA	AAGAGCCTGT	GACGGAAAAC	1100
55	ACCAAGAAAG	TGGCTCGCTG	CTTCTATGCT	TTGGAGCAGA	ATCGTGCCGA	1150
	CCGCAAACGT	TATCCGGCTG	TAAACCCCAT	CGATAGTTAC	TCGAAGTACA	1200
	TCGAATATCC	CGAATTCGAG	AGCTATATAT	CGAACCACAT	CAGTTTACTC	1250
	ATTATATTCA	ACAGAAGTTG	GCAGATATAT	GGATCAAATC	TTACAGCAGA	1300
	CTGGACTACT	AAGGTGAATG	AGCTGAAGAT	GCGCTTGCAT	CAGGGTAAAG	1350
60	AAAT					1354

2) INFORMATION FOR SEQ ID NO: 716

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1788 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
 (B) STRAIN: Type 4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 716

20	TTTGACTCAA	GGGAAGATTA	TAAAAGTATC	GGGACCTCTA	GTTATTGCAT	50
	CAGGTATGCA	GGAGGCTAAT	ATTCAAGATA	TTTGCCGTGT	AGGTAAGCTA	100
	GGGTTAATCG	GTGAAATTAT	TGAAATGAGA	AGAGATCAGG	CATCTATCCA	150
	AGTCTATGAA	GAAACATCTG	GTCTTGGTCC	GGGAGAACCT	GTTGTTACAA	200
	CTGGAGAACC	TCTCTCGGTT	GAATTAGGGC	CAGGATTGAT	TTCTCAAATG	250
25	TTTGATGGCA	TACAACGCCC	ATTAGATCGA	TTTAAATTGG	CTACTCATAA	300
	TGATTTTCTA	GTTTCGTGGG	TAGAAAGTTC	AAGTTTGGAT	AGAGATATTA	350
	AGTGGCATT	TGATTCCACT	ATAGCAATTG	GTCAAAAAGT	GAGTACGGGT	400
	GATATTCTTG	GAAGTGTCAA	GGAAACCGAG	GTAAGTTAATC	ATAAAATTAT	450
	GGTTCCTTAT	GGAGTATCTG	GAGAAGTCGT	TTCTATTGCA	TCTGGCGATT	500
30	TTACAATTGA	TGAAGTTGTA	TATGAAATAA	AAAAATTGGA	CGGTAGTTTC	550
	TATAAAGGAA	CGCTTATGCA	AAAATGGCCT	GTCCGCAAGG	CGCGTCCTGT	600
	TTCTAAACGT	TTAATTCCAG	AAGAACCATT	AATCACAGGT	CAACGAGTTA	650
	TTGATGCATT	TTTCCAGTA	ACCAAGGGG	GAGCTGCAGC	AGTTCCTGGA	700
	CCGTTTGGAG	CAGGAAAGAC	AGTTGTACAA	CACCAAGTAG	CTAAATTTGC	750
35	CAATGTTGAT	ATTGTTATTT	ATGTCGGTTG	TGGAGAACGT	GGAAATGAAA	800
	TGACGGATGT	ACTGAATGAG	TTTCCTGAGT	TGATTGACCC	TAATACCGGA	850
	CAATCAATTA	TGCAACGGAC	AGTTCTGATT	GCTAATACTT	CAAATATGCC	900
	TGTTGCTGCT	CGTGAGGCTT	CAATTTATAC	AGGAATTACC	ATGGCTGAGT	950
	ATTTTCGTGA	TATGGGCTAC	TCTGTCGCCA	TTATGGCTGA	TTCAACTTCA	1000
40	CGTTGGGCAG	AAGCGCTACG	TGAAATGTCA	GGACGTCTAG	AAGAAATGCC	1050
	TGGTGATGAG	GGTTATCCTG	CTTATCTGGG	AAGTCGTATC	GCTGAATATT	1100
	ATGAAAGAGC	AGGACGTTCT	CAGGTTCTAG	GGCTTCCAGA	ACGTGAAGGA	1150
	ACGATTACTG	CTATTGGAGC	TGTATCGCCA	CCTGGTGGAG	ATATTTTCTG	1200
	ACCAGTTACT	CAAAACACTT	TACGGATTGT	GAAAGTTTTT	TGGGGGCTTG	1250
45	ATGCTCCGTT	GGCACAGCGA	CGTCATTTTC	CTGCAATTAA	CTGGCTTACA	1300
	TCTTATTCAC	TATATAAAGA	CAGTGTGGGC	ACTTATATAG	ATGGTAAAGA	1350
	GAAGACAGAT	TGGAATAGTA	AAATAACTCG	TGCGATGAAC	TACTTACAAC	1400
	GGGAATCTAG	TTTAGAGGAA	ATTGTTTCGT	TTGTTGGAAT	TGATTCTCTG	1450
	TCTGATAATG	AACGACTAAC	GATGGAAATT	GCTAAACAAA	TTCGAGAAGA	1500
50	TTATTTTCAA	CAGAACGCTT	TTGATTCCGT	AGATACATTC	ACTTCGTTTG	1550
	CAAAACAAGA	AGCAATGCTA	AGTAATATTC	TCACTTTTGC	TGATCAGGCA	1600
	AATCATGCTT	TAGAGTTGGG	TTCTTACTTT	ACAGAGATTA	TGGAAGGTAC	1650
	CGTGGCAGTT	CGAGACCGTA	TGGCGAGAAG	TAAATATGTT	TCAGAAGATA	1700
	GATTAGATGA	AATCAAAATT	ATATCAAATG	AGATTACACA	TCAAATTCAT	1750
55	TTGATATTAG	AAACAGGAGG	TCTATAAATG	AGTGTTAT		1788

2) INFORMATION FOR SEQ ID NO: 717

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Burkholderia mallei*
 (B) STRAIN: GB8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 717

```

15  CGATCCTGGT GTGCTCGGCC GCTGACGGCC CGATGCCGCA AACGCGTGAG      50
    CACATCCTGC TGGCGCGTCA GGTCTGGTGTG CCGTACATCA TCGTGTTCCCT    100
    GAACAAGTGC GACATGGTGG ACGACGCGGA GCTGCTCGAG CTGGTCGAAA      150
    TGGAAAGTGC CGAACTGCTG TCGAAGTACG ACTTCCCGGG CGACGACACG      200
    CCGATCATCA AGGGTTCGGC GAAGCTGGCG CTGGAAGGCG ACAAGGGCGA      250
    20  GCTGGGCGAA GTGGCGATCA TGAACCTGGC CGACGCGCTG GACACGTACA      300
    TCCCGACGCC GGAGCGTGCG GTCGACGGCG CGTTCTTGAT GCCGGTGGAA      350
    GACGTGTTCT CGATCTCGGG CCGTGGTACG GTGGTGACGG GTCGTGTCTGA      400
    GCGCGGCGTG ATCAAGGTTG GCGAGGAAAT CGAAATCGTC GGTATCAAGG      450
    CGACGGCGAA GACGACCTGC ACGGGCGTGG AAATGTTCCG CAAGCTGCTG      500
    25  GACCAGGGTC AGGCGGGCGA CAACGTCGGT ATCCTGCTGC GCGGCACAAA      550
    GCGTGAAGAC GTGGAGCGCG GCCAGGTTCT GGCGAAGCCG GGTTCGATCA      600
    CGCCGCACAC GCACCTTCACG GCAGAAAGTGT ACGTGCTGAG CAAGGACGAA      650
    GCGGCGCCGC ACACGCCGTT CTTCAACAAC TACCGTCCGC AGTTCTACTT      700
    CCGTACGACG GACGTGACGG GCTCGATCGA GCTGCCGAAG GACAAGGAAA      750
    30  TGGTGATGCC GGGCGACAAC GTGTCGATCA CGGTGAAGCT GATCGCGCCG      800
    ATCGCGATGG AAGAAGGTCT GCG                                     823
  
```

35 2) INFORMATION FOR SEQ ID NO: 718

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Burkholderia pseudomallei*
 (B) STRAIN: 1026B

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 718

```

50  GCGATCCTGG TGTGCTCGGC CGCTGACGGC CCGATGCCGC AAACGCGTGA      50
    GCACATCCTG CTGGCGCGTC AGGTCTGGTGT GCCGTACATC ATCGTGTTCC      100
    TGAACAAGTG CGACATGGTG GACGACGCGG AGCTGCTCGA GCTGGTCGAA      150
    ATGGAAGTGC GCGAACTGCT GTCGAAGTAC GACTTCCCGG GCGACGACAC      200
    55  GCCGATCATC AAGGGTTCGG CGAAGCTGGC GCTGGAAGGC GACAAGGGCG      250
    AGCTGGGCGA AGTGCGGATC ATGAACCTGG CCGACGCGCT GGACACGTAC      300
    ATCCCGACGC CGGAGCGTGC GGTCTGATGG GCGTTCCTGA TGCCGGTGGA      350
    AGACGTGTTT TCGATCTCGG GCCGTGGTAC GGTGGTGACG GGTCTGTCTG      400
    AGCGCGGCGT GATCAAGGTT GGCGAGGAAA TCGAAATCGT CCGTATCAAG      450
    60  GCGACGGCGA AGACGACCTG CACGGGCGTG GAAATGTTCC GCAAGCTGCT      500
  
```

	GGATCAGGGT	CAGGCGGGCG	ACAACGTCGG	TATCCTGCTG	CGCGGCACGA	550
	AGCGTGAAGA	CGTGGAGCGC	GGCCAGGTTT	TGGCGAAGCC	GGGTTCGATC	600
	ACGCCGCACA	CGCACTTCAC	GGCTGAAGTG	TACGTGCTGA	GCAAGGACGA	650
	AGGCGGCCGC	CACACGCCGT	TCTTCAACAA	CTACCGTCCG	CAGTTCTACT	700
5	TCCGTACGAC	GGACGTGACG	GGCTCGATCG	AGCTGCCGAA	GGACAAGGAA	750
	ATGGTGTATG	CGGGCGACAA	CGTGTGATC	ACGGTGAAGC	TGATCGCGCC	800
	GATCGCGATG	GAAGAAGGTC	TGCG			824

2) INFORMATION FOR SEQ ID NO: 719

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 800 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium beijerincki* (deposited as *Clostridium butyricum*)
 (B) STRAIN: ATCC 8260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 719

	TGTATCAGCA	GCAGATGGTC	CAATGCCACA	AACAAGAGAA	CATATACTAC	50
	TAGGATCAAG	AGTTGGTATC	CAATATATCG	TAGTATTCTT	AAATAAAGCA	100
30	GATATGGTAG	ACGATCCAGA	ATTATTAGAA	TTAGTAGAAA	TGGAAGTAAG	150
	AGAATTATTA	AGCGAATATG	ACTTCCCAGG	AGACGATATT	CCAGTAATAA	200
	CAGGATCAGC	ATTAAAAGCA	TTAGAAAATC	CAACAGATGA	AGAAGCAATT	250
	AAGCCAATCA	TGGATTTAAT	GGAAGCAGTA	GATAGCTATA	TCCCAACTCC	300
	AGAAAGAGCA	ACAGATAAGC	CATTCTTAAT	GCCAATCGAA	GATGTATTCA	350
35	CAATTACAGG	AAGAGGAACA	GTTGCAACAG	GAAGAGTTGA	AGCTGGAGTA	400
	CTTCATGTAG	GAGATGAAGT	AGAAATCGTT	GGATTAAACAG	AAGAAAAGAA	450
	GAAAGTTGTA	GTAAGTGGAA	TCGAAATGTT	CAGAAAGTTA	TTGGATGAAG	500
	CACAAGCTGG	AGATAACATC	GGAGCATTAT	TAAGAGGAGT	TCAAAGAACT	550
	GATATTGAAA	GAGGTCAAGT	TTTATCAAAA	CCAAATTCAG	TACACCCTCA	600
40	CACTAAATTT	GTAGGTCAAG	TATACGTACT	TAAAAAAGAA	GAAGGTGGAA	650
	GACATACTCC	ATTCTTTGAT	GGATACAGAC	CACAATTCTA	TTTCAGAACA	700
	ACAGACGTTA	CAGGRTCAAT	CAAGTTACCA	GATGGAATGG	AAATGGTAAT	750
	GCCTGGAGAT	CACATTGATA	TGAATGTTGA	ATTAATCACT	CCAATCGCAA	800

2) INFORMATION FOR SEQ ID NO: 720

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium innocuum*
 (B) STRAIN: ATCC 14501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 720

```

5  GGTGCTATCC TGGTTGTTGC TGCATCTGAT GGTCCCTATGC CTCAGACTCG      50
   TGAGCACATC CTGCTTGCTC GTCAGGTAGG TGTTCCTTAC ATCGTTGTAT      100
   TCCTGAACAA ATGCGACATG GTTGATGACG AAGAACTGAT CGACCTTGTT      150
   GAAATGGAAG TACGTGAGCT GTTAAGCGAG TACGGATTCTG ACGGAGATAA      200
   CGCTCCGTTT ATCCGTGGTT CTGCACTGAA GGCTCTGGAA GGTGACGACA      250
   AATACGTTGG CGCTATCAAA GAACTGATGG ATGCAGTTGA TGAATTCATC      300
   CCAGATCCAA CTCGTGAAAC TGACAAACCA TTCCTGATGT CTGTAGAAGA      350
10  CGTTATGACA ATCACAGGAC GTGGTACAGT TGCTACAGGA CGTGTGAGC      400
   GTGGGGTAGT AAAACTGGGA GAAGAAGTTG AAATCGTTGG TATCAAGGAT      450
   ACTCAGAAAA CTGTTGTTAC CGGACTGGAA ATGTTCCGTA AGCAGCTGGA      500
   CTTTCGCAGAA TCCGGAGACA ACATCGGTGC TCTGCTGCGT GGTATCAACC      550
   GTGACCCAGT TCAGCGTGGA CAGGTTCTTG CTAAACCAGG ATCCGTACAT      600
15  CCACACACAA AGTTCAAGGC TCAGGTTTAT GTATTAACAA AAGAAGAAGG      650
   TGGACGTCAC ACTCCATTCG TTTCTAACTA CCGTCCTCAG TTCTACTTCC      700
   GTACAACCTG CGTAACTGGT GTTATTACAT TACCGGAAGG AACTGAAATG      750
   GTTATGCCTG GTGACAACGT TGAAATGAAC GTTGAGCTGA TTGCTCCAA      799

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20

2) INFORMATION FOR SEQ ID NO: 721

(i) SEQUENCE CHARACTERISTICS:

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25  (A) LENGTH: 789 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

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30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

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    (A) ORGANISM: Clostridium novyi
    (B) STRAIN: ATCC 19402

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35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 721

```

40  TTGTATCAGC AGCAGATGGT CCAATGCCAC AAACAAGAGA ACACATCCTA      50
   TTAGCATCAA GAGTAGGAGT TAACCACATA GTAGTATTCT TAAACAAAGC      100
   AGACCAAGTA GATGATCCAG AATTACTAGA ATTAGTAGAA ATGGAAGTAA      150
   GAGAATTATT AAGCGAATAC GGATTTGACG GAGACGAATG TCCAGTAGTA      200
   GTAGGATCAG CATTAAAAGC AATCGAAGAA GGGGATGACC AATGCATCCT      250
   AGACTTAATG AAAGCTGTAG ATGAATATAT CCCAACTCCA GAAAGAGCAA      300
   CAGATCAACC ATTCTTAATG CCTGTAGAAG ATGTATTTAC AATTACAGGA      350
45  AGAGGAACAG TTGCAACAGG AAGAGTTGAA AGAGGAGTAC TACACGTAGG      400
   AGATGAAGTA CAAATCGTAG GAATGAAAGA AGAAATCGGA AAGACAACAA      450
   TCACAGGAGT AGAAATGTTT AGAAAGATGT TAGATGAAGC AATGGCTGGA      500
   GATAACATCG GAGCATTATT AAGAGGAGTA CAAAGAGACG AAATCGAAAG      550
   AGGTCAAGTA CTAGCAAAAC CAGGTTTCAGT AACACCTCAC AAAAAATTCG      600
50  TAGGTCAAGT TTACGTATTA AAGAAAGAAG AAGGTGGAAG ACACACTCCA      650
   TTCTTTAACG GATACAGACC ACAATTCTAC TTCAGAACAA CAGACGTAAC      700
   AGGATCAATC GCTTTACCAG AAGGAGTAGA AATGGTAATG CCAGGAGACC      750
   ATATAGACAT GAACGTAGAA TTAATCACAC CAGTAGCAA      789

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55

2) INFORMATION FOR SEQ ID NO: 722

(i) SEQUENCE CHARACTERISTICS:

```

60  (A) LENGTH: 798 bases

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(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Clostridium septicum*
 (B) STRAIN: ATCC 12464

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 722

	G TTCAGCAGC	A GACGGTCCA	A TGCCACAAA	C AAGAGAACA	T TACTACTA	50
	G CATCAAGAG	T TGGTGTTGA	C TATATCGTA	G TATTCTTAA	A CAAGGCAGA	100
15	T ATGGTAGAT	G ACGAAGAAT	T ATTAGAATT	A GTAGAAATG	G AAGTTAGAG	150
	A ATTATTATC	A GAATACAAC	T TCCAGGAG	A TGATATTCC	A GTAATCAAG	200
	G GATCAGCTT	T AGTAGCATT	A GAAAACCCA	A CAGATGAAA	A ATCAATCGC	250
	T CCAATCTTA	G AATTAATGG	A AGCAGTAGA	T AGCTACATT	C CAACACCAG	300
	A AAGAGCAAC	A GATAAGCCA	T TCTTAATGC	C AGTAGAAGA	T GTATTACAC	350
20	A TAACTGGTA	G AGGAACAGT	T GCAACAGGA	A GAGTTGAAA	G AGGAGTTCT	400
	T CATGTAGGA	G ACGAAGTAG	A AATCGTTGG	A TTATCAGAA	G AAAGCAGAA	450
	A AGTAGTAGT	A ACAGGAATA	G AAATGTTCA	G AAAGTTACT	A GACGAAGCA	500
	C AAGCTGGAG	A TAATGTTGG	A GTACTTTTA	A GAGGTGTTT	A AAGAACAGA	550
	T ATCGAAAGA	G GTCAAGTAT	T AGCAAAGAC	T GGATCAGTT	A AGCCACACA	600
25	G CAAGTTCGT	A AGTCAAGTA	T ACGTACTTA	A GAAAGAAGA	A GGTGGAAGA	650
	C TACTCCAT	T CTTCGATGG	A TACAGACCA	C AATTCTACT	T CAGAACAAC	700
	A GACGTTACT	G GATCAATCA	A ATTACCAGA	C GGAATGGAA	A TGGTATATG	750
	C AGGAGACCA	C ATTGATATG	A ACGTTGAAT	T AATCACTCA	A GTAGCAA	798

30

2) INFORMATION FOR SEQ ID NO: 723

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 799 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Clostridium tertium*
 (B) STRAIN: ATCC 14573

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 723

	G TTCAGCAGC	A GATGGTCCA	A TGCCTCAAA	C AAGAGAACA	C TACTACTA	50
	G CTTCAAGAG	T TGGTGTTGA	C TACATAGTT	G TTTTCTTAA	A CAAGGCAGA	100
50	T ATGGTAGAT	G ACGAAGAAT	T ATTAGAATT	A GTTGAAATG	G AAGTAAGAG	150
	A ATTATTATC	A GAATACAAC	T TCCAGGAG	A TGATATTCC	A GTAATAAAG	200
	G GTTCAGCTT	T ACAAGCATT	A GAAAACCCA	A CAGATGAAA	A AGCAATCGC	250
	T CCAATCCTT	G AGTTAATGG	A AGCTGTAGA	T AGCTACATT	C CAACTCCAG	300
	A AAGAGCAAC	A GATAAGCCA	T TCTTAATGC	C AGTAGAAGA	T GTATTACAC	350
55	A TCACTGGTA	G AGGAACAGT	T GCTACAGGA	A GAGTTGAAA	G AGGAGTTCT	400
	T CACGTAGGA	G ACGAAGTAG	A AATCGTTGG	A TTATCAGAA	G ACAGCAGAA	450
	A AGTAGTAGT	A ACAGGAATA	G AAATGTTCA	G AAAGTTACT	A GACGAAGCG	500
	C AAGCTGGAG	A CAACGTAGG	A GTTCTTTTA	A GAGGAGTTC	A AAGAACTGA	550
	C ATCGAAAGA	G GTCAAGTTT	T AGCAAAAGT	T GGATCAGTT	A AGCCACACA	600
60	A GAAATTTGT	A AGTCAAGTA	T ACGTACTTA	A AAAAGAAGA	A AGGTGGAAGA	650

CATACTCCAT	TCTTCGATGG	ATACAGACCA	CAATTCTACT	TCAGAACAAAC	700
AGAYGTTACT	GGTTCAATCA	AGTTACCAGA	TGGAATGGAA	ATGGTTATGC	750
CAGGAGACCA	CATTGATATG	AACGTTGAAT	TAATCACTCA	AGTAGCTAT	799

5

2) INFORMATION FOR SEQ ID NO: 724

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 801 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium tetani*
 (B) STRAIN: ATCC 19406

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 724

25	TAGTAAGTGC	AGCAGATGGT	CCAATGCCAC	AAACAAGAGA	ACACATACTA	50
	TTAGCATCCA	GAGTTGGAGT	TGAGCACATA	GTAGTATTCT	TAAATAAAGC	100
	AGACCAAGTA	GATGACGCAG	AGTTAATCGA	ATTAGTAGAA	ATGGAAGTAA	150
	GGGAATTAAT	GAACGAATAC	GGATTCACAG	GAGATGACGC	ACCAGTAGTA	200
	GTAGGATCCG	CATTAAAAGC	ATTAGAAAAT	CCAGAAGATG	ATGCAGCAAC	250
	ACAATGCATA	ATGGACTTAA	TGGCAGCAGT	AGATGAATAT	ATACCAACAC	300
	CAGAAAGAGC	AACAGATAAG	CCATTCTTAA	TGCCAGTAGA	AGATATCTTC	350
30	ACAATCACAG	GAAGAGGAAC	AGTTGCAACA	GGAAGAGTAG	AAAGAGGAAT	400
	TCTAAAAGTA	GGAGACGAAA	TAGAAATCGT	AGGATTAAGT	GATGAAAGCA	450
	AGAAATCAGT	AATCACAGGA	ATAGAAATGT	TCAGAAAAC	ATTAGATGAA	500
	GCACAAGCAG	GAGATAACAT	CGGAGCATT	TTAAGAGGTG	TTCAAAGAGA	550
	TGAAATCCAA	AGAGGTCAAG	TATTAGCAGC	AACAGGATCA	GTAAAACCAC	600
35	ATAAGAGTTT	TACAGGTCAA	GTATATGTAT	TAAAGAAAGA	AGAAGGAGGA	650
	AGACACACTC	CATTCTTTAA	CGGATACAGA	CCACAATTCT	ACTTTAGAAC	700
	AACAGACGTA	ACAGGTTCAA	TCGCACTACC	AGAAGGAGTA	GAAATGGTAA	750
	TGCCAGGAGA	CCACATAGAC	ATGAAGGTAG	AATTAATAAC	AAGAGTAGCA	800
40	A					801

2) INFORMATION FOR SEQ ID NO: 725

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 633 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus malodoratus*
 (B) STRAIN: ATCC 43197

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 725

60	TATGCCTCAA	ACTCGTGAAC	ACATCTTGTT	ATCTCGTAAC	GTTGGTGTTC	50
	CTTACATCGT	TGTATTCTTA	AACAAAATGG	ATATGGTTGA	TGATGAAGAA	100

```

TTACTAGAAT TAGTTGAAAT GGAAGTTCGT GACTTATTGT CAGAATACGA 150
CTTCCCAGGC GACGACACTC CAGTTATCGC TGGTTCAGCT TTGAAAGCTT 200
TAGAAGGCGA TGCTTCATAC GAAGAAAAAA TCTTAGAATT AATGGCTGCT 250
GTTGATGAAT ATATCCCAAC ACCAGTTCGT GATACTGACA AACCATTTCAT 300
5 GATGCCAGTC GAAGATGTAT TCTCAATCAC TGGTCGTGGA ACTGTTGCAA 350
CTGGTCGTGT TGAACGTGGA CAAGTTCGCG TTGGTGACGA AGTTGAAATC 400
GTTGGTATTG CTGAAGCAAC TGCTAAAACA ACTGTTACAG GTGTTGAAAT 450
GTTCCGTAAA TTGTTAGATT ACGCTGAAGC AGGCGATAAC ATTGGTGCA 500
TGTTACGTGG TGTTCACGCT GAAGACATCC AACGTGGACA AGTATTGGCT 550
10 AAACCAGCTT CAATCACTCC ACATACAAA TTCTCTGCAG AAGTTTACGT 600
TTTAACTAAA GAAGAAGGCG GACGTCATAC TCC 633

```

15 2) INFORMATION FOR SEQ ID NO: 726

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 623 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus sulfureus*
 (B) STRAIN: ATCC 49903

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 726

```

30 CACGTGAACA CATETTGTTA TCTCGTAACG TAGGTGTTCC TTACATCGTT 50
GTATTCTTAA ACAAATGGA TATGGTTGAT GACGAAGAAT TATTAGAATT 100
AGTAGAAATG GAAGTTCGTG ACTTATTATC AGAATACGAT TTCCCAGGCG 150
ATGACACTCC AGTTGTTGCA GGTTCGTGCTT TGAAAGCTTT AGAAGGCGAC 200
35 GCTTCTTACG AAGAAAAAAT CATGGAATTA ATGGCTGCAG TTGACGAGTA 250
CATCCCAACT CCAACTCGTG ACACTGACAA ACCATTTCATG ATGCCAGTTG 300
AGGATGTATT CTCAATCACT GGACGTGGTA CTGTTGCTAC AGGTCGTGTT 350
GAACGTGGAC AAGTTCGCGT TGGTGACGTT GTAGATATCG TTGGTATCGC 400
TGACGAAACT GCTCAAACA CTGTAACAGG TGTGAAATG TTCCGTAAAT 450
40 TATTAGACTA CGCTGAAGCA GCGGATAACA TCGGTGCTTT ATTACGTGGT 500
GTTGCTCGTG AAGACATCCA ACGTGGACAA GTTTTAGCTA AACCAGCTTC 550
AATCACTCCA CATACAAAT TCTCTGCTGA AGTATACGTA TTAAGCAAAG 600
AAGAAGGTGG ACGTCATACT CCA 623

```

45

2) INFORMATION FOR SEQ ID NO: 727

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 646 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactococcus garvieae*
 (B) STRAIN: ATCC 49156

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 727

	CGGTCCTATG	CCTCAAACCTC	GTGAACACAT	CTTGTTATCA	CGTAACGTTG	50
	GCGTACCATA	CATCGTTGTT	TTCTTGAACA	AAATGGATAT	GGTTGATGAC	100
5	GAAGAATTGC	TAGAATTAGT	TGAAATGGAA	GTTTCGTGACC	TATTGTCTGA	150
	ATATGACTTC	CCAGGCGACG	ATGTTCTCTG	AATCGCTGGT	TCTGCTTTGA	200
	AAGCTCTTGA	AGGAGATCCT	TCATACGAAG	AAAAAATCAT	GGAATTGATG	250
	GCTGCAGTTG	ACGAATACGT	TCCAACCTCA	GAACGTGATA	CTGACAAACC	300
	ATTCATGATG	CCAGTCGAAG	ACGTATTCTC	AATCACTGGA	CGTGGTACTG	350
10	TTGCTACAGG	CCGTGTTGAA	CGTGGACAAG	TTCGCGTTGG	TGATGAAGTA	400
	GAAATCGTTG	GTATTGCTGA	CGAAACTGCT	AAAACAACTG	TAACAGGTGT	450
	TGAAATGTTT	CGTAAATTGT	TAGACTATGC	TGAAGCAGGG	GATAACATTG	500
	GTGCATTGCT	ACGTGGGGTT	GCTCGTGAAG	ACATCCAACG	TGGACAAGTA	550
	TTGGCTAAAG	CTGGTACAAT	CACACCTCAT	ACAAAATTCA	AAGCTGAAGT	600
15	TTATGTTTTT	ACAAAAGAAG	AAGGTGGACG	TCACACTCCA	TTCTTC	646

2) INFORMATION FOR SEQ ID NO: 728

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycoplasma pirum*
- (B) STRAIN: ATCC 25960D

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 728

	GAGCAATTTT	AGTTGTTTCT	GCAACTGATG	GTCCAATGCC	TCAAACCTCGT	50
35	GAACATATCT	TATTAGCACG	CCAAGTTGGT	GTTCTTAAAA	TGGTTGTTTT	100
	CTTAAACAAA	TGTGATGTTG	CTTCTGATCC	AGAAATGCAA	GAATTAGTTG	150
	CTGAAGAAGT	AAAAGACTTA	TTAAAATCTT	ATGGTTTTGA	TGGTGACAAAT	200
	ACTCCAATTA	TTCGTGGTTC	AGCATTAGAA	GCATTAAATG	GTAAACCTGA	250
	ATGAGAAGAA	AAAATTAAG	AATTAATGAA	GGCAGTGGAT	GACACTATTC	300
40	CTGATCCAGT	TCGTGATACT	GAAAAGCCAT	TCTTGTTACC	AATTGAAGAC	350
	GTAATGACAA	TTACAGGTCG	TGGTACTGTT	GTTACAGGTC	GTGTAGAACG	400
	TGGTACTCTA	AAATTAAATG	ATGAAGTTGA	AATTGTTGGT	TTAGGTGAAA	450
	CATTTAAATC	TGTTGTAACA	GGTATTGAAA	TGTTCCGTAA	AGAATTAGAT	500
	GAAGCTCGTG	CTGGTGACAA	TGCTGGTATT	TTACTTCGTG	GTGTTGACCG	550
45	TGGTCAAGTA	CAACGTGGTC	AAGTTCTTGC	TAAACCAGGT	TCTATTACTC	600
	CTCATACTAA	ATTTAAAGCT	GAAATTTATG	CTTTGAAAAA	AGAAGAAGGT	650
	GGTCGTCATA	CTGCTTTCCT	AAACGGTTAT	CGTCCTCAAT	TCTATTTCAG	700
	AACAACCTGAT	GTTACAGGTT	CTATTAAATT	AAAAGATGGA	ACTGAAATGG	750
	TTATGCCTGG	TGACAATACT	GAAATCACTG	TAGAATTAAT	TTCACCAATT	800
50	GCTTGTAATA	AGGAAGTAAG	TTT			823

2) INFORMATION FOR SEQ ID NO: 729

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 826 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Mycoplasma salivarium*
(B) STRAIN: ATCC 23064

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 729

```

10 GGAGCAATCT TAGTTGTTGC TGCAACTGAT GGTGCGATGC CTCAAACTCG      50
   TGAACACGTT TTA CTTGCAA AACAAGTTGG TGTTCTTAAA ATCGTTGTTT      100
   TCTTAAACAA AATCGATATG TTCAAGCCAG AAGAAAGAGC CGAAATGGTT      150
   GAAATGGTTG AAATGGACAT TCGTGACTTA TTAAACAAAT ACGACTTTGA      200
   TGGTGACAAT ACTCCTATTA TTGCTGGTTC AGCATTAAAA GCATTACAAG      250
15 GTGATCCAGA ATATGAAAAG AATATTCTAG AACTTATGGA TGCAGTAGAC      300
   ACATACATTG ATGAACCTAC TCGTGATAAA GATAAACCAT TCTTAATGGC      350
   TGTAGAAGAC GTATTTACAA TTACTGGTCG TGGAAGTGTG GCTACTGGTA      400
   GAGTAGAACG TGGTACATTA CATCTAAATG ATGAAGTTGA AATCGTTGGT      450
   CTACGTCCAA CAATTAAAAC TGTGTGTTACT GGAATTGAAA TGTTCCGTAA      500
20 AAATTTAAAA GAAGCTCAAG CTGGAGATAA TGCAGGACTT TTACTACGTG      550
   GAATTGATAG AGATCAAGTA GAACGTGGAC AAGTTTTGGC CAAACCAAAA      600
   AGTATTATTC CTCACACAGA ATTTGAAGCT GCTGTGTATG TTCTAAAAGC      650
   TGAAGAAGGT GGACGTCACA CTCCATTCTT TGAACACTAT AAACCACAAT      700
   TTTACTTTTCG TACAACCGAC GTTACTGGTG GAATTAAATT CAAACCTGGA      750
25 CGTGAAATGG TTATGCCTGG CGAAAATGTT GAATTTACAG TTACTTTAAT      800
   TGCTCCTATT GCAGTTGAAG AAGGAA                                     826

```

30 2) INFORMATION FOR SEQ ID NO: 730

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 810 bases
(B) TYPE: Nucleic acid
35 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria polysaccharea*
(B) STRAIN: ATCC 43768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 730

```

45 TGGTATGTTT CGCAGCYGAY GGYCCTATGC CTCAAACTCG CGAACACATC      50
   CTGYTGGCTC GCCAAGTAGG YGTACCTTAC ATCATCGTRT TCATGAACAA      100
   ATGCGACATG GTTGACGATG CCGAGCTGTT GGAAGTGGTT GAAATGGAAA      150
   TCCGYGACCT GYTGTCMAGC TACGACTTCC CMGGCGACGA CTGCCCAATC      200
50 GTACAAGGTT CTGCACTGAA AGCTTTGGAA GGYGAYGCTG GTTACGAAGA      250
   GAAAAATCTT GAAYTGGCTG CTGCTTTGGA CAGCTACATC CCAACTCCTG      300
   AGCGTGCTGT GGACAAACCK TTCYTGyTGC CTATCGAAGA CGTRTTCTCT      350
   ATCTCTGGYC GYGGTACMGT AGTAACYGGY CGTGTAAGAG GCGGTRTCAT      400
   CCACGTTGGT GACGAGATYG AAATCGTAGG TCTGAAAGAA ACCCAAAAAA      450
55 CCACCTGTAC CGGCGTTGAA ATGTTCCGCA AACTGCTGGA CGAAGGTCAA      500
   GCWGGTGACA ACGTAGGCGT ATTGYTGCCT GGTACCAARC GTGAAGACGT      550
   AGAGCGTGGT CAAGTATTGG CYAAACCAGG YACCATYACT CCSCACACCA      600
   AATTCAAAGC AGAAGTATAC GTACTGAGCA AAGAAGAGGG TGGTCGYCAC      650
   ACTCCATTCT TCGCYAACTA CCGYCCMCAA TTCTACTTCC GTACYACTGA      700
60 CGTAACYGGT GCAGTTACTT TGGAAGAAGG TGTAGAAATG GTAATGCCAG      750

```

GTGAGAACGT AACCATTACY GTAGAACTGA TTGCGCCTAT CGCTAGGAAG 800
AAGGTCTGCG 810

5

2) INFORMATION FOR SEQ ID NO: 731

(i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 813 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
serotype *enteritidis*
- (B) STRAIN: ATCC 13076

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 731

CTGGTTGTTG CTGCGACTGA CGGCCCGATG CCGCAGACCC GTGAGCACAT 50
CCTGCTGGGT CGTCAGGTAG GCGTTCGTA CATCATCGTG TTCCTGAACA 100
25 AATGCGACAT GGTGATGAC GAAGAGCTGC TGGAACTGGT TGAAATGGAA 150
GTTCGYGAAC TGCTGTCTCA GTACGACTTC CCGGGCGACG ACACTCCGAT 200
CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGACGCA GAGTGGGAAG 250
CGAAAATCAT CGAACTGGCT GGCTTCCTGG ATTCTTACAT CCCGGAACCA 300
GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG ACGTATTCTC 350
30 CATCTCCGGT CGTGGTACCG TTGTTACCG TCGTGTAGAA CGCGGTATCA 400
TCAAAGTGGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA GACTCAGAAG 450
TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAAGTCTGG ACGAAGGCCG 500
TGCCGGTGAG AACGTAGGTG TTCTGCTGCG TGGTATCAA CCGTGAAGAAA 550
TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCACCATCAA GCCGCACACC 600
35 AAGTTCGAAT CTGAAGTGTA CATTCTGTCC AAAGATGAAG GCGGCCGTCA 650
CACTCCGTTT TTCAAAGGCT ACCGTCCGCA GTTCTACTTC CGTACTACTG 700
ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTAGAGAT GGTAATGCCG 750
GGCGACAACA TCAAAATGGT TGTACCCTG ATCCACCCGA TCGCAATGGA 800
CGACGGTCTG CGT 813

40

2) INFORMATION FOR SEQ ID NO: 732

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

50

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
serotype *gallinarum*
- (B) STRAIN: ATCC 9184

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 732

60 CTGGTTGTTG CTGCGACTGA CGGCCCGATG CCGCAGACCC GTGAGCACAT 50
550

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CCTGCTGGGT CGTCAGGTAG GCGTTCGGTA CATCATCGTG TTCCTGAACA 100
AATGCGACAT GGTGTGATGAC GAAGAGCTGC TGGAAGTGGT TGAAATGGAA 150
GTTTCGYGAAC TGCTGTCTCA GTACGACTTC CCGGGCGACG AACTCCGAT 200
CGTTCGTGGT TCTGCTCTGA AAGCGCTGGA AGGCGACGCA GAGTGGGAAG 250
5 CGAAAATCAT CGAACTGGCT GGCTTCCTGG ATTCTTACAT CCCGGAACCA 300
GAGCGTGCGA TTGACAAGCC GTTCCTGCTG CCGATCGAAG ACGTATTCTC 350
CATCTCCGGT CGTGGTACCG TTGTTACCGG TCGTGTAGAA CGCGGTATCA 400
TCAAAGTGGG CGAAGAAGTT GAAATCGTTG GTATCAAAGA GACTCAGAAG 450
TCTACCTGTA CTGGCGTTGA AATGTTCCGC AAAGTGTGGT ACGAAGGCCG 500
10 TGCCGGTGAG AACGTAGGTG TTCTGCTGCG TGGTATCAAA CGTGAAGAAA 550
TCGAACGTGG TCAGGTACTG GCTAAGCCGG GCACCATCAA GCCGCACACC 600
AAGTTCGAAT CTGAAGTGTA CATTCTGTCC AAAGATGAAG GCGGCCGTCA 650
CACTCCGTTT TCAAAGGCT ACCGTCCGCA GTTCTACTTC CGTACTACTG 700
ACGTGACTGG CACCATCGAA CTGCCGGAAG GCGTAGAGAT GGTAATGCCG 750
15 GGCGACAACA TCAAATGGT TGTACCCTG ATCCACCCGA TCGCAATGGA 800
CGACGGTCTG CG 812

```

20 2) INFORMATION FOR SEQ ID NO: 733

(i) SEQUENCE CHARACTERISTICS:

```

25 (A) LENGTH: 814 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Salmonella choleraesuis subsp. choleraesuis
    serotype paratyphi B
    (B) STRAIN: ATCC 8759

```

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 733

```

TGGTTGTTGC TCGACTGAC GGYCCGATGC CGCAGACCCG TGAGCACATC 50
CTGCTGGGTC GTCAGGTAGG CGTTCCGTAC ATCATCGTGT TCCTGAACAA 100
ATGCGACATG GTTGATGACG AAGAGCTGCT GGAAGTGGTT GAAATGGAAG 150
40 TTCGYGAACT GCTGTCTCAG TACGACTTCC CCGGCGACGA CACTCCGATC 200
GTTTCGTGGT CTGCTCTGAA AGCGCTGGAA GGCGACGCAG AGTGGGAAGC 250
GAAAATCATC GAAGTGGCTG GCTTCCTGGA TTCTTACATT CCGGAACCAG 300
AGCGTGCGAT TGACAAGCCG TTCCTGCTGC CGATCGAAGA CGTATTCTCC 350
ATCTCTGGTC GTGGTACCGT TGTACCCTG CGTGTAGAAC GCGGTATCAT 400
45 CAAAGTGGGC GAAGAAGTTG AAATCGTTG TATCAAAGAG ACTCAGAAGT 450
CTACCTGTAC TGGCGTTGAA ATGTTCCGCA AACTGCTGGA CGAAGGCCGT 500
GCGGGTGAGA ACGTAGGTGT TCTGCTGCGT GGTATCAAAC GTGAAGAAAT 550
CGAACGTGGT CAGGTACTGG CTAAGCCGGG CACCATCAAG CCGCACACCA 600
AGTTTCGAATC TGAAGTGATC ATTCTGTCCA AAGATGAAGG CGGCCGTCAT 650
50 ACTCCGTTCT TCAAAGGCTA CCGTCCGCAG TTCTACTTCC GTACTACTGA 700
CGTGAAGTGC ACCATCGAAC TGCCGGAAGG CGTAGAGATG GTAATGCCGG 750
GCGACAACAT CAAATGGTT GTTACCCTGA TCCACCCGAT CGCAATGGAC 800
GACGGTCTGC GTTT 814

```

55

2) INFORMATION FOR SEQ ID NO: 734

(i) SEQUENCE CHARACTERISTICS:

```

60 (A) LENGTH: 828 bases

```

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype *virchow*

10 (B) STRAIN: ATCC 51955

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 734

	GGCGCGATCC	TGGTTGTTGC	TGCGACTGAC	GGCCCGATGC	CGCAGACCCG	50
15	TGAGCACATC	CTGCTGGGTC	GTCAGGTAGG	CGTTCCGTAC	ATCATCGTGT	100
	TCCTGAACAA	ATGCGACATG	GTTGATGACG	AAGAGCTGCT	GGAAGTGGTT	150
	GAAATGGAAG	TTCGTGAACT	TCTGTCTCAG	TACGACTTCC	CGGGCGACGA	200
	CACTCCGATC	GTTCTGTGGT	CTGCTCTGAA	AGCGCTGGAA	GGCGACGCAG	250
	AGTGGGAAGC	GAAAATCATC	GAAGTGGCTG	GCTTCCTGGA	TTCTTACATT	300
20	CCGGAACCAG	AGCGTGCGAT	TGACAAGCCG	TTCCTGCTGC	CGATCGAAGA	350
	CGTATTCTCC	ATCTCCGGTC	GTGGTACCGT	TGTTACCGGT	CGTGTAGAAC	400
	GCGGTATCAT	CAAAGTGGGC	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAG	450
	ACTCAGAAGT	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
	CGAAGGCCGT	GCCGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAAC	550
25	GTGAAGAAAT	CGAACGTGGT	CAGGTACTGG	CTAAGCCGGG	CACCATCAAG	600
	CCGCACACCA	AGTTCGAATC	TGAAGTGTAC	ATTCTGTCCA	AAGATGAAGG	650
	CGGCCGTCAT	ACTCCGTTCT	TCAAAGGCTA	CCGTCCGCAG	TTCTACTTCC	700
	GTACTACTGA	CGTGACTGGC	ACCATCGAAC	TGCCGGAAGG	CGTAGAGATG	750
	GTAATGCCCG	GCGACAACAT	CAAAATGGTT	GTTACCCTGA	TCCACCCGAT	800
30	CGCAATGGAC	GACGGTCTGC	GTTTCGCA			828

2) INFORMATION FOR SEQ ID NO: 735

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 825 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

45 (A) ORGANISM: *Serratia grimesii*

(B) STRAIN: ATCC 14460

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 735

50	GGCGCTATCC	TGGTTGTTGC	TGCGACTGAT	GGCCCAATGC	CACAGACCCG	50
	TGAGCACATC	CTGCTGGGTC	GTCAGGTTGG	CGTTCCTTTC	ATCATCGTAT	100
	TCATGAACAA	ATGCGACATG	GTTGATGATG	AAGAGCTGCT	GGAAGTGGTA	150
	GAAATGGAAG	TTCGTGAACT	TCTGTCTGCT	TATGACTTCC	CTGGTGATGA	200
	CCTGCCAGTT	GTTCTGTGGT	CAGCGCTGAA	AGCACTGGAA	GGCGAAGCTG	250
55	AGTGGGAAGC	TAAAATCATC	GAAGTGGCTG	GCTACCTGGA	TTCTTACATC	300
	CCAGAACCAG	AGCGTGCTAT	CGACAAGCCG	TTCCTGCTGC	CAATCGAAGA	350
	CGTATTCTCC	ATCTCCGGYC	GTGGTACYGT	AGTTACCGGT	CGTGTAGAGC	400
	GCGGTATCGT	TAAAGTTGGC	GAAGAAGTTG	AAATCGTTGG	TATCAAAGAC	450
	ACCGTTAAGT	CTACCTGTAC	TGGCGTTGAA	ATGTTCCGCA	AACTGCTGGA	500
60	CGAAGGCCGT	GCTGGTGAGA	ACGTAGGTGT	TCTGCTGCGT	GGTATCAAGC	550

GTGAAGACAT	CGAACGTGGT	CAGGTACTGG	CTAAACCAGG	TTCAATCAAG	600
CCACACACCA	AATTCGACTC	AGAAGTTTAC	ATCCTGAGCA	AAGAAGAAGG	650
TGGTCGTCAC	ACTCCATTCT	TCAAAGGCTA	CCGTCCACAG	TTCTACTTCC	700
GTACAACTGA	CGTGACCGGT	ACCATCGAAC	TGCCAGAAGG	CGTAGAGATG	750
5 GTAATGCCAG	GCGATAACGT	GAACATGGTT	GTAACCCCTGA	TTCACCCAAT	800
CGCGATGGAC	GACGGTCTGC	GTTTC			825

10 2) INFORMATION FOR SEQ ID NO: 736

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 798 bases
 (B) TYPE: Nucleic acid
 15 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Clostridium difficile*
 (B) STRAIN: ATCC 9689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 736

25 TATTAGTTTG	TTCAGCAACA	GATGGACCAA	TGCCACAAAC	AAGAGAGCAT	50
ATACTATTAT	CAAGACAAGT	TGGAGTACCA	TATATAGTAG	TATTCTTAAA	100
CAAATGTGAC	ATGGTAGATG	ATGAAGAGTT	ATTAGAGTTA	GTAAGAGATGG	150
AAGTAAGAGA	TTTATTAACA	GAATATGATT	TCCCAGGAGA	TGACACTCCA	200
30 ATAGTAAGAG	GTTTCAGCATT	AATGGCATT	GAAGATCCAA	AGAGYGAGTG	250
GGGAGATAAG	ATAGTAGAAT	TATTCGAGCA	AATAGATGAG	TATATACCAG	300
CTCCAGAGAG	AGATACAGAT	AAACCATTCT	TAATGCCAGT	AGAGGACGTA	350
TTCTCAATCA	CAGGAAGAGG	AACAGTTGCA	ACAGGAAGAG	TGGAAAGAGG	400
AGTACTAAAA	GTACAAGACG	AAGTAGAKTT	AGTAGGATTA	ACAGAAGCAC	450
35 CAAGAAAAGT	AGTAGTAACA	GGAGTAGAGA	TGTTTCAGAAA	ATTATTAGAC	500
CAAGCACAAG	CAGGGGATAA	TATAGGAGCA	TTATTAAGAG	GAGTACAAAG	550
AAACGAGATA	GAAAGAGGAC	AAGTACTAGC	AAAGACTGGA	TCAGTAAAGG	600
CACACACAAA	GTTTACAGCA	GAAGTATATG	TACTTAAAAA	AGAAGARGGT	650
GGAAGACATA	CACCATTCTT	TGATGGATAT	AGACCACAAT	TCTATTTTCAG	700
40 AACCAACAGAC	GTAACAGGAG	CTTGTAAGTT	ACCAGAAGGA	ATAGAGATGG	750
TAATGCCTGG	AGATAACGTA	ACAATGGAAG	TAGACTTAAT	AAACTCAA	798

45 2) INFORMATION FOR SEQ ID NO: 737

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 411 bases
 (B) TYPE: Nucleic acid
 50 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Burkholderia pseudomallei*
 (B) STRAIN: 1026B

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 737

60

```

      GTCAACATGA TGGAGCTCAT CAACAACATC GCGAAGGAGC ACGGCGGTTA      50
      CTCCGTGTTT GCGGGCGTGG GCGAGCGTAC CCGTGAAGGG AACGACTTCT      100
      ACCACGAAAT GAAGGACTCG AACGTTCTCG ACAAGGTCGC GCTGGTGTAC      150
      GGCCAGATGA ACGAGCCGCC GGGCAACCGT CTGCGCGTGG CGCTGACGGG      200
5     CCTCACGATG GCCGAGCACT TCCGTGACGA AGGCCTCGAC GTGCTGTTCT      250
      TCGTCGACAA CATCTACCGT TTCACGCTGG CCGGTACCGA AGTGTGCGCG      300
      CTGCTCGGCC GTATGCCGTC GGCAGTGGGC TATCAGCCGA CGCTGGCTGA      350
      AGAAATGGGC AAGCTGCAAG AGCGCATCAC GTCGACGAAG AAGGGCTCGA      400
      TCACGTCGGT T                                     411
10

```

2) INFORMATION FOR SEQ ID NO: 738

```

15     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 394 bases
        (B) TYPE: Nucleic acid
        (C) STRANDEDNESS: Double
        (D) TOPOLOGY: Linear
20
        (ii) MOLECULE TYPE: Genomic DNA
        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Clostridium bifermentans
25         (B) STRAIN: ATCC 638

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 738

```

30     TACAAGAGCT TATTAACAAT ATAGCTACTC AACACGGTGG TATATCAGTA      50
      TTCGCAGGTG TTGGAGAGAG AACAAAGAGAA GGTAACGACT TATTCCATGA      100
      GATGAGCGAT ACAGGAGTTA TAAATAAAAC AGCTCTAGTA TTCGGACAAA      150
      TGAATGAGCC ACCTGGAGCA AGAATGAGAG TTGCTTTAAC TGGTCTTACA      200
      ATGGCTGAAT ACTTCAGAGA TCAACAAGGG CAAGACGTTT TATTATTCGT      250
      AGATAATATA TTCCGTTTCA CTCAAGCAGG ATCTGAGGTT TCTGCACTTC      300
35     TTGGACGTAC TCCATCAGCA GTTGGATACC AACCAACATT AGCAACAGAG      350
      ATGGGTAGAT TACAAGAGAG AATAACATCT ACAAATAAAG GGTC          394

```

40 2) INFORMATION FOR SEQ ID NO: 739

```

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 394 bases
            (B) TYPE: Nucleic acid
45         (C) STRANDEDNESS: Double
            (D) TOPOLOGY: Linear
        (ii) MOLECULE TYPE: Genomic DNA
        (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Clostridium beijerincki (deposited as
            Clostridium butyricum)
            (B) STRAIN: ATCC 8260

```

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 739

```

      TTAATAAACA ACATAGCTAA ACAACATGGT GGTTTATCAG TATTTACTGG      50
      AGTTGGTGAA AGATCAAGAG AAGGTAATGA CTTATATCAT GAAATGAGAG      100
      AGTCAGGAGT TATTGATAAG ACAGCATTAG TATTTGGACA AATGAATGAG      150
60     CCACCGGGTG CCAGAATGAG AGTTGCATTA ACAGGTCTTA CTATGGCAGA      200

```

GTATTTTAGA	GATAAAGGTC	AAGATGTGTT	ACTATTCATA	GATAACATAT	250
TCAGATATAC	TCAAGCAGGT	TCAGAGGTTT	CAGCATTACT	TGGAAGAACA	300
CCTTCAGCGG	TTGGATATCA	GCCAACACTT	GCAACTGAAA	TGGGTGCACT	350
TCAGGAAAGA	ATTACATCAA	CAGTTAATGG	TTCTATTACG	TCAG	394

5

2) INFORMATION FOR SEQ ID NO: 740

- 10 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 393 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 15 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Clostridium difficile*
 - (B) STRAIN: ATCC 9689
- 20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 740

TTATAAACAA	TATTGCTAAG	CAACATGGTG	GTATTTCTGT	ATTTTCAGGA	50
GTAGGAGAAA	GAACAAGAGA	AGGTAACGAC	CTTTATGGCG	AAATGAGTGA	100
GTCTGGAGTT	ATAAATAAAA	CAGCTCTAGT	ATTTGGTCAA	ATGAATGAAC	150
CACCTGGAGC	GAGAATGAGA	GTTGCTTTAA	CTGGACTTAC	AATGGCAGAA	200
CATTTTAGAG	ATGAGCAAGG	ACAAGACGTT	TTACTTTTCG	TTGATAATAT	250
ATTCCGTTTC	ACACAAGCTG	GTTCAGAAGT	TTCAGCACTT	CTAGGACGTA	300
TGCCATCAGC	TGTTGGTTAT	CAGCCAACAT	TAGCTACTGA	AATGGGTGCA	350
CTTCAAGAGA	GAATAACATC	AACTAAGAAA	GGTTCAATAA	CAT	393

35 2) INFORMATION FOR SEQ ID NO: 741

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 398 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- 40 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Clostridium ramosum*
 - (B) STRAIN: ATCC 25582
- 45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 741

TTGATTCAAG	AATTCATTAA	TAACATTGCT	ACAGAACATG	GTGGTTTATC	50
AGTTTTTGCT	GGAGTTGGTG	AACGTAGCCG	TGAAGGTAAT	GATTTATATT	100
ATGAAATGAA	GGAAAGTGGT	GTTTTATCTA	AAACAACACT	AGTATTTGGA	150
CAGATGAATG	AACCCCCAGG	AGCTCGTTTA	AGAGTTGCTT	TAACGGGTCT	200
TACTATGGCA	GAAGAATTCC	GTGATGAACA	AGGTCAGGAT	GTCTTATTAT	250
TCATCGATAA	TATTTTCCGT	TTTACTCAAG	CTGGATCTGA	AGTATCTGCC	300
TTACTTGGAC	GGGTACCATC	ACAAGCTGGG	TATCAGCCAA	CTTTAGCAAC	350
CGAAATGGGT	GCTTTACAAG	AACGGATTAC	ATCAACTAAA	AAAGGATC	398

60

2) INFORMATION FOR SEQ ID NO: 742

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium septicum*
 (B) STRAIN: ATCC 12964

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 742

	TAGCTAAGGA	ACACGGTGA	CTTTCAGTAT	TCACAGGTGT	TGGAGAAAGA	50
	TCAAGAGAAG	GTAATGATTT	ATATTACGAA	ATGAAAGAAT	CAGGAGTTAT	100
20	AGACAAGACA	GCTCTAGTGT	TTGGACAAAT	GAATGAATCT	CCAGGAGCTA	150
	GAATGAGAGT	ATCTTTAACA	GGATTAACATA	TGGCTGAATA	TTTCAGAGAT	200
	CAAGGTCAAG	ATGTGCTTTT	ATTCATAGAT	AACATATTTA	GATTTACTCA	250
	AGCTGGATCA	GAAGTATCGG	CTTTACTTGG	AAGAATACCA	TCAGCAGTTG	300
	GTTATCAACC	AACACTAGCA	ACTGAAATGG	GTGCACTTCA	AGAAAGAATT	350
25	ACTTCAACTA	AAAATGGATC	AATAACTTCA			380

2) INFORMATION FOR SEQ ID NO: 743

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium tertium*
 (B) STRAIN: ATCC 14573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 743

45	TTAATAAATA	ATATAGCAAA	AGAGCATGGT	GGTCTTTCTG	TATTTACAGG	50
	AGTTGGAGAA	AGGTCAAGAG	AAGGTAACGA	CTTATATTAT	GAAATGAAAG	100
	AGTCAGGGGT	TATAGATAAG	ACAGCTTTAG	TATTTGGACA	AATGAATGAA	150
	TCACCAGGAG	CAAGAATGAG	AGTTTCATTA	ACTGGATTAA	CTATGGCTGA	200
	ATATTTTGA	GATCAAGGTC	AAGACGTTCT	TTTATTTATA	GATAATATAT	250
50	TTAGATTTAC	TCAAGCGGGA	TCAGAAGTTT	CTGCGTTATT	AGGAAGAATT	300
	CCTTCAGCAG	TTGGATATCA	ACCAACTCTT	GCAACTGAAA	TGGGAGCACT	350
	TCAAGAAAGA	ATAACATCAA	CAAAGAATGG	ATCAATCAC		389

2) INFORMATION FOR SEQ ID NO: 744

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 843 bases
 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Comamonas acidovorans*

(B) STRAIN: ATCC 15668

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 744

	TTCCCCCGCA	CGCATGCCCA	AGGTGTTCTGA	TGCCCTGAAG	CTCGACGGCT	50
	CGGCCCTGAC	GCTGGAAGTG	CAGCAACTGC	TGGGTGACGG	CGTTGTGCGT	100
	ACCATCGCCC	TGGGTTCGTC	CGACGGTCTG	CGTCGCGGCC	TGATGGTGTC	150
15	CAACACCGGC	AACCCCATCA	CCGTGCCCCGT	GGGCAAGGCG	ACGCTGGGTC	200
	GCATCATGGA	CGTGCTGGGC	AATCCCATCG	ACGAACGTGG	TCCCGTGGAT	250
	CAGGCGCTGA	CGGCTCCCAT	CCACCGCAAG	GCACCGGCTT	ATGACGAGCT	300
	GTCGCCTTCG	CAGGAACTGC	TGGAAACCGG	CATCAAGGTG	ATCGACCTGA	350
	TCTCGCCCTT	CGCCAAGGGC	GGCAAGGTGG	GTCTGTTTCGG	TGGCGCCGGT	400
20	GTGGGCAAGA	CCGTGAACAT	GATGGAAGTC	ATCAACAACA	TCGCCAAGGG	450
	CCACGGTGGT	CTGTCCGGTG	TCGCCGGTGT	GGGTGAACGT	ACCCGCGAAG	500
	GCAATGACTT	CTATCACGAA	ATGTCGGACG	CCGGCGTGGT	CAACCAGGAG	550
	TCGCTGAACG	ACTCCAAGGT	GGCCATGGTC	TACGGCCAGA	TGAACGAACC	600
	CCCGGGCAAC	CGTCTGCGCG	TGGCGCTGAC	CGGCCTGACC	ATGGCCGAAG	650
25	CCTTCCGTGA	CGAAGGCAAG	GACGTGCTGT	TCTTCGTGGA	CAACATCTAC	700
	CGCTACACGC	TGGCCGGTAC	CGAAGTGTCC	GCTCTGCTGG	GTGCGATGCC	750
	TTCCGCCGTG	GGCTACCAGC	CCACGCTGGC	CGAGGAAATG	GGCCGCCTGC	800
	AAGAGCGCAT	CACCTCGACC	AAGGTCGGTT	CGATCACTTC	CAC	843

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2) INFORMATION FOR SEQ ID NO: 745

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 819 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

40

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella pneumoniae* subsp.
rhinoscleromatis

45

(B) STRAIN: ATCC 13884

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 745

	GCCGTACCAC	GCGTGTACGA	AGCCCTTGAG	GTACAGAATG	GTAATGAAGT	50
50	TCTGGTGCTG	GAAGTTCAGC	AGCAGCTGGG	CGGCGGTATC	GTACGTACCA	100
	TCGCCATGGG	TTCTTCTGAT	GGTCTGCGCC	GCGGTCTGGA	TGTAAAAGAC	150
	CTCGAGCACC	CGATCGAAGT	CCCGGTAGGT	AAAGCAACGC	TGGGTCGTAT	200
	CATGAACGTA	CTGGGTCAAC	CGGTTGACAT	GAAAGGCGAC	ATCGGCGAAG	250
	AAGAGCGTTG	GGCTATCCAC	CGCGCGGCAC	CGTCCTATGA	AGAGCTGTCC	300
55	AGCTCTCAGG	AACTGCTGGA	AACCGGCATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTCCGC	AAGGGCGGTA	AGTTTGGTCT	GTTCGGCGGT	GCGGGTGTAG	400
	GTA AAAACTGT	AAACATGATG	GAGCTGATCC	GTAACATCGC	GATCGAGCAC	450
	TCCGGTTACT	CTGTGTTTGC	GGGCGTAGGT	GAGCGTACTC	GTGAGGGTAA	500
	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTATCGAT	AAAGTATCCC	550
60	TGGTGTACGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCG	600

	CTGACCGGCC	TGACCATGGC	TGAGAAATTC	CGTGACGAAG	GTCGTGACGT	650
	ACTGCTGTTC	GTCGATAACA	TCTATCGTTA	CACCCTGGCC	GGTACTGAAG	700
	TATCCGCGCT	GCTGGGTCGT	ATGCCTTCAG	CGGTAGGTTA	TCAGCCGACC	750
	CTGGCGGAAG	AGATGGGCGT	TCTGCAGGAA	CGTATCACCT	CCACCAAAC	800
5	CGGTTCTATC	ACCTCCGTA				819

2) INFORMATION FOR SEQ ID NO: 746

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria canis*
 (B) STRAIN: ATCC 14687

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 746

25	GCGATTCTAT	TCCGCGCGTA	TATGATGCTC	TTAAACTAGT	GGATAGAGAA	50
	CTGACGCTTG	AAGTACAACA	ACAGTTGGGT	GATGGTGTCTG	TTCGTACTAT	100
	TGCGATGGGT	AGTTCCGACG	GCCTCAAACG	AGGTTTGCGC	GTAGTTAACA	150
	CCGGTGCTCC	AATTACAGTG	CCTGTGGGCA	AAGCAACATT	AGGCCGTATT	200
	ATGGACGTAT	TAGGTAATCC	GGTTGATGAA	GCTGGTCCGA	TTGGCTCCGA	250
30	GCAAACCCGA	GCAATCCACC	AACCTGCTCC	TAAGTTCGAC	GAGCTTTCTA	300
	GCGCCACAGA	GATTTTGGAA	ACAGGTATTA	AAGTAATTGA	TTTGCTTTGC	350
	CCGTTTGCCA	AAGGCGGTAA	AGTAGGTTTG	TTTGGTGGTG	CGGGAGTGGG	400
	CAAAACCGTA	AATATGATGG	AGTTGATTAA	CAACATCGCG	AAAGCACACA	450
	GCGGTTTGTC	TGTATTTGCC	GGTGTGGGTG	AACGGACGCG	TGAAGGTAAT	500
35	GACTTTTATC	ATGAGATGAA	AGATTCCAAT	GTATTAGATA	AAGTAGCCAT	550
	GGTTTACGGT	CAGATGAACG	AGCCTCCCAG	TAACCGTTTG	CGCGTTGCGC	600
	TAACTGGCTT	GTCTATGGCC	GAATTCTTCC	GTGACGAGAA	AGATGAAAAC	650
	GGTAAAGGCC	GTGATGTATT	GTTCTTTGTA	GACAATATTT	ACCGCTATAC	700
	CCTAGCCGGT	ACAGAAGTAT	CTGCATTGCT	TGGCCGTATG	CCTTCGGCAG	750
40	TAGGTTATCA	GCCGACGTTG	GCAGAGGAAA	TGGGCCGCTT	GCAAGAGCGT	800
	ATTACYTCAM	CCCAAACAGG	CTCT			824

2) INFORMATION FOR SEQ ID NO: 747

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria cinerea*
 (B) STRAIN: ATCC 14685

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 747

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CGCGACGCTA TCCCGCATGT TTACGATGCC CTGAAATTGG ACGAGAACGG      50
TCTGACTCTG GAGGTTCAAC AGCTTCTGGG CGACGGCGTT GTCCGTACTA      100
TTGCAATGGG TAGTTCAGAC GGCCTTAAAC GCGGTATGTC TGTAAGCAAT      150
ACTGGTGCGC CAATCACTGT GCCGGTAGGT AAAGGTACAT TGGGTCGTAT      200
5  TGTCGACGTA TTGGGTACGC CTGTTGATGA AGCAGGTCCG ATCGATAACG      250
ACAAAAGCCG TGCCATTAC CAAACTGCTC CGAAATTCTGA CGAGTTGTCT      300
TCAGCTACCG AATTGTTGGA AACCAGGTATT AAAGTGATCG ACTTGCTGTG      350
TCCGTTTGCT AAAGGCGGTA AAGTAGGTCT GTTCGGTGGT GCCGGTGTGG      400
GCAAAACCGT GAACATGATG GAATTGATCA ACAACATCGC CAAAGCGCAC      450
10 AGCGGTCTGT CCGTGTTCGC AGGTGTGGGT GAGCGTACCC GTGAAGGTAA      500
CGACTTCTAC CACGAGATGA AAGATTCCAA CGTATTGGAT AAAGTAGCCA      550
TGGTGTATGG CCAAATGAAC GAACCTCCGG GCAACCGTCT GCGCGTTGCT      600
TTGACCGGTT TGACTATGGC CGAATACTTC CGTGACGAAA AAGACGAAAA      650
CGGTAAAGGC CGCGACGTAT TGTTCCTTCGT TGACAACATC TACCGTTACA      700
15 CTTTGGCCGG TACTGAAGTA TCTGCACTGT TGGGCCGTAT GCCTTCTGCA      750
GTGGGTTACC AACCACATT GGCTGAAGAA ATGGGTCGTT TGCAAGAGCG      800
TATTACCTCT ACCCAAACCG GTTCATTAC T      831

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2) INFORMATION FOR SEQ ID NO: 748

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 862 bases
25 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:
(A) ORGANISM: Neisseria cuniculi
(B) STRAIN: ATCC 14688

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 748

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CCGTGGCCAA GTACCACAAA TTTATGACGC ACTGAGTGTT GATGGCACCG      50
AAACAACCTT GGAAGTTCAA CAGCAGTTGG GTGATGGCGT GGTGCGTACC      100
ATTGCGATGG GTTCAACCGA AGGCTTGAAG CGTGGTTTGA CTGTATCTAA      150
40 CTCTGGTGCA CCGATTTCTG TGCCAGTGGG TCAAGCGACT TTGGGTCGTA      200
TTATGGATGT GTTGGGTCGT CCAATCGACG AGGCAGGTCC TGTAATGCT      250
CAAGAAAAAT GGTCAATTCA CCGTGAAGCA CCAAGCTATG ATGAGCAATC      300
AAACTCAACT GAGCTGCTAG AAACAGGCAT CAAAGTAATT GATTTGCTTT      350
GCCCATTTGC TAAAGGTGGT AAAGTTGGCT GTTCGGTGG TGCAGGTGTG      400
45 GGTAAAACCG TGAATATGAT GGAGCTGATT AATAATATCG CTCTGAAGCA      450
TTCAGGTCTT TCTGTTTTTG CAGGTGTTGG TGAGCGTACT CGTGAGGGTA      500
ACGATTTTTT TCACGAAATG CAAGAAGCAG GCGTTGTTAA TACCGAAGAC      550
TTCACCAAGT CAAAAGTAGC GATGGTTTAT GGTCAGATGA ATGAGCCACC      600
AGGAAACCGT TTGCGTGTG CATTGACAGG CTTGACGATG GCAGAATATT      650
50 TCCGTGACGA AAAAGATGAA GCAACAGGCA AAGGGCGTGA TGTTCTATTG      700
TTCGTTGATA ACATCTATCG TTACACACTG GCTGGTACGG AAGTGTCAGC      750
ACTTCTAGGT CGTATGCCAT CAGCAGTAGG TTATCAACCG ACTCTGGCTG      800
AAGAAATGGG TGCGTTGCAA GAGCGTATTA CCTCAACGCA ATCGGGTTCTG      850
ATCACTTCGG GG      862

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2) INFORMATION FOR SEQ ID NO: 749

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(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 844 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria elongata* subsp. *elongata*
 (B) STRAIN: ATCC 25295

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 749

	GGA	ACT	CCCA	CGT	GAC	GCTA	TCC	CGCAT	GT	TTTT	GAT	GCA	TTAA	AATTAG	50
15	TTG	AAA	ATGA	CCT	AAC	CTTA	GA	AGTT	CAAC	AACT	TTT	TGGG	GGAT	GGTGTA	100
	GTG	CGT	ACCA	TTG	CGAT	GGG	TAG	TTCA	GAT	GGAT	TAA	AAGC	GTGG	TATGGC	150
	TGT	GA	AATAAT	ACC	GGAG	CTC	CG	ATT	ACTGT	TCCT	GTT	TGGC	CGT	GAACTT	200
	TGG	GTC	GTAT	CAT	GGAT	GTA	TTG	GGTA	ATC	CGG	TTG	ATGA	GGC	AGGTCCG	250
	GTA	AA	TGCAT	CCA	ATAC	ACG	TGC	GAT	CCAT	CA	AGAG	GCTC	CTA	AGTTGA	300
20	TG	AGCT	TTTCT	TCA	ACA	ACGG	AAT	TAT	TAGA	AACT	TGG	CATT	AAG	GTTATCG	350
	ACT	TG	TTATG	TCC	GTT	TGCC	AA	AGG	TGGTA	AAG	TAG	GTCT	GTT	TGGTGGT	400
	GCG	GT	GTAG	GTA	AA	ACCGT	AA	TAT	GATG	GAG	TAA	TATTA	ACA	ACATTGC	450
	CA	AGG	CACAT	AG	CGG	TTTGT	CT	GTG	TTTGC	AGG	CGT	TGGT	GA	ACGTACTC	500
	GT	GA	AGGTAA	TG	ACT	TCTAT	CAC	GAG	ATGA	AAG	ATT	TCCAA	CGT	TATTGGAC	550
25	AA	AGT	TGGCAA	TG	GTT	TACGG	TC	GAT	TGAAC	GA	ACC	TCCAG	GCA	ACCGTCT	600
	GCG	CGT	TGCT	TT	GAC	CGGT	TG	ACT	ATGGC	CGA	ATA	CTTC	CGT	GACGAAA	650
	AAG	AC	GAAAA	CGG	TAA	AGGT	CG	C	GACGTAT	TG	TTCT	TCGT	GG	ACAACATT	700
	TAC	CGT	TACA	CT	TTG	GCCGG	TAC	GGA	AGTA	TCC	G	CATTGC	TGGG	TCGTAT	750
	GC	CTT	CAGCA	GT	AGG	TTACC	AA	CCG	ACATT	GG	CTG	AAGAA	AT	GGGTCGTT	800
30	TG	CA	AGAGCG	TAT	TAC	CTCT	AC	CC	CAGACAG	GCT	CT	TATTAC	TT	CC	844

2) INFORMATION FOR SEQ ID NO: 750

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria flavescens*
 (B) STRAIN: ATCC 13120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 750

50	CGC	GAC	GCTA	TTCC	GCAT	GT	TTAC	GAT	GCC	CTGA	AATT	TGG	ACG	AGA	AACGG	50				
	TCT	GACT	CTG	GA	AGTT	CAAC	AG	CTT	CTGGG	TG	ACG	GCGTT	GT	CCG	TACTA	100				
	TTG	CAAT	TGGG	TAG	TTCA	GAC	GG	C	TGAAAC	G	CGG	CATGTC	TG	TAA	GCAAT	150				
	AC	CGGT	TGCGC	CA	ATC	ACTGT	G	CCG	G	TAGGT	AA	AGG	TACAT	T	G	GCCGTAT	200			
	TGT	CG	ACGTA	TT	G	GTACGC	CT	G	TTGATGA	AG	C	AGGTCCG	AT	C	GATACCG	250				
55	ACA	AG	AGCCG	TG	CC	ATTAC	CAA	ACT	GCTC	CG	AA	ATT	TCGA	TG	AG	TTGTCT	300			
	TCA	ACT	ACCG	AAT	TG	TTGGA	A	ACC	G	G	TATT	AA	AG	TGATCG	ACT	TG	CTGTG	350		
	TCC	G	TTTGCT	A	AGG	GCGGTA	A	AG	TAGGTCT	G	TT	C	G	G	TGGT	G	CC	G	TGG	400
	G	CA	AAACCGT	GA	AC	ATGATG	GA	ATT	GATCA	ACA	AC	ATCGC	CAA	AG	CGCAC	450				
	AG	CG	G	CCTGT	CC	G	TGTT	CGC	AG	G	TG	TGGGT	GA	AC	G	TACCC	500			
60	CG	ACT	TCTAC	CAC	G	AGATGA	A	AG	ATTCCAA	CG	T	ATTG	GAT	AA	AG	TAGCCA	550			

	TGGTGTATGG	TCAAATGAAC	GAACCTCCAG	GCAACCGTCT	GCGCGTTGCT	600
	TTGACCGGTT	TGACTATGGC	CGAATACTTC	CGTGACGAAA	AAGATGAAAA	650
	CGGTAAAGGT	CGCGACGTAT	TGTTCTTCGT	TGACAACATC	TACCGTTACA	700
	CTCTGGCCGG	TACCGAAGTA	TCCGCACTGT	TGGGTCGTAT	GCCTTCTGCA	750
5	GTGGGTTACC	AACCGACATT	GGCTGAAGAA	ATGGGTCGTT	TGCAGGAGCG	800
	TATTACTTCT	ACGCAAACCG	GTTCCATTAC	TTCC		834

10 2) INFORMATION FOR SEQ ID NO: 751

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 834 bases
	(B) TYPE: Nucleic acid
15	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

	(A) ORGANISM: <i>Neisseria gonorrhoeae</i>
	(B) STRAIN: ATCC 31426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 751

25	CGCGACATGA	TTCCGCGCGT	TTACGACGCT	TTGAAATTAG	ACGAAAACGG	50
	TCTGACTTTG	GAAGTCCAAC	AGCTTTTGGG	TGATGGCGTA	GTCCGTACCA	100
	TCGCTATGGG	CAGCTCGGAC	GGTTTGAAAC	GCGGCATGAC	TGTGAGCAAT	150
	ACTGGTTTCG	CCATTACTGT	GCCGGTAGGT	AAAGGTACGT	TGGGACGCAT	200
30	TGTCGATGTA	TTGGGAACCT	CTGTTGACGA	GGCAGGTCCA	ATTGATACCG	250
	ACAAGAGTCG	TGCCATCCAC	CAAGCCGCTC	CTAAGTTTGA	CGAACTGTCT	300
	TCCACAACCG	AATTGCTCGA	AACGGGCATT	AAAGTGATTG	ACTTGCTGTG	350
	TCCGTTTGCC	AAAGCGGTA	AAGTAGGTCT	GTTTCGGCGGT	GCCGGTGTGG	400
	GTAAAACCGT	GAACATGATG	GAAATTGATCA	ACAACATCGC	CAAAGCGCAC	450
35	AGCGGCTTGT	CCGTGTTCTC	AGGCGTGGGT	GAGCGTACCC	GCGAAGGTAA	500
	CGACTTCTAC	CACGAGATGA	AAGATTCCAA	CGTATTGGAT	AAAGTAGCCA	550
	TGGTGTATGG	CCAAATGAAC	GAACCTCCAG	GCAACCGTCT	GCGCGTTGCT	600
	TTGACCGGTT	TGACTATGGC	TGAATACTTC	CGTGACGAAA	AAGACGAAAA	650
	CGGTAAAGGT	CGTGACGTAT	TGTTCTTCGT	TGACAACATC	TACCGTTACA	700
40	CTCTGGCCGG	TACCGAAGTA	TCCGCACTGT	TGGGCCGTAT	GCCTTCTGCA	750
	GTGGGTTACC	AACCGACATT	GGCTGAAGAA	ATGGGTCGTT	TGCAAGAGCG	800
	TATTACCTCT	ACCCAAACCG	GTTCCATTAC	TTCC		834

45 2) INFORMATION FOR SEQ ID NO: 752

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 825 bases
50	(B) TYPE: Nucleic acid
	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55 (vi) ORIGINAL SOURCE:

	(A) ORGANISM: <i>Neisseria gonorrhoeae</i>
	(B) STRAIN: ATCC 27628

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 752

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ACATGATTCC GCGCGTTTAC GACGCTTTGA AATTAGACGA AAACGGTCTG      50
ACTTTGGAAG TCCAACAGCT TTTGGGTGAT GGCGTAGTCC GTACCATCGC      100
TATGGGCAGC TCGGACGGTT TGAAACGCGG CATGACTGTG AGCAATACTG      150
5 GTTCGCCCAT TACTGTGCCG GTAGGTAAAG GTACGTTGGG ACGCATTGTC      200
GATGTATTGG GAACGCCTGT TGACGAGGCA GGTCCAATTG ATACCGACAA      250
GAGTCGTGCC ATCCACCAAG CCGCTCCTAA GTTTGACGAA CTGTCTTCCA      300
CAACCGAATT GCTCGAAACG GGCATTAAAG TGATTGACTT GCTGTGTCCG      350
TTTGCCAAAG GCGGTAAAGT AGGTCTGTTC GGCGGTGCCG GTGTGGGTAA      400
10 AACCGTGAAC ATGATGGAAT TGATCAACAA CATCGCCAAA GCGCACAGCG      450
GCTTGTCGGT GTTCTCAGGC GTAGGTGAGC GTACCCGCGA AGGTAACGAC      500
TTCTACCACG AGATGAAAGA TTCCAACGTA TTGGATAAAG TAGCCATGGT      550
GTATGGCCAA ATGAACGAAC CTCCAGGCAA CCGTCTGCGC GTTGCTTTGA      600
CCGGTTTGAC TATGGCTGAA TACTTCCGTG ACGAAAAAGA CGAAAACGGT      650
15 AAAGGTCGTG ACGTATTGTT CTTTCGTTGAC AACATCTACC GTTACACTCT      700
GGCCGGTACC GAAGTATCCG CACTGTTGGG CCGTATGCCT TCTGCAGTGG      750
GTTACCAACC GACATTGGCT GAAGAAATGG GTCGTTTGCA AGAGCGTATT      800
ACCTCTACCC AAACCGGTTT CATT      825

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2) INFORMATION FOR SEQ ID NO: 753

- (i) SEQUENCE CHARACTERISTICS:
- 25 (A) LENGTH: 831 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear
- 30 (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Neisseria lactamica*
(B) STRAIN: ATCC 23970
- 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 753

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GATGCGATTG CGCATGTTTA CGATGCCCTG AAATTGGACG AGAACGGTCT      50
GACCCGTGGA GTCCAACAGC TTTTGGGTGA CGGCGTTGTC CGTACTATTG      100
40 CAATGGGTAG TTCAGACGGC CTGAAACGCG GCATGTCTGT CAGCAATACC      150
GGTGCGCCAA TCACTGTGCC GGTAGGTAAA GGTACGTTGG GCCGTATTGT      200
CGACGTATTG GGTACACCTG TTGACGAAGC AGGTCCGATC GATACCGACA      250
AGAGCCGCGC CATCCACCAA ACCGCCCGCA AATTCGACGA GTTGTCTTCA      300
ACTACCGAAT TGTTGGAAAC CGGCATTAAA GTGATCGATT TGCTGTGTCC      350
45 GTTTGCTAAG GGCGGTAAAG TAGGTCTGTT CGGTGGTGCC GGTGTGGGCA      400
AAACCGTGAA CATGATGGAA TTGATCAACA ACATCGCCAA AGCGCACAGC      450
GGTCTGTCCG TGTTTGCAGG CGTGGGCGAG CGTACCCGCG AAGGTAACGA      500
CTTCTACCAC GAGATGAAAG ATTCCAACGT ATTGGATAAA GTAGCCATGG      550
TGTATGGTCA GATGAACGAA CCTCCGGGCA ACCGTCTGCG CGTTGCTTTG      600
50 ACCGGTTTGA CGATGGCCGA ATAATTCCGC GACGAAAAAG ACGAAAACGG      650
CAAAGGCCGC GACGTATTGT TCTTCGTGGA CAACATCTAC CGTTACACCC      700
TGGCCGGTAC CGAAGTATCC GCACTGTTGG GCCGTATGCC TTCCGCAGTG      750
GGTTACCAAC CGACATTGGC TGAAGAAATG GGTCGTTTGC AAGAGCGTAT      800
TACCTCTACC CAAACCGGTT CCATTACTTC C      831
55

```

2) INFORMATION FOR SEQ ID NO: 754

- 60 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 836 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria meningitidis*

(B) STRAIN: 2241C

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 754

	CCACGCGACA	TGATTCCGCG	CGTTTACGAC	GCTTTGAAAT	TAGACGAAAA	50
15	CGGTCTGACT	TTGGAAGTCC	AACAGCTTTT	GGGCGACGGC	GTAGTCCGTA	100
	CCATTGCGAT	GGGCAGCTCG	GACGGTTTGA	AACGCGGCAT	GA CTGTGAGC	150
	AATACCGGTG	CGCCATTAC	TGTGCCGGTA	GGTAAAGGTA	CGTTGGGACG	200
	CATTGTCGAT	GTATTGGGAA	CGCCTGTTGA	CGAGGCAGGT	CCAATCGATA	250
	CCGACAAGAG	CCGTGCCATC	CACCAAGCCG	CTCCTAAGTT	TGACGAACTG	300
20	TCTTCCACAA	CCGAATTGCT	CGAAACGGGC	ATTAAAGTGA	TTGACTTGCT	350
	GTGTCCGTTT	GCCAAAGGCG	GTAAAGTAGG	TCTGTTCCGG	GGTGCCGGTG	400
	TGGGTAAAAC	CGTGAACATG	ATGGAATTGA	TCAACAACAT	CGCCAAAGCG	450
	CACAGCGGCT	TGTCCGTGTT	CGCAGGCGTG	GGTGAGCGTA	CCCGCGAAGG	500
	TAACGACTTC	TACCACGAGA	TGAAAGATTG	CAACGTATTG	GATAAAGTGG	550
25	CAATGGTTTA	CGGTCAGATG	AACGAACCTC	CGGGCAACCG	TTTGCGCGTC	600
	GCATTGACCG	GTTTGACCAT	GGCGGAATAC	TTCCGTGACG	AAAAAGACGA	650
	AAACGGCAAA	GGCCGCGACG	TATTGTTCTT	CGTGGACAAC	ATCTACCGTT	700
	ACACTCTAGC	TGGTACCGAA	GTATCCGCAT	TGTTGGGCCG	TATGCCGTCT	750
	GCA GTGGGCT	ACCAACCGAC	ATTGGCAGAA	GAAATGGGTC	GTTTGCAGGA	800
30	GCGTATTACC	TCTACCCAAA	CCGGTTCTAT	TACTTC		836

2) INFORMATION FOR SEQ ID NO: 755

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 837 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria mucosa*

(B) STRAIN: ATCC 19696

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 755

50	CCGCGTGATG	CCATTCCGCG	TGTTTACGAC	GCCCTGAAAT	TGGATGCAAA	50
	CGGCC TGACT	TTGGAAGTGC	AACAGCTTCT	GGGTGACGGC	G TAGTTCGTA	100
	CTATTGCAAT	GGGTAGTTCC	GATGGTTTGA	AACGCGGCAT	GA CTGTAAGC	150
	AATACAGGTG	CGCCGATTAC	AGTACCGGTA	GGTAAAGGTA	CTTTGGGACG	200
	TATTGTGCGAT	GTATTGGGTA	CGCCTGTTGA	CGAAGCAGGT	CCGATTGATA	250
55	CCGACAAACA	CCGTGCCATC	CATCAGACAG	CTCCGAAATT	TGATGAACTG	300
	TCTGCGACTA	CTGAGCTGCT	GGAAACCGGC	ATTAAAGTGA	TTGACTTGCT	350
	GTGTCCGTTT	GCCAAAGGCG	GTAAAGTAGG	TCTGTTCCGG	GGTGCCGGTG	400
	TAGGCAAAAC	CGTCAACATG	ATGGAATTAA	TTAACAACAT	CGCCAAAGCA	450
	CATAGCGGTT	TGTCCGTGTT	TGCAGGTGTG	GGTGAGCGTA	CCCGTGAAGG	500
60	TAATGACTTC	TACCACGAGA	TGAAAGATTG	CAACGTATTG	GACAAAGTGG	550

	CGATGGTTTA	CGGTCAGATG	AACGAACCTC	CGGGTAACCG	TCTGCGTGTA	600
	GCCTTGACCG	GTTTGACGAT	GGCCGAATAC	TTCCGTGATG	AAAAAGACGA	650
	AAGCGGCAAA	GGCCGTGACG	TATTGTTCTT	CGTGGACAAT	ATCTACCGTT	700
	ACACCCTGGC	CGGTACCGAA	GTATCCGCAT	TGTTGGGTCG	TATGCCTTCA	750
5	GCAGTAGGTT	ACCAACCGAC	ATTGGCTGAA	GAAATGGGTC	GTTTGCAAGA	800
	GCGTATTACC	TCTACCCAAA	CAGGCTCCAT	TACCTCC		837

10 2) INFORMATION FOR SEQ ID NO: 756

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 834 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria subflava*
(B) STRAIN: ATCC 14221

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 756

25	CGCGACGCTA	TCCCGCATGT	TTACGATGCC	CTGAAATTGG	ACGAGAACGG	50
	TCTGACTCTG	GAAGTTCAAC	AGCTTCTGGG	TGACGGCGTT	GTCCGTACTA	100
	TTGCAATGGG	TAGTTCAGAC	GGCCTGAAAC	GCGGCATGTC	TGTAAGCAAT	150
	ACTGGTGCGC	CAATCACTGT	GCCGGTAGGT	AAAGGTACAT	TGGGTCGTAT	200
30	TGTCGACGTA	TTGGGTACGC	CTGTTGATGA	AGCAGGTCCG	ATCGATACCG	250
	ACAAGAGCCG	TGCCATTAC	CAAACCTGCTC	CGAAATTCTGA	CGAGTTGTCT	300
	TCAACTACCG	AATTGCTGGA	AACCGGTATT	AAAGTGATCG	ACTTGCTGTG	350
	TCCGTTTGCT	AAGGGCGGTA	AAGTAGGTCT	GTTCCGGTGGT	GCCGGTGTGG	400
	GCAAAACCGT	GAACATGATG	GAATTGATCA	ACAACATCGC	CAAAGCGCAC	450
35	AGCGGTCTGT	CCGTGTTTCGC	AGGTGTGGGT	GAACGTACCC	GTGAAGGTAA	500
	CGACTTCTAC	CACGAGATGA	AAGATTCCAA	CGTATTGGAT	AAAGTAGCCA	550
	TGGTGTATGG	CCAAATGAAC	GAACCTCCGG	GCAACCGTCT	GCGCGTTGCT	600
	TTGACCGGTT	TGACTATGGC	CGAATACTTC	CGTGACGAAA	AAGACGAAAA	650
	CGGTAAAGGT	CGCGACGTAT	TGTTCTTCGT	TGACAACATC	TACCGTTACA	700
40	CTCTGGCCGG	TACCGAAGTA	TCTGCACTGT	TGGGCCGTAT	GCCTTCTGCA	750
	GTGGGTTACC	AACCGACATT	GGCTGAAGAA	ATGGGTTCGT	TGCAAGAGCG	800
	TATTACCTCT	ACCCAAACTG	GTTCCATTAC	TTCC		834

45 2) INFORMATION FOR SEQ ID NO: 757

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 833 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

55 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria weaveri*
(B) STRAIN: ATCC 51223

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 757

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      CCCGTGATGC TATTCCCATG TATACGATGC CCTGAAATTG GTAGATAACG      50
      ATCTGACCCT GGAAGTGCAA CAACTTTTATG GTGATGGTGT GGTTTCGTACC      100
      ATTGCAATGG GTAGTTCAGA CGGCCTAAAA CGTGGTATGG CTGTTAACAA      150
5     TACCGGCGCT CCGATTACTG TTCCGGTGGG GAAAGCCACC TTGGGACGTA      200
      TTATGGATGT GTTGGGTAAT CCGGTTGATG AAGCAGGTCC TGTTGTATCA      250
      GAAGAACTC GCGCTATTCA TCAAGCTGCC CCTAAATTTG ACGAACTGTC      300
      TTCAGCAACT GAGTTGTTGG AAACAGGCAT TAAAGTAATT GACTTGCTGT      350
      GCCCGTTTGC CAAAGGTGGT AAAGTAGGTT TGTTTGGTGG TGCCGGCGTG      400
10    GGTAAAACCG TAAATATGAT GGAGTTGATC AACAACATCG CGAAGGCACA      450
      TAGTGGTTTG TCTGTATTCG CCGGTGTAGG TGAGCGTACC CGTGAAGGTA      500
      ACGACTTCTA CCATGAAATG AAAGACTCTA ACGTATTGGA TAAAGTAGCC      550
      ATGGTTTATG GCCAGATGAA TGAACCTCCG GGTAACCGTT TGC GCGTTGC      600
      TTTGACTGGT TTGACTATGG CCGAATATTT CCGTGACGAG AAAGATGAAA      650
15    ACGGCAAAGG TCGTGACGTC TTGTTCTTTG TGGATAATAT CTATCGCTAT      700
      ACTCTGGCCG G TACTGAAGT GTCTGCACTG TTAGGTCGTA TGCCGTCTGC      750
      AGTAGGTTAT CAGCCTACAT TGGCAGAAGA AATGGGTCGC TTGCAGGAGC      800
      GTATTACTTC TACTCAAACA GGTTCGATTA CTT      833

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20

2) INFORMATION FOR SEQ ID NO: 758

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      (i) SEQUENCE CHARACTERISTICS:
25     (A) LENGTH: 833 bases
      (B) TYPE: Nucleic acid
      (C) STRANDEDNESS: Double
      (D) TOPOLOGY: Linear

      (ii) MOLECULE TYPE: Genomic DNA

      (vi) ORIGINAL SOURCE:
      (A) ORGANISM: Neisseria animalis
      (B) STRAIN: ATCC 19573

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35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 758

```

      CGCGATGCCA TTCCTCACGT TTACGATGCC CTGAAATTGG ACGACACCGG      50
      TCTGACTTTG GAAGTACAAC AACTTCTGGG CGACGGTGTG GTACGTACCA      100
40    TTGCAATGGG TAGTTCAGAC GGCCTGAAAC GGGGTTTGTC TGTGAGCAAT      150
      ACCGGTTCTC CGATTGCCGT TCCTGTCCGT AAAGCGACTT TGGGTCGTAT      200
      TATGGACGTA TTGGGCAATC CGGTTGATGA AGCCGGTCCG GTTGCTACCG      250
      AAGAGAAACG TGCTATTAC CAAAGCCGCAC CGAAGTTTGA TGAATTGTCA      300
      TCAGCTACCG AGTTGTTGGA AACCGGTATT AAAGTAATCG ACTTGCTGTG      350
45    TCCGTTTGCA AAAGGCGGTA AAGTAGGTCT GTTCGGCGGT GCCGGTGTGG      400
      GCAAACCGT AAACATGATG GAATTGATCA ACAACATCGC CAAAGCACAC      450
      AGCGGTCTGT CTGTGTTTGC CGGTGTAGGT GAACGTACCC GCGAAGGTAA      500
      CGACTTCTAC CACGAGATGA AAGATTCCAA CGTGTTGGAT AAAGTAGCCA      550
      TGGTGTACGG TCAGATGAAT GAGCCGCCGG GCAACCGCTT GCGCGTGGCT      600
50    TTGACCGGCC TGACTATGGC CGAATACTTC GTGACGAAA AGACGAAAAC      650
      GGCAAAGGTC GTGACGTATT GTTCTTCGTG GACAACATTT ACCGCTACAC      700
      ACTGGCCGGT ACCGAAGTAT CAGCATTTGT GGGCCGTATG CCGTCTGCAG      750
      TAGGTTATCA GCCGACATTG GCAGAGGAAA TGGGTCGCTT GCAAGAGCGT      800
      ATTACCTCTA CCCAAACCGG TTCGATTACC TCT      833

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55

2) INFORMATION FOR SEQ ID NO: 759

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      (i) SEQUENCE CHARACTERISTICS:

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60

(A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Proteus penneri*
 (B) STRAIN: ATCC 33519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 759

15	AGCGTCCCTA	AAGTATACGA	CGCTCTTGAG	GTTATGAATG	GTAAAGAAAA	50
	ACTGGTGCTG	GAAGTTCAGC	AACAGTTAGG	CGGTGGTATC	GTTTCGTTGTA	100
	TCGCAATGGG	TACATCAGAC	GGTTTAAGCC	GTGGCTTAAA	AGTTGAAGAT	150
	TTAGGCCACC	CAATTGAAGT	ACCAGTAGGT	AAAGCAACAC	TGGGACGTAT	200
	CATGAACGTT	CTGGGTACAC	CTATTGATAT	GAAAGGTGAT	ATTGCAACTG	250
	AAGAACGTTG	GTCTATTCAC	CGTGAAGCAC	CAACCTACGA	AGAGTTATCA	300
20	AACTCACAAG	AACTGCTTGA	AACCGGTATC	AAAGTAATGG	ACTTAATCTG	350
	TCCGTTTGCT	AAAGGTGGTA	AAGTAGGTCT	GTTTCGGTGGT	GCGGGTGTGG	400
	GTAAACACAG	TAACATGATG	GAATTGATCC	GTAATATCGC	GATCGAGCAC	450
	TCAGGTTACT	CTGTATTTGC	TGGTGTGGT	GAGCGTACTC	GTGAGGGTAA	500
	CGACTTCTAT	CATGAAATGA	CAGATTCTAA	CGTTCTTGAC	AAAGTATCGT	550
25	TAGTTTATGG	TCAGATGAAT	GAGCCACCAG	GAAACCGTCT	GCGTGTAGCA	600
	CTGACTGGTC	TGACTATGGC	TGAAAAATTC	CGTGATGAAG	GCCGTGACGT	650
	ACTGTTATTC	GTCGATAACA	TTTATCGTTA	CACCTTAGCC	GGTACAGAAG	700
	TATCAGCACT	GTTAGGTCGT	ATGCCATCAG	CGGTAGGTTA	CCAGCCAACA	750
	TTGGCTGAAG	AGATGGGTGT	TCTGCAAGAA	CGTATCACTT	CAACCAAAAC	800
30	AGGTTCAATC	ACCTCTGTA				819

2) INFORMATION FOR SEQ ID NO: 760

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 819 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype *enteritidis*
 (B) STRAIN: ATCC 13076

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 760

50	GCCGTACCAC	GCGTGTACGA	TGCCCTTGAG	GTGCAGAATG	GTAATGAGAA	50
	GCTGGTGCTG	GAAGTTCAGC	AGCAGCTTGG	CGGCGGTATC	GTGCGTACCA	100
	TCGCGATGGG	GTCTTCTGAC	GGTCTGCGTC	GCGGTCTGGA	TGTAAAAGAT	150
	CTCGAACACC	CGATCGAAGT	CCCGGTAGGT	AAAGCCACGC	TGGGTCGTAT	200
55	CATGAACGTC	CTGGGCGAAC	CGGTCGACAT	GAAAGGCGAG	ATCGGCGAAG	250
	AAGAGCGTTG	GGCGATTAC	CGCGCAGCAC	CTTCCTACGA	AGAGTTGTCA	300
	AACTCTCAGG	AACTGCTGGA	AACCGGTATC	AAAGTTATCG	ACCTGATGTG	350
	TCCGTTTCGG	AAGGGCGGTA	AAGTCGGTCT	GTTTCGGTGGT	GCGGGTGTAG	400
	GTAAACCGGT	AAACATGATG	GAGCTTATTC	GTAACATCGC	GATCGAGCAC	450
60	TCCGGTTACT	CAGTGTGTTG	GGGCGTAGGG	GAACGTACTC	GTGAGGGTAA	500

	CGACTTCTAC	CACGAAATGA	CCGACTCCAA	CGTTATCGAT	AAAGTATCCC	550
	TGGTGTATGG	CCAGATGAAC	GAGCCGCCGG	GAAACCGTCT	GCGCGTTGCA	600
	CTGACCGGCC	TGACCATGGC	GGAGAAATTC	CGTGACGAAG	GTCGTGACGT	650
	ACTGCTGTTC	GTCGATAACA	TCTATCGTTA	CACCCTGGCC	GGTACGGAAG	700
5	TATCCGCACT	GCTGGGCCGT	ATGCCTTCCG	CAGTAGGTTA	CCAGCCGACT	750
	CTGGCGGAAG	AGATGGGCGT	TCTGCAGGAA	CGTATCACCT	CCACCAAAAC	800
	CGGTTCTATC	ACCTCCGTA				819

10

2) INFORMATION FOR SEQ ID NO: 761

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 812 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia pestis*
- (B) STRAIN: RRBK1M27

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 761

	ACCAAAAGTG	TACAACGCCC	TTGAGGTAGA	AGGTACAAC	GAAAAGTTAG	50
	TGCTGGAAGT	TCAGCAACAG	TTGGGCGGTG	GTGTTGTTTCG	TTGTATCGCA	100
	ATGGGCTCTT	CCGATGGTCT	GAGCCGTGGG	TTGAAAGTAA	CCAACCTAGA	150
30	ACACCCGATC	GAAGTACCGG	TTGGTAAAGC	GACCCTTGGC	CGTATCATGA	200
	ACGTATTGGG	TGAACCAATC	GACATGAAAG	GTCCTATCGG	TGAAGAAGAG	250
	CGTTGGGCAA	TCCATCGCGA	AGCGCCTTCT	TATGAAGAGC	TTGCTAGCTC	300
	ACAAGATCTG	TTAGAAACCG	GTATCAAGGT	TATGGACCTG	ATTTGTCCGT	350
	TTGCTAAGGG	CGGTAAAGTC	GGTCTGTTTCG	GTGGTGCGGG	TGTAGGTAAA	400
35	ACAGTAAACA	TGATGGAGCT	GATCCGTAAC	ATCGCGATCG	AGCACTCTGG	450
	GTATTCTGTA	TTTGCCCGTG	TAGGTGAGCG	TACCCGTGAG	GGTAATGACT	500
	TCTACCATGA	AATGACTGAC	TCCAACGTTT	TGGACAAAGT	ATCCTTGTTT	550
	TACGGCCAGA	TGAATGAGCC	ACCAGGTAAC	CGTCTACGCG	TTGCACTGAC	600
	CGGCCTGACC	ATGGCGGAGA	AATTCCGTGA	TGAAGGTCGT	GACGTACTGC	650
40	TGTTTATCGA	TAATATCTAT	CGTTATACCC	TAGCTGGTAC	GGAAGTATCC	700
	GCATTGCTGG	GTCGTATGCC	ATCAGCGGTA	GGTTATCAGC	CAACACTGGC	750
	TGAAGAGATG	GGTGTGTTGC	AGGAACGTAT	TACTTCCACT	AAGACGGGTT	800
	CAATCACCTC	TG				812

45

2) INFORMATION FOR SEQ ID NO: 762

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 408 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Burkholderia mallei*
- (B) STRAIN: GB8

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 762

```

5  CGACGTGATC GAGCCCTTCT TCGTCGACGT GATGCGCTCT TGCAGCTTGC 50
   CCATTTCTTC AGCCAGCGTC GGCTGATAGC CCACTGCCGA CGGCATACGG 100
   CCGAGCAGCG CCGACACTTC GGTACCGGCC AGCGTGAAAC GGTAGATGTT 150
   GTCGACGAAG AACAGCACGT CGAGGCCTTC GTCACGGAAG TGCTCGGCCA 200
   TCGTGAGGCC CGTCAGCGCC ACGCGCAGAC GGTGCCCCGG CGGCTCGTTC 250
   ATCTGGCCGT ACACCAGCGC GACCTTGTCG AGAACGTTTC AGTCCTTCAT 300
   TTCGTGGTAG AAGTCGTTCC CTTACGGGT ACGCTCGCCC ACGCCCGCGA 350
10 ACACGGAGTA ACCGCCGTGC TCCTTCGCGA TGTGTTGAT GAGCTCCATC 400
   ATGTTGAC 408

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15 2) INFORMATION FOR SEQ ID NO: 763

(i) SEQUENCE CHARACTERISTICS:

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20  (A) LENGTH: 400 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

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    (A) ORGANISM: Clostridium sordellii
    (B) STRAIN: ATCC 9714

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 763

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30  GAACTTATAA ACAACATAGC TACTCAACAT GGTGGTATAT CAGTATTCGC 50
   AGGTGTTGGA GAGAGAACAA GAGAAGGTAA CGACCTTTAC GGAGAAATGA 100
   GTGAGTCTGG AGTTATAAAC AAGACAGCTC TAGTATTCGG ACAAATGAAT 150
   GAGCCACCTG GAGCAAGAAAT GAGAGTTGCT TTAAGTGGTC TTACAATGGC 200
35  TGAATATTTT AGAGATCAAG AAGGACAAGA CGTTTTATTA TTCGTAGATA 250
   ATATATTCCG TTCTACTCAA GCAGGATCTG AGGTTTCTGC ACTTCTTGGA 300
   CGTACTCCAT CAGCAGTTGG ATACCAACCA ACATTAGCTA CAGAGATGGG 350
   TAGATTACAA GAGAGAATAA CATCTACAA TAAAGGTCT ATAACATCAG 400

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40

2) INFORMATION FOR SEQ ID NO: 764

(i) SEQUENCE CHARACTERISTICS:

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45  (A) LENGTH: 405 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear

```

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

```

    (A) ORGANISM: Clostridium novyi
    (B) STRAIN: ATCC 19402

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55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 764

```

   TTAATTCAAG AATTAATCAA CAATATAGCG AAGGAACACG GTGGATTATC 50
   TGTATTTACA GGAGTTGGAG AAAGAACAAG AGAAGGTAAT GACCTTTACT 100
60  ATGAAATGAA AGAATCTGGT GTTATAAATA AAACAGCACT AGTATTTGGT 150

```


	CAAATGAATG	AGCCACCTGG	AGCAAGAATG	AGAGTTGCTC	TTACAGGACT	200
	TACTATGGCA	GAATATTTCA	GGGATCAAGG	ACAAAACGTA	CTTTTATTTCA	250
	TAGACAACAT	ATTTAGATTG	ACTCAAGCAG	GTTTCAAGGT	GTCAGCTTTA	300
	CTTGGAAGAA	TACCTAGTGC	CGTTGGATAC	CAACCAACAC	TAGCAACAGA	350
5	AATGGGTGCG	CTTCAAGAAA	GAATAACATC	TACAAAGCAT	GGTTCTATAA	400
	CATCA					405

10 2) INFORMATION FOR SEQ ID NO: 765

(i) SEQUENCE CHARACTERISTICS:

	(A)	LENGTH: 393 bases
	(B)	TYPE: Nucleic acid
15	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Clostridium botulinum</i>
	(B)	STRAIN: 20:3.1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 765

25	AATTAATAAA	TAACATAGCT	AAAGAACATG	GTGGATTATC	AGTGTTTACT	50
	GGAGTTGGAG	AAAGATCTAG	AGAAGGTAAT	GATCTTTATC	ATGAAATGAG	100
	AGAATCAGGC	GTTATAGATA	AAACCGCATT	AGTATTTGGT	CAAATGAATG	150
	AGCCACCTGG	TGCTAGAATG	AGAGTTGCAT	TAACAGGGTT	AACTATGGCT	200
30	GAATATTTTA	GAGATAAAGG	TCAAGATGTA	TTACTATTTA	TAGATAATAT	250
	ATTTAGATTT	ACTCAAGCTG	GATCAGAAGT	TTCAGCATTA	CTTGGAAGAA	300
	TACCATCAGC	AGTTGGTTAC	CAACCAACTT	TAGCAACTGA	AATGGGTGCA	350
	CTTCAAGAGA	GAATTACATC	AACTAAGAAT	GGTTCTATAA	CAT	393

35

2) INFORMATION FOR SEQ ID NO: 766

(i) SEQUENCE CHARACTERISTICS:

40	(A)	LENGTH: 399 bases
	(B)	TYPE: Nucleic acid
	(C)	STRANDEDNESS: Double
	(D)	TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

	(A)	ORGANISM: <i>Clostridium histolyticum</i>
	(B)	STRAIN: ATCC 19401

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 766

	AGGAACTTAT	AAATAATATT	GCAAAACAAT	ATGGAGGTCT	ATCTGTATTT	50
	ACAGGTGTTG	GTGAAAGAAC	AAGAGAAGGT	AATGACCTAT	ATAATGAAAT	100
55	GAAAGATTCT	GGGGTTATAG	AGAAAAGTGC	ACTAGTATTT	GGACAGATGA	150
	ATGAACCACC	AGGAGCGAGA	ATGAGAGTAG	CATTGACAGG	ACTTACTATG	200
	GCAGAATATT	TTAGAGATCA	AGGGCAAGAT	GTACTTTTAT	TTATAGATAA	250
	TATATTTAGA	TTTACGCAGG	CTGGTTCTGA	AGTTTCTGCA	TTGTTAGGAA	300
	GAATTCCAAG	TGCAGTTGGA	TATCAACCAA	CCCTTGCAAC	TGAAATGGGT	350
60	GCATTACAAG	AAAGAATAAC	ATCCACAAAA	AATGGATCAA	TTACTTCAG	399

2) INFORMATION FOR SEQ ID NO: 767

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Peptostreptococcus prevotii*
 (B) STRAIN: ATCC 9321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 767

20	CATGATGGAA	CTGATCCGTA	ACATCGCCAT	CGAGCACAGC	GGTTATTCCG	50
	TGTTCCGCCGG	TGTGGGTGAG	CGTACTCGTG	AGGGTAACGA	CTTCTACCAC	100
	GAGATGAAGG	ACTCCAACGT	TCTGGACAAA	GTGGCACTGG	TCTACGGTCA	150
	GATGAACGAG	CCGCCGGGTA	ACCGTCTGCG	CGTAGCACTG	ACTGGCCTGA	200
	CCATGGCCGA	GAAGTTCCGT	GACGAAGGTA	ACGACGTTCT	GTTGTTTCGTC	250
25	GACAACATCT	ACCGTTACAC	CCTGGCCGGT	ACTGAAGTAT	CCGCACTGCT	300
	GGGCCGTATG	CCTTCGGCAG	TAGGTTACCA	GCCGACCCTG	GCTGAAGAGA	350
	TGGGCGTTCT	GCAAGAACGT	ATCACTTCGA	CCAAGGAAGG		390

2) INFORMATION FOR SEQ ID NO: 768

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 953 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Absidia corymbifera*
 (B) STRAIN: ATCC 46775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 768

	AGGTCTTGTT	CGTGGCAAAA	GGTCATTGAC	ACTGGTGCTC	CTATCACCAT	50
	TCCTGTTGGT	AACGAAGTCC	TTGGTCGTAT	CATTAACGTC	ATTGGTGAGC	100
	CCATTGATGA	GCGTGGTCCY	ATCAAGTCCA	AGGCCACTCG	TGCTATCCAC	150
50	GCTGATGCTC	CCGAGTTCGT	TGATCAATCC	CCCACTCCCG	AGATTCTCGA	200
	GACTGGTATC	AAGGTTGTCT	ATTGCTTGC	TCCCTATGCT	CGTGGTGCTA	250
	AGATTGGTCT	TTTCGGTGGT	GCCGGTGTCT	GCAAGACTGT	CTTGATTCAA	300
	GAATTGATCA	ACAACATTGC	CAAGGCTCAC	GGTGGTTACT	CTATCTTCTG	350
	TGGTGTCGGT	GAACGTACTC	GTGAAGGCAA	CGATTTGTAC	CACGAAATGA	400
55	TTTCCACTGG	TGTCATCAAG	CTTGAAGGTG	AATCCAAGTG	TGCTCTTGTC	450
	TTTGGTCAAA	TGAACGAACC	CCCCGGAGCT	CGTGCCCGTG	TTGCCTTGAC	500
	TGGTTTGACC	ATTGCCGAAT	ACTTCCGTGA	TGAGGAAGGT	CAAGATGTGT	550
	TGCTCTTCAT	TGACAACATT	TTCCGTTTCA	CTCAAGCCGG	TTCTGAAAGT	600
	TCCGCTTTGC	TTGGTCGTAT	TCCCTCTGCT	GTCGGTTACC	AACCCACTCT	650
60	YTCCACTGAT	ATGGGTGGTA	TGCAAGAGCG	TATTACTACC	ACCAAGAACG	700

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5 GTTCCATTAC CTCCGTGCAA GCTGTCTACG TCCCTGCTGA CGATTTGACT 750
  GATCCTGCTC CTGCTACTAC TTTTGCTCAC TTGGACGCCA CCACTGTGTT 800
  GTCTCGTTCC ATTGCTGAGT TGGGTATCTA CCCTGCTGTC GATCCCCTTG 850
  ACTCCAAGTC CCGTATCTTG GATCCCCGTA TCGTTGGTGA TGAGCACTAC 900
  TCTGTTGCCA CTGGTGTCCA ACAAATCCTT CAAAACCTACA AGTCGCTTCA 950
  AGA 953

```

10 2) INFORMATION FOR SEQ ID NO: 769

(i) SEQUENCE CHARACTERISTICS:

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15 (A) LENGTH: 1343 bases
  (B) TYPE: Nucleic acid
  (C) STRANDEDNESS: Double
  (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: Genomic DNA

20 (vi) ORIGINAL SOURCE:

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  (A) ORGANISM: Alternaria alternata
  (B) STRAIN: ATCC 62099

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 769

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25 CGCGGTTCCA AGGCCACCGA CACCGGTGCC CCCATCAAGA TTCCCGTTGG 50
  TCACGGTACC CTTGGTCGTA TCATGAACGT CACTGGTGAC CCCATTGACG 100
  AGCGTGGTCC CATCAAGGCC ACCAAGTACG CTCCCATCCA CGCCGACCCC 150
  CCGGAGTTCA CCGAGCAATC CACCTCCGCT GAGGTCCTCG TTACCGGTAT 200
30 CAAGGTTGTC GACCTGTTGG CTCCTTACGC TCGTGGTGGA AAGATTGGTC 250
  TCTTCGGAGG TGCTGGTGTC GGAAAGACTG TCTTCATTCA GGAGCTGATT 300
  GTAAGGAGAC AACTGTCTA CTGGCTGAGC ATTAGCTAAC GGCAGGCAGA 350
  ACAACATCGC CAAGGCCAC GGTGGTTTCT CTGTCTTCAC TGGTGTCCGT 400
  GAGCGTACCC GTGAGGGTAA CGATCTGTAC CACGAGATGC AGGAGACTTC 450
35 CGTCATTAG CTTGACGGTG ACTCCAAGGT CGCCCTCGTC TTCGGTCAGA 500
  TGAACGAGCC CCCGGGTGCC CGTGCCCGTG TCGCTCTTAC TGGTCTTACT 550
  GTTGCTGAGT AAGTCTTGAA TTCACTGTGT TGACAACGTC GTGGCTAATG 600
  GGAAAAAAGA TACTTCCGTG ACGAAGAGGG ACAGGATGTG CTTCTCTTCA 650
  TCGACAGTAA GTGCTGTGAC GAATGCCTG TGAGACATAC ACTGACTTCG 700
40 GCAATAGACA TTTTCCGTTT CACCCAGGCC GGTTCGAGG TGTCCGCTCT 750
  TCTTGGTCGT ATCCCCTCTG CCGTCGGTTA CCAGCCACC CTCGCCATTG 800
  ACATGGGTGT CATGCAGGAG CGTATTACCA CCACCACCAA GGGTTCCATC 850
  ACCTCCGTCC AGGCCGTCTA CGTGCCCGCT GACGATTGTA CTGACCCCTGC 900
  CCCC GCCACC ACCTTCGCCC ATTTGGACGC CACCACTGTC TTGTCCCGTG 950
45 GTATCTCCGA GTTGGGTATC TACCCCGCCG TCGACCCTCT TGACTCCAAG 1000
  TCCCGTATGT TGGACCCCCG TGTCAATTGGT CAGGACCACT ACGACACCGC 1050
  CACCCGCGTT CAGCAGATT TCCAGGAGTA CAAGTCGCTC CAGGATATCA 1100
  TTGCCATTCT CGGTATGGAC GAGTTGTCGG AAGCTGACAA GCTTACCGTC 1150
  GAGCGTGCCC GTAAGATCCA GCGTTTCTTG AGCCAGCCTT TCGCTGTCGC 1200
50 CCAGGTCTTC ACTGGTATTG AGGGCAAGCT TGTGACCTC AAGGACACCA 1250
  TCCGATCATT CAAGGCTATC TTGACTGGTG AGGGTGACGA CCTTCCCGAG 1300
  GGTGAGTCTC GACTATCTCC GCATTATAG CGTATAACTG ACA 1343

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2) INFORMATION FOR SEQ ID NO: 770

(i) SEQUENCE CHARACTERISTICS:

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60 (A) LENGTH: 480 bases
  (B) TYPE: Nucleic acid

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(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Aspergillus flavus*

(B) STRAIN: ATCC 26947

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 770

	TTCAGGAGTT	GATTGTATGT	TCACCTGCAA	CATAAGACTT	CCCATTCTCC	50
	ACTCTTTTCT	AACTCTTCAC	AGAACAACAT	TGCCAAGGCT	CACGGTGGTT	100
	ACTCTGTCTT	CACTGGTGTC	GGTGAGCGTA	CCCGTGAGGG	TAACGATCTG	150
15	TACCACGAAA	TGCAGGAGAC	TGGTGTCAAT	CAGCTCGAGG	GTGAATCTAA	200
	GGTCGCCCTT	GTCTTCGGTC	AGATGAACGA	GCCCCAGGT	GCCCCGTGCC	250
	GTGTCGCCCT	TACCGGTCTG	ACCATCGCCG	AGTACTTCCG	TGACGAGGAA	300
	GGTCAGGATG	TGCTGCTCTT	CATTGACAAC	ATTTTCCGTT	TCACCCAGGC	350
	CGGTTCTGAG	GTGTCTGCCC	TTCTTGGTCG	TATCCCCTCC	GCTGTCGGTT	400
20	ACCAGCCCAC	TCTGGCCGTC	GACATGGGTG	GTATGCAGGA	GCGTATTACC	450
	ACCACCACCA	AGGGTTCCAT	TACCTCCGTC			480

25 2) INFORMATION FOR SEQ ID NO: 771

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1174 bases

(B) TYPE: Nucleic acid

30 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

35 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mucor circinelloides*

(B) STRAIN: ATCC 38592

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 771

40	CTCGAACAAG	AYAACTTGCC	YGCCATTTTG	AACGCCCTTG	AAGTCAAGGA	50
	YCACTCTGGT	GGACGTCTCG	TYCTCGAAGT	CTCTCAACAT	TTGGGTGAGA	100
	ACACTGTCCG	TACTATTGCT	ATGGATGGTA	CTGAAGGTAA	GTTATGTYCA	150
	TCCCANNGGA	TACAGTCARA	CAGMAATGTC	TAGTGGTTAT	AGCAGYAGCA	200
45	GATGATTGAC	CAATATGTTA	GGTCTTGTC	GGTGGTCAA	AGGTTGTTGA	250
	CACTGGTGCT	CCCATTACCA	TCCCCGTTGG	TAAGGAAGTC	CTTGGTCGTA	300
	TCATCAACGT	TATTGGTGAA	CCCATTGATG	AACGTGGTCC	CATTGACGCC	350
	AAGACTCACC	GTCTATTCA	CGCTGAAGCT	CCCGAATTCT	TTGATCAATC	400
	CCCCACTCCC	GAAATCCTCG	AGACTGGTAT	CAAGGTYGTC	GATTTGTTGG	450
50	CTCCTTATGC	TCGTGGTGGT	AAGATTGGTC	TCTTCGGTGG	TGCTGGTGTC	500
	GGTAAGACTG	TCTTGATTCA	AGAATTGATT	AACAACATYG	CCAAGGCTCA	550
	CGGTGGTTAC	TCTATCTTCT	GTGGTGTCGG	TGAACGTACT	CGTGAGGGTA	600
	ACGATTTGTA	CCATGAAATG	ATTGAAACCG	GTGTCATTCA	ATTGGAAGGC	650
	GAGTCCAAGT	GTGCTCTCGT	CTTTGGTCAA	ATGAACGAAC	CCCCAGGTGC	700
55	TCGTGCCCCG	GTGCTTTTGA	CTGGTTTGAC	TATTGCTGAA	TACTTCCGTG	750
	ATGATGAGGG	TCAAGATGTC	TTGCTTTTCA	TTGATAACAT	TTTCAGATTC	800
	ACTCAAGCTG	GTTCTGAGGT	ATCTGCCCTT	TTGGGTCGTA	TTCTTCCGC	850
	TGTCGGTTAC	CAACCCACTC	TTTCCACYGA	TATGGGTGGT	ATGCAAGAGC	900
	GTATTACTAC	CACCAAGAAC	GGTTCCATTA	CCTCCGTCCA	AGCTGTCTAC	950
60	GTCCCTGCTG	ATGATTTGAC	CGATCCTGCT	CCTGCCACCA	CTTTTGCTCA	1000

CTTGGATGCC	ACCACTGTCT	TGTCTCGTTC	CATCGCTGAA	TTGGGTATCT	1050
AYCCCGCTGT	CGATCCTCTT	GATTCCAAGT	CTCGTATCCT	CGATCCCCGT	1100
ATTGTCGGTG	ATGAGCACTA	CAAGGTTGCC	ACTGAAGTTC	AACAAATCCT	1150
CCAAAACACTAC	AAGTCTCTCC	AAGA			1174

5

2) INFORMATION FOR SEQ ID NO: 772

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Piedraia hortai*
 (B) STRAIN: ATCC 24292

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 772

AGGAGCTTAT	CAACAACATC	GCCAAGGCTC	ACGGTGGTTA	CTCCGTCTTC	50
ACTGGTGTCTG	GTGAGCGTAC	TCGTGAGGGT	AACGATTTGT	ACCACGAGAT	100
GCAAGAGACT	TCCGTCATTC	AGCTTGACSG	CGAGTCCAAG	GTCGCTCTCG	150
TGTTTCGGTCA	GATGAACGAG	CCCCCGGGTG	CCCGTGCCCG	TGTTGCCCTG	200
ACTGGTCTTA	CCATCGCTGA	GTACTTCCGT	GATGCCGAGG	GTCAGGATGG	250
TAAGTTCTAT	AACTCTTGTC	GCAAAGGTTT	CATTCTGGTC	GCTAACTTGC	300
TCAGTGCTCC	TGTTTCATCGA	CAACATTTTC	CGTTTCACCC	AGGCTGGTAT	350
GGAGGTGTCT	GCCCTCCTCG	GTCGTATTCC	TTCTGCCGTC	GGTTACCAAC	400
CTACTCTCGC	CGTCGACATG	GGTGGTATGC	AAGAGCGTAT	TACCACTACC	450
AAGAAGGGAT	CCATTAC				467

35

2) INFORMATION FOR SEQ ID NO: 773

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudallescheria boydii*
 (B) STRAIN: ATCC 44331

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 773

TTGCCAAGGC	CCACGGTGGT	TACTCTGTCT	TCACTGGTGT	CGGTGAGCGT	50
ACCCGTGAGG	GTAACGATCT	GTACCACGAA	ATGCAGGAAA	CCTCCGTCAT	100
TCAGCTTGAT	GGCGAGTCCA	AGGTCGCGCT	TGTCTTCGGT	CAGATGAACG	150
AGCCCCCTGG	TGCCCCGTGCT	CGTGTCGCTC	TTACTGGTCT	TACCGTTGCC	200
GAGTACTTCC	GTGATGAGGA	GGGTCAGGAT	GGTAAGTTAT	ATCGTTTTTA	250
TTATCTTCTT	TGCCACCACC	CCTCTACGAA	TCCATGCCTC	CGTTGGTGAA	300
GGCATCGTTT	GTAGGGCGGG	TCGGAGTTTG	CGGCAATTTT	TGCCGTCGGC	350
TTGAAGCCGC	GGATGCCCGA	TGTTTGACGC	GTATCGATGC	TAACAACAAT	400

60

GACAACAGTG	CTTCTCTTCA	TTGACAACAT	TTTCCGATTC	ACCCAGGCCG	450
GTTCCGAGGT	GTCTGCCCTT	CTCGGTCGTA	TTCCCTCTGC	CGTCGGTTAC	500
CAGCCCACTC	TTGCCGTAGA	CATGGGTGCC	ATGCAGGAAC	GTATTACCAC	550
CACCAAGAAG	GGTTCGATTA	CCTCCGTC			578

5

2) INFORMATION FOR SEQ ID NO: 774

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1123 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

20 (A) ORGANISM: *Rhizopus oryzae*
 (B) STRAIN: ATCC 56015

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 774

AACTTACCYG	CTATCTTGAA	CGCTCTCGAA	GTCCAAGATC	ACTCTGGTGG	50
ACGTCTTGTC	CTTGAAGTTC	GCTCAACACT	TGGGTGAAAA	TACTGTCCGT	100
ACTATTGCTA	TGGATGGTAC	TGAAGGTAAG	CTATACTATA	ACCGTKTTAT	150
CCGAGTATGA	TATTAACCTG	AAAAAAGGTC	TCGTYCGTGG	TCAAAAGGTT	200
ATTGACACTG	GTGCTCCCAT	TACCATTCCT	GYTGGTAAGG	AAGTTCTCGG	250
TCGTATCATT	AACGTCATTG	GTGAACCCAT	CGATGAACGT	GGTCCTATCA	300
ACGCCAAGAG	CCAACGTCCC	ATTCACGCCG	AAGCTCCCGA	ATTCGTTGAC	350
CAATCTCCTA	CTCCCGAAAT	TCTTGAAACT	GGTATCAAGG	TTGTCGACTT	400
GTTGGCTCCT	TATGCTCGTG	GTGGTAAGAT	TGGTCTTTTC	GGTGGTGCTG	450
GTGTCGGTAA	GACTGTGTTG	ATTCAAGAAT	TGATTAACAA	CATCGCCAAG	500
GCTCACGGTG	GTTACTCTAT	TTTCTGTGGT	GTCGGTGAAC	GTACTCGTGA	550
AGGTAACGAT	CTTTACCACG	AAATGATTGA	AACTGGTGTC	ATCAAGCTCG	600
ATGGTGACTC	CAAGTGTGCT	CTTGTCTTTG	GTCAAATGAA	CGAACCCCA	650
GGAGCTCGTG	CCCGTGTTGC	CTTGACTGGT	TTGACCATTG	CTGAATACTT	700
CCGTGATGAT	GAAGGTCAAG	ATGTGTTGCT	TTTCATTGAT	AACATTTTCC	750
GTTTCACCCA	AGCTGGTTCW	GAAGTATCTG	CCCTTTTGGG	TCGTATTCCC	800
TCCGCTGTGC	GTTACCAACC	CACTCTTTCT	ACTGATATGG	GTGGTATGCA	850
AGAACGTATT	ACAACCACCA	AGAACGGTTC	CATTACATCC	GTCCAAGCTG	900
TCTACGTCCC	TGCTGATGAT	TTGACCGATC	CTGCTCCCGC	CACCACTTTT	950
GCTCACTTGG	ATGCCACCAC	TGTCTTGTCT	CGTTCCATTG	CCGAATTGGG	1000
TATTTACCCT	GCCGTCGATC	CTCTTGAYTC	CAAGTCTCGT	ATCTTGGATC	1050
CTCGTATCGT	TGGTGACGAA	CACTACAAGG	TCGCTACCGA	AGTTCAACAA	1100
ATCCTTCAAA	ACTACAAGTC	TCT			1123

50 2) INFORMATION FOR SEQ ID NO: 775

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 477 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

60 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Scopulariopsis koningii*

(B) STRAIN: ATCC 38745

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 775

5
 ATTCAGGAGC TCATCAACAA CATTGCCAAG GCTCACGGTG GTTACTCTGT 50
 GTTCACTGGT GTCGGTGAGC GTACCCGTGA GGGTAACGAT CTGTACCACG 100
 AAATGCAGGA GACTTCGGTC ATTCACTCG AGGGCGAGTC CAAGGTCGCG 150
 CTTGTGTTTC GTCAGATGAA CGAGCCCCC GGTGCCCCGTG CCCGTGTCTGC 200
 10 CCTTACCGGT CTGACCGTTG CCGAGTACTT CCGTGACGAG GAGGGCCAGG 250
 ATGGTGAGTA ACCGACGAAG TCTGAGATCT TGTCGGGCAT TATTCTAACG 300
 ACAACTAGTG CTTCTCTTCA TCGACAACAT TTTCCGCTTC ACCCAGGCCG 350
 GTTCCGAGGT GTCCGCGCTT CTCGGCCGTA TCCCCTCTGC CGTCGGTTAC 400
 CAGCCCACCC TGGCCGTCGA CATGGGAGGT ATGCAGGAGC GTATTACCAC 450
 15 GACTCAGAAG GGCTCGATTA CCTCGGT 477

2) INFORMATION FOR SEQ ID NO: 776

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 610 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

30

- (A) ORGANISM: *Trichophyton mentagrophytes*
 (B) STRAIN: ATCC 8125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 776

35 TCCGGAGTTG ATTGTAAGTC ATTTGAAACC CAGCCCCAAG AAACAGAAGC 50
 TAGGCGAAAA TTGGACAATT GAGCAATTTA GCCATTGGAG AAAAGAAATT 100
 TCGAGTATTA ATTGTTTTTA TAGAACAACA TTGCCAAGGC TCACGGTGGT 150
 TACTCTGTCT TCACTGGTGT CGGAGAGCGT ACCCGTGAAG GAAACGATCT 200
 CTACCATGAA ATGCAGGAGA CCCGTGTCAT TCAGCTTGAT GGCGAGTCCA 250
 40 AGGTCGCCCT GGTCTTCGGC CAGATGAACG AGCCCCCAGG TGCCCGTGCC 300
 CGTGTGCTC TTACTGGTTT GACCATTTGCT GAGTACTTCC GTGATGAGGA 350
 AGGTCAAGAC GGTGAGTTTY TTATGGATAA AARATTTTTT TTTTTTTTTT 400
 TTTTTTMAAR AAATTCATGT TCTAACAAAG TATATCCTAG TGCTTCTCTT 450
 CATCGACAAC ATTTTCCGTT TCACTCAGGC TGGTTCCGAA GTGTCTGCCC 500
 45 TGCTTGGTCTG TATCCCATCT GCCGTCGGTT ACCAACCAC TCTTGCCGTC 550
 GACATGGGTG GTATGCAGGA ACGTATTACC ACCACCAAGA AGGGATCCAT 600
 TACCTCCGTC 610

50

2) INFORMATION FOR SEQ ID NO: 777

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 593 bases
 55 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichophyton tonsurans*
 (B) STRAIN: ATCC 56185

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 777

	GGAGTTGATT	GTAAGTCATT	TGAAACCCAG	CCCCAAGAAA	CAGAAGCTAG	50
	GTGAAAATTG	GACAATTGAA	CAATTTAGCC	CTTGGAGAAA	AGAAATTTTCG	100
	AGTATTAATT	ATTTTATAG	AACAACATTG	CCAAGGCTCA	CGGTGGTTAC	150
10	TCTGTCTTCA	CTGGTGTGCG	AGAGCGTACC	CGTGAAGGAA	ACGATCTCTA	200
	CCATGAAATG	CAGGAGACCC	GTGTCATTCA	GCTTGATGGC	GAGTCCAAGG	250
	TCGCCCTGGT	CTTCGGCCAG	ATGAACGAGC	CCCCAGGTGC	CCGTGCCCGT	300
	GTTGCTCTTA	CTGGTTTGAC	CATTGCTGAG	TACTTCCGTG	ATGAGGAAGG	350
	TCAAGACGGT	GAGTTTCTTA	TGGATGAAAG	ATTTTTTTTT	TTCAAGAAAT	400
15	TCATGTTCTA	ACAAAGTGTA	TTCTAGTGCT	TCTCTTCATC	GACAACATTT	450
	TCCGTTTCAC	TCAGGCTGGT	TCCGAAGTGT	CTGCCCTGCT	TGGTCGTATC	500
	CCATCTGCCG	TCGGTTACCA	ACCCACTCTT	GCCGTCGACA	TGGGTGGTAT	550
	GCAGGAACGT	ATTACCACCA	CCAAGAAGGG	ATCCATTACC	TCC	593

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2) INFORMATION FOR SEQ ID NO: 778

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 1141 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

30 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trichosporon cutaneum*
 (B) STRAIN: ATCC 62965

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 778

	CCGTGGTCAA	GAAGTTATTG	ACACTGGTGC	CCCAATTACC	ATTCCTGTTG	50
	GTCGTGGTAC	TCTTGGTAGA	ATTATCAACG	TCATGGGTGA	ACCAATTGAC	100
40	GAACGTGGCC	CTATCAAGGC	TTCTAAGTAT	GCTCCTATCC	ATACTGAACC	150
	ACCAACCTTT	GCTGAACAA	CTACTTCTGC	TGAAGTTCTT	GAAACCGGTA	200
	TCAAGGTTGT	CGATCTTCTT	GCTCCTTACG	CCCGTGGTGG	TAAGATTGGT	250
	CTTTTCGGTG	GTGCTGGTGT	CGGTAAGACT	GTCTTCATTC	AAGAACTTAT	300
	TAACAACATT	GCCAAGGCTC	ACGGTGGTTT	CTCTGTCTTC	ACTGGTGTCTG	350
45	GTGAAAGAAC	CCGTGAAGGT	AACGATCTTT	ACCGTGAAAT	GAAGGAAACT	400
	GGTGTCATCA	ACCTCGAAGG	TGACTCCAAG	GTCGCTCTCG	TTTTCGGTCA	450
	AATGAACGAA	CCTCCAGGTG	CCCGTGCCCC	TGTCGCTTTG	ACTGGTCTTA	500
	CCATTGCCGA	ATACTTCCGT	GATGAAGAAG	GACAAGATGT	CTTGCTTTTC	550
	GTTGACAACA	TTTTTCAGATT	CACCCAAGCC	GGTTCTGAAG	TCTCTGCTCT	600
50	TTTGGGTCTG	ATTCCATCTG	CCGTCGGTTA	CCAACCTACC	CTTGCTACCG	650
	ATATGGGTGC	CCTCCAAGAA	CGTATTACCA	CCACCCAAAA	GGGTTCCGTC	700
	ACATCTGTCC	AAGCCGTCTA	TGTCCAGCA	GACGATTGGA	CTGATCCTGC	750
	CCCAGCCACC	ACTTTCGCTC	ACTTGGACGC	CACCACTGTC	TTGTCTCGTT	800
	CCATTTCCGA	ATTGGGTATC	TACCCAGCTG	TCGATCCTCT	CGATTCCAAG	850
55	TCTCGTCTTT	TGGATCCTGA	AGTTATTGGA	CACGAACACT	ACGAAGTTGC	900
	CACTCAAGTT	CAACAAACCC	TCCAAGCTTA	CAAGTCTCTC	CAAGATATCA	950
	TTGCCATTTT	GGGTATGGAT	GAATTGTCTG	AAGCTGATAA	GCTTACTGTC	1000
	GAACGTGCCC	GTAAGATCCA	AAGATTCTTT	TCCCAACCAT	TCGCTGTTGC	1050
	CGAAGTTTTT	ACTGGTATCG	AAGGTCGTCT	CGTTCCATTG	AAGGAAACCG	1100
60	TCAGATCTTT	CAAGGAAATC	CTTGAAGGTA	AGTACGATCA	C	1141

2) INFORMATION FOR SEQ ID NO: 779

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1093 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cladophialophora carrionii*
 (B) STRAIN: ATCC 22864

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 779

20	GCTGAAGGCC	GAACGTGAGC	GTGGTATCAC	CATCGATATC	GCGCTCTGGA	50
	AGTTCGAGAC	TCCCAAGTAC	TTCGTCACCG	TCATCGATGC	CCCTGGTCAT	100
	CGTGACTTCA	TCAAGAACAT	GATCACTGGT	ACCTCCCAGG	CTGATTGTGC	150
	TATTCTCATC	ATTGCCGCTG	GTACTGGTGA	GTTCGAGGCC	GGTATCTCCA	200
	AGGATGGCCA	GACCCGTGAG	CATGCTCTGC	TCGCCTACAC	CCTGGGCGTG	250
25	AAGCAGCTTA	TCGTCGCCAT	CAACAAGATG	GACACCACCA	AATGGTCTGA	300
	GGATCGTTTC	AACGAAATCA	TCAAGGAGAC	TTCCAAC TTC	ATCAAGAAGG	350
	TCGGATACAA	CCCCAAGTCC	GTTCCATTTC	TGCCCATCTC	CGGCTTCAAC	400
	GGTGACAACA	TGATCGACGT	CTCCACCAAT	GCCCCCTGGT	ACAAGGGCTG	450
	GGAAAAGGAG	TCCAAGGCTG	GCAAGGCCAC	CGGCAAGACC	CTCCTTGAGG	500
30	CTATCGACTC	CATCGACCCT	CCTGCTCGTC	CCACCGACAA	GCCTCTCCGT	550
	CTCCCCACTCC	AGGATGTCTA	CAAGATTTCT	GGTATCGGCA	CGGTGCCCCGT	600
	CGGTCGTGTT	GAGACTGGTA	CCATCAAGGC	CGGTATGGTC	GTCACCTTTG	650
	CCCCCGCCAA	CGTCACCACT	GAAGTCAAGT	CCGTCGAAAT	GCACCACGAA	700
	CAGCTCGCCG	AGGGCGTTCC	GGGTGACAAC	GTCGGCTTCA	ACGTCAAGAA	750
35	CGTCTCCGTG	AAGGAGGTTC	GTCGTGGAAA	CGTTGCTGGT	GACTCCAAGA	800
	ACGACCCCCC	CAAGGGTGCC	GACTCCTTCA	ACGCCCAGGT	CATCGTCCTC	850
	AACCACCCTG	GTCAGGTCGG	TGCTGGCTAC	GCCCCGGTCT	TGGATTGCCA	900
	CACTGCCCAC	ATTGCCTGCA	AGTTCTCTGA	GCTCCTCGAG	AAGATCGATC	950
	GTCGTACCGG	CAAGTCCATG	GAAAACAACC	CCAAGTTCAT	CAAGTCTGGT	1000
40	GATGCTGCCA	TCGTGAAGAT	GGTTCCCAGC	AAGCCTATGT	GCGTTGAGGC	1050
	TTTCACCGAC	TACCCTCCTC	TTGGTCGTTT	CGCCGTCCGT	GAC	1093

2) INFORMATION FOR SEQ ID NO: 780

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 752 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cunninghamella bertholletiae*
 (B) STRAIN: ATCC 42115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 780

TACTTGTA AAA TGGTCTCAAG ATCGTTACAA CGAAATTGTT AAGGAAGTTT 50
 CTTCCCTTCAT CAAGAAGATT GGTACAAATC CTAAATCCGT TCCTTTCGTY 100
 CCTATCTCTG GTTGGCACGG TGATAACATG TTGGAAGCTT CTACCAACAT 150
 GCCTTGGTAC AAGGGATGGA CCAAGGAAAC TAAAGCTGGT TCTTCCACTG 200
 5 GTAAGACTCT CTTAGAAGCC ATTGACAGCA TTGAACCTCC TACCCGTCCT 250
 TCTGACAAGC CTTTACGTCT TCCTTTACAA GATGTTTACA AGATTGGTGG 300
 TATTGGTACT GTCCCTGTTG GTCGTGTTGA AACTGGTGTC ATCAAGGCTG 350
 GTATGGTTGT TACYTTCGCT CCCGCTAACG TCACCACTGA AGTTAAGTCC 400
 GTTGAAATGC ATCACGAACA ATTAGAACAA GGTGTTCCCTG GTGACAACGT 450
 10 TGGTTTCAAC GTCAAGAACG TTTCCGTTAA GGATATCCGT CGTGGTAACG 500
 TCTGTTCCGA CTCCAAGAAC GACCCCGCTA AGGAATCTGC TTCCTTCAAC 550
 GCTCAAGTTA TCGTCTTGAA CCACCCTGGT CAAATTGGTG CTGGTTATGC 600
 CCCAGTTCTT GACTGTCACA CTGCTCACAT TGCTTGTAAG TTCGCTGAAT 650
 TATTAGAAAA GATCGATCGT CGTTCGCGTA AGAAACTCGA AGATGCTCCT 700
 15 AAATTCGTTA AATCTGGTGA CTCTGCTATC GTTAAGATGG TTCCTTCCAA 750
 GC 752

20 2) INFORMATION FOR SEQ ID NO: 781

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 728 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Curvularia lunata*
 (B) STRAIN: ATCC 26425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 781

35 CAAGTGGTCT GAGGACCGTT ACCAGGAAAT CATCAAGGAG ACCTCCAAC 50
 TCATCAAGAA GGTGGGCTAC AACCCCAAGC ACGTTCCCTT CGTCCCCATC 100
 TCCGGTTTCA ACGGAGACAA CATGATTGAG GCCTCCACCA ACTGCCCTG 150
 GTACAAGGGT TGGGAGAAGG AGACCAAGGC CAAGGCCACT GGTAAGACCC 200
 40 TCCTTGAGGC CATCGACGCC ATCGACCCTC CTGTCCGTCC TACCGACAAG 250
 CCCCTCCGCC TTCCCTCCA GGATGTTTAC AAGATTGGTG GTATTGGCAC 300
 GGTCCCCGTC GGTGCTGTCG AGACCGGTAT CATCAAGCCC GGTATGGTGC 350
 TCACCTTCGC CCCCGCTGGT GTCACCACCG AAGTCAAGTC CGTCGAGATG 400
 CACCACGAGC AGCTTACTGA GGGTGTCCCC GGTGACAACG TCGGCTTCAA 450
 45 CGTCAAGAAC GTCTCCGTCA AGGAGATCCG TCGTGGTAAC GTTGCCGGTG 500
 ACTCCAAGAA CGACCCCCC AAGGGTTGCG AGTCCTTCAA CGCCAGGTC 550
 ATCGTCCTCA ACCACCCTGG TCAGGTCCGT GCCGGTTACG CCCAGTCCT 600
 TGA CTGCCAC ACTGCCACA TTGCTGCAA GTTCTCCGAG CTCCTCGAGA 650
 AGATCGACCG CCGTACCGGA AAGTCTGTTG AGAACTCCCC CAAGTTCATC 700
 50 AAGTCCGGTG ACGCCGCCAT CGTCAAGA 728

2) INFORMATION FOR SEQ ID NO: 782

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1145 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Fonsecaea pedrosoi*
(B) STRAIN: ATCC 18831

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 782

```

10 TGAAGTCCGA GCGTGAGCGT GGTATCACCA TCGATATCGC CCTCTGGAAG      50
   TTCGAGACTC CCAAGTAAGG CTCAACAGAC ACAACAAGCA AATGCATACT      100
   CGCTAACCTA TTCACCCACC ACAGGTACAA CGTCACCGTC ATTGACGCCC      150
   CCGGTCACCG TGATTTTCATC AAGAACATGA TCACTGGTAC CTCCCAGGCT      200
   GACTGCGCCA TTCTCATCAT TGCCGCCGGT ACTGGTGAGT TCGAGGCCGG      250
15 TATCTCCAAG GACGGTCAGA CCCGTGAGCA CGCTCTTCTC GCCTACACCC      300
   TTGGTGTCAA GCAGCTCATC GTTGCCATCA ACAAGATGGA CACCACCAAG      350
   TGGTCTGAGG CCCGTTACCA GGAGATCATC AAGGAGACCT CCGGTTTCAT      400
   CAAGAAGGTC GGCTTCAACC CCAAGCACGT TCCCTTCGTG CCCATCTCCG      450
   GTTTC AACGG TGACAACATG ATCGACGTCT CCACCAACTG CCCCTGGTAC      500
20 AAGGGTTGGG AGAAGGAGAC CAAGGCCAAG GCCACCGGCA AGACCCTCCT      550
   CGAGGCCATT GACGCCATCG ACCCCCCCAC TCGTCCCACC GACAAGCCCC      600
   TCCGTCTTCC CCTYCAGGAT GTCTACAAGA TCGGTGGTAT TGGCACGGTT      650
   CCCGTCGGTC GTGTCGAGAC CGGTACCATC AAGGCCGGCA TGGTCGTCAC      700
   CTTCGCCCCC GCTGGGTGTC CCACTGAGGT CAAGTCCGTC GAGATGCACC      750
25 ACGAGCAGGT TCCCGAGGCT CTCCCCGGTG ACAACGTCGG CTTCAACGTC      800
   AAGAACGTCT CCGTCAAGGA GATCCGTCGT GGCAACGTCG CCGGTGACTC      850
   CAAGAACGAC CCCCCCAAGG GCTGCGACAG CTTCAACGCC CAGGTCATCG      900
   TCCTCAACCA CCCC GGTCAG GTCGGCGCCG GCTACGCGCC CGTCCTCGAC      950
   TGCCACACTG CTCACATTGC TTGCAAGTTC TCTGAGCTCC TCGAGAAGAT      1000
30 CGACCGCCGT ACCGGCAAGT CCATTGAGGC CAGCCCCAAG TTCATCAAGT      1050
   CTGGTGACGC CGCCATCGTC AAGATGGTTC CCTCCAAGCC TATGTGCGTT      1100
   GAGGCCTTCA CCGACTACCC CCCTCTTGGA CGTTTCGCCC TCCGT          1145

```

35

2) INFORMATION FOR SEQ ID NO: 783

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 1151 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

45

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Microsporium audouinii*
(B) STRAIN: ATCC 11347

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 783

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GCTCAAGGCT GAGCGTGAGC GTGGTATCAC CATTGACATC GCCCTCTGGA      50
AGTTCGAGAC CCCCAAGTAC ATGGTCACCG TCATCGGTAT GCTTTATCTG      100
TTTCCCATT ATAGTTGCGA CAAGTAACTA ATAAAAAGTA GATGCCCCCG      150
55 GACACCGTGA CTTTCATCAAG AACATGATTA CTGGTACCTC CCAGGCCGAC      200
   TGCGCTATTC TCATCATTGC TGCCGGTACT GGTGAGTTTC AGGCTGGTAT      250
   CTCCAAGGAT GGCCAGACTC GTGAGCACGC CCTGCTCGCT TTCACCTCG      300
   GTGTCAAGCA GCTCATCGTT GCCATCAACA AGATGGACAC CACCAACTGG      350
   TCTGAGTCCC GTTTCGGTGA AATCATCAAG GAAGTCACCA ACTTCATCAA      400
60 GAAGGTCGGC TACGACCCCA AGGGTGTCCC ATTCGTCCCA ATCTCTGGCT      450

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	TCAACGGTGA	CAACATGATT	GAGCCCTCCA	CCAACTGCCC	ATGGTACAAG	500
	GGATGGAACA	AGGAGACCAA	GGCCGGTGGC	AAATCCTCTG	GTAAGACCCT	550
	CCTTGAGGCC	ATCGATGCCA	TTGACATGCC	CACTCGTCCC	ACCGACAAGC	600
	CTCTCCGTCT	CCCACTCCAG	GATGTCTACA	AGATCTCTGG	TATCGGAACA	650
5	GTACCAGTCG	GTCGTGTTGA	GACTGGTATC	ATCAAGCCTG	GTATGGTTGT	700
	CACTTTTCGCC	CCCGCCAACG	TCACCACTGA	AGTCAAGTCC	GTCGAAATGC	750
	ACCACCAGCA	GCTCGTTTCAG	GGTGTTCCTG	GTGACAACGT	TGGCTTCAAC	800
	GTCAAGAACG	TCTCTGTCAA	GGAAGTCCGC	CGTGGTAACG	TTGCCGGTGA	850
	TTCCAAGAAC	GACCCACCAT	CTGGCTGCGC	CTCTTTCAAG	GCCCAGGTCA	900
10	TCGTCCCTCAA	CCACCCCGGC	CAGATCGGTG	CTGGTTACGC	CCCAGTCCTC	950
	GACTGCCACA	CTGCCACAT	TGCTTGCAAG	TTCTCTGAGC	TTCTTGAGAA	1000
	GATTGACCGC	CGTACTGGTA	AATCCGTCTG	AACCAGCCCT	AAGTTCGTCA	1050
	AGTCTGGTGA	TGCCGCTATT	GCCACCATGG	TTCCATCCAA	GCCCATGTGC	1100
	GTTGAGGCTT	TCACTGACTA	CCCACCACTT	GGTCGTTTCG	CCGTCCGTGA	1150
15	C					1151

2) INFORMATION FOR SEQ ID NO: 784

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 979 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

25 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

30 (A) ORGANISM: *Mucor circinelloides*

(B) STRAIN: ATCC 38592

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 784

35	CCAAGTGGTC	TCAAGATCGT	TACAACGAAA	TTGTCAAGGA	AGTTTCCGGT	50
	TTCATCAAGA	AGATCGGTTT	CAACCCCAAG	TCCGTTCCCT	TCGTTCCCAT	100
	TTCTGGCTGG	CACGGTGATA	ACATGTTGGA	TGAATCCACC	AACATGCCCT	150
	GGTTCAAGGG	ATGGAACAAG	GAGACCAAGG	CCGGTTCCAA	GACTGGTAAG	200
	ACTCTCCTCG	AAGCCATCGA	TGCCATTGAG	CCCCCTGTCC	GTCTTCTGA	250
40	CAAGCCTCTC	CGTCTTCCTC	TTCAAGATGT	CTACAAGATT	GGTGGTATTG	300
	GTACAGTTCC	CGTCGGTCGT	GTTGAAACTG	GTACTATCAA	GGCTGGTATG	350
	GTTGTCAACT	TCGCTCCCGC	TGCTGTCACC	ACTGAAGTTA	AGTCCGTTGA	400
	AATGCATCAC	GAAACCCTCT	CTGAAGGTCT	CCCCGGTGAC	AACGTTGGTT	450
	TCAACGTCAA	GAACGTCTCC	GTCAAGGATA	TCCGTCGTGG	TAACGTCTGT	500
45	TCCGACTCCA	AGAACGATCC	CGCTAAGGAA	TCTGCCTCTT	TCACTGCTCA	550
	AGTTATTATC	TTGAACCATC	CCGGTCAAAT	CTCTGCTGGT	TACGCACCAG	600
	TTCTCGATTG	TCACACTGCT	CACATCGCCT	GTAAGTTCTC	TGAACTCATT	650
	GAGAAGATTG	ATCGTCGTTC	CGGTAAGTAC	CTGCATCTGT	CAGAATTGAA	700
	GGTCCGCCGT	TATAGCAAAG	GCTGGGTTTA	AATGTTGGGG	TTTGTCTGAT	750
50	CTATAATGAT	GATTGCTCCT	TCAATTTTTG	ACATAATTTG	ATGATCTGAA	800
	TTGTGTTGCT	AACGTCGCAT	TTGCTTCTTT	TGCTTCTTTT	GCATGTAGGT	850
	AAGAAGATGG	AAGATGCTCC	CAAAGTAAGT	ATTACGATTG	ATGGACAATT	900
	AAAATAGAAT	ACTAACAATT	ATTGTTTATA	GTTCGTCAAG	TCTGGTGACT	950
55	CTGCTATCGT	CAAGATGGTT	CCCTCCAAG			979

2) INFORMATION FOR SEQ ID NO: 785

60 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1099 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

5

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Phialaphora verrucosa*
 (B) STRAIN: ATCC 38561

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 785

	GGACAAGCTG	AAGGCCGAAC	GTGAGCGTGG	TATCACCATC	GATATCGCGC	50
15	TCTGGAAGTT	CGAGACTCCC	AAATACTTCG	TCACCGTCAT	TGATGCCCCT	100
	GGTCATCGTG	ACTTCATCAA	GAACATGATC	ACTGGTACCT	CCCAGGCTGA	150
	TTGTGCCATC	CTCATCATTG	CCGCCGGTAC	CGGTGAGTTC	GAAGCCGGTA	200
	TCTCCAAGGA	TGGCCAGACC	CGTGAGCACG	CTCTCCTCGC	CTACACCCTA	250
	GGTGTAAGC	AGCTTATCGT	CGCCATCAAC	AAGATGGACA	CCGCCAAATG	300
20	GTCCGAGGAT	CGGTTCAACG	AAATCATCAA	GGAGACTTCC	AACTTCATCA	350
	AGAAGGTCGG	ATACAACCCC	AAGTCCGTCC	CGTTCGTGCC	CATCTCCGGT	400
	TTCAACGGTG	ACAACATGAT	CGACGTCTCC	TCCAACGCCC	CCTGGTACAA	450
	GGGTTGGGAG	AAGGAGACCA	AGGCCGGCAA	GGCCACTGGC	AAGACCTCC	500
	TCGAGGCCAT	CGACGCGATT	GACCCCTCCTA	CTCGTCCAC	CGACAAGCCC	550
25	CTCCGTCTCC	CTCTCCAGGA	TGTCTACAAG	ATCTCTGGTA	TCGGCACGGT	600
	GCCCGTTGGT	CGTGTTGAGA	CCGGTACCAT	CAAAGCCGGT	ATGGTCGTCA	650
	CCTTCGCTCC	CGCCAACGTC	ACCACTGAAG	TCAAGTCCGT	CGAAATGCAC	700
	CACGAACAGC	TCGCCGAAGG	TGTTCCAGGT	GACAATGTCG	GCTTCAACGT	750
	CAAGAACGTC	TCCGTCAAGG	AGGTTTCGTCG	TGGAAACGTT	GCCGGTGACT	800
30	CCAAGAATGA	CCCCCCCCAAG	GGTGCCGACT	CCTTCAACGC	TCAGGTCATC	850
	GTCCTCAACC	ACCCTGGTCA	GGTCGGTGCC	GGCTACGCCC	CGGTCTTGGA	900
	TTGCCACACT	GCCCACATTG	CTTGCAAGTT	CTCTGAGCTC	CTCGAGAAGA	950
	TCGATCGTCG	TACCGGCAAG	TCCATGGAAA	ACAACCCCAA	GTTTATCAAG	1000
	TCTGGTGATG	CTGCCATCGT	GAAGATGGTT	CCCAGCAAGC	CTATGTGCGT	1050
35	TGAGGCCTTC	ACCGACTATC	CTCCTCTTGG	TCGTTTCGCC	GTCCGTGAC	1099

2) INFORMATION FOR SEQ ID NO: 786

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 750 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Saksenaea vasiformis*
 (B) STRAIN: ATCC 60625

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 786

55	ACCACCAAGT	GGTCTGAGGC	CCGTTACCAG	GAGATCATCA	AGGAGACCTC	50
	CGGYTTCATC	AAGAAGGTCG	GCTTCAACCC	CAAGCACGTT	CCCTTCGTGC	100
	CCATCTCCGG	TTTCAACGGT	GACAACATGA	TCGACGTCTC	CACCAACTGC	150
	CCCTGGTACA	AGGGTTGGGA	GAAGGAGACC	AAGGCCAAGG	CCACCGGCAA	200
	GACCMTCCTC	GAGGCCATTG	ACGCCATCGA	CCCCCYAGY	CGTCCCACCG	250
60	ACAAGCCCCT	YCGTCTTCCC	CTMCAGGATG	TYTACAAGAT	TGGCGGTATT	300

5 GGCACGGTTC CCGTCGGTCG TGTYGAGACC GGTRCCATCA AGGGTGGCAT 350
 GGTGCGTCACC TTCCCCCCCC CTGGTGTAC CACTGAGGTC AAGTCCGTCG 400
 AGATGCACCA CGAGCAGCTC GCCGAGGGS TCCCCGGTGA CAACGTCGGC 450
 TTCAACGTCA AGAACGTCTC CGTCAAGGAG ATCCGTCGTG GCAACGTTGC 500
 CCGTGACTCC AAGAACGACC CCCCCAAGGG CTGCGACAGC TTCAACGCCC 550
 AGGTCATCGT CCTCAACCAC CCCGGTCAGG TCGGCGCCGG CTACGCGCCS 600
 GTCCTSGACT GCCACACTGC TCACATTGCC TGCAAGTTCT CTGAGCTCCT 650
 CGAGAAGATC GACCGCCGTT CCGGCAAGTC CATCGAGTCC GGCCCCAAGT 700
 TCATCAAGTC TGGTGACGCC GCCATCGTCA AGATGGTTCC CTCCAAGCCC 750
 10

2) INFORMATION FOR SEQ ID NO: 787

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1084 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
 20
 (ii) MOLECULE TYPE: Genomic DNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Syncephalastrum racemosum*
 25 (B) STRAIN: ATCC 32330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 878

30 GCTCAAGGCC GAGCGTGAGC GTGGTATCAC CATCGATATC GCTCTCTGGA 50
 AGTTCGAGAC CCCCAGGTAC CACGTCACCG TCATTGATGC CCCCAGGCCAT 100
 CGTGATTTCA TCAAGAACAT GATCACTGGT ACCTCGCAGG CTGACTGCGG 150
 TATCCTCATC ATTGCCGCCG GTACTGGTGA GTTCGAGGCT GGTATCTCCA 200
 AGGATGGCCA GACCCGTGAG CACGCTCTGC TTGCCTTCAC CCTCGGTGTC 250
 CGTCAGCTGA TCGTCGCCAT CAACAAGATG GACTCGACCA AGTACTCTGA 300
 35 GGCCCGTTAC AACGAAATCG TCAAGGAGGT CTCCACCTTC ATCAAGAAGA 350
 TCGGTTTCAA CCCCAGGTCC GTTCCCTTCG TCCCCTCTC TGGCTGGAAC 400
 GGTGACAACA TGTTGGAGGA GTCCTCCAAC ATGCCCTGGT TCAAGGGCTG 450
 GAAGAAGGAG ACCAAGGCTG GCGAGAAGTC CCGCAAGACC CTCCTTGAGG 500
 CCATTGACAA CATTGACCCC CCGGTCCGTC CCTCGGACAA GCCCCTCCGT 550
 40 CTTCCCCTCC AGGATGTCTA CAAGATCGGT GGTATCGGCA CAGTCCCCGT 600
 CGGTGCTGTC GAGACTGGTG TCATCAAGGC TGGTATGGTC GTGACCTTCG 650
 CCCCCGCCAA CGTCACCACT GAAGTCAAGT CCGTCGAGAT GCACCACGAG 700
 CAGCTCGTCG AGGGTGTCCC CCGTGACAAC GTCGGTTTCA ACGTCAAGAA 750
 CGTTTCCGTC AAGGATATCC GCCGTGGTAA CGTCTGCTCT GACTCCAAGA 800
 45 ACGACCCCGC CAAGGAGTCT GCCTCGTTCA CCGCCAGGT CATCGTCCTG 850
 AACCACCCCG GTCAGATCGG TGCCGGTTAC GCCCCGGTTC TTGACTGCCA 900
 CACCGCTCAC ATTGCCTGCA AGTTCGCTGA GCTCCTCGAG AAGATCGACC 950
 GTCGTTCCGG YAAGAAGCTC GAAGAGTCCC CCAAGTTCGT CAAGTCGGGT 1000
 GACTCCGCCA TCGTCAAGAT GGTTCCTTCC AAGCCCATGT GCGTTGAGGC 1050
 50 CTACACTGAG TACCCCCCTC TTGGCCGTTT CGCC 1084

2) INFORMATION FOR SEQ ID NO: 788

- 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1155 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 60 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Trichophyton tonsurans*
(B) STRAIN: ATCC 56185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 788

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10 GCTCAAGGCC GAGCGTGAGC GTGGTATCAC CATCGATATC GCCCTCTGGA      50
   AGTTCGAGAC CCCCAAGTAC AATGTCACCG TCATTGGTAT GTTTTTCTTT      100
   ACCTTTCCCC TCCATCGTCT TGCTGTGCCA TAACTAACGA GAGTAGACGC      150
   CCCCGGTCAC CGTGACTTCA TCAAGAACAT GATCACTGGT ACCTCCCAGG      200
   CTGACTGTGC TATTCTCATC ATTGCTGCCG GTACTGGTGA GTTCGAGGCT      250
15 GGTATCTCCA AGGATGGCCA GACCCGTGAG CACGCTCTGC TCGCCTTCAC      300
   CCTTGGTGTC AAGCAGCTCA TCGTTGCCAT CAACAAGATG GACACCACCA      350
   ACTGGTCCGA GGACCGTTTC AAGGAAATCA TCAAGGAAGT CACCAACTTC      400
   ATCAAGAAGG TTGGCTACGA CCCCAAGGGT GTTCCATTCT TTCCAATCTC      450
   TGGTTTCAAC GGTGACAACA TGATTGAGGC CTCCAGCAAC TGCCCATGGT      500
20 ACAAGGGATG GAACAAGGAG ACCAAGGCCG GTGGTGCCAA GACTGGCAAG      550
   ACCCTYCTCG AGGCCATCGA TGCCATCGAC ATGCCAACCC GTCCTACCGA      600
   CAAGCCCCTY CGTCTCCAC TCCAGGATGT CTACAAGATC TCTGGTATCG      650
   GAACTGTACC AGTCGGTCGT GTTGAGACCG GTATCATCAA GCCTGGTATG      700
   GTCGTCACCT TCGCCCCTGC CAACGTCACC ACTGAAGTCA AGTCCGTCGA      750
25 AATGCACCAC CAGCAGCTTC AGCAGGGTGT CCCCGGTGAC AACGTCGGCT      800
   TCAACGTCAA GAACGTTTCC GTCAAGGAAG TCCGCCGTGG TAACGTTGCC      850
   GGTGACTCCA AGAACGACCC ACCATCCGGC TGTGCCTCCT TCAACGCCCCA      900
   GGTCAATCGT CTCAACCACC CCGGCCAGAT CCGTGCTGGT TACGCCCCAG      950
   TCCTCGACTG CCACACTGCT CACATTGCTT GCAAGTTCGC TGAGCTCCTC      1000
30 GAGAAGATTG ACCGCCGTAC CGGTAAATCC GTCGAAGCCA ACCCCAAGTT      1050
   CGTCAAGTCT GGTGATGCCG CTATCGCCAA GATGGTTCCC TCCAAGCCCCA      1100
   TGTGCGTTGA GGCTTTCAT GACTACCCCC CACTTGGTGC TTTCCGCCGC      1150
   CGTGA

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35

2) INFORMATION FOR SEQ ID NO: 789

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 1138 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

45 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 50 (A) ORGANISM: *Trichophyton mentagrophytes*
(B) STRAIN: ATCC 8125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 789

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TCAAGGCCGA GCGTGAGCGT GGTATCACCA TCGATATCGC CCTCTGGAAG      50
TTTCGAGACCC CCAAGTACAA TGTCACCGTC ATTGGTATGT TTCTCTTTAC      100
55 CTTTCCCCTC CATCGTCTTG CTGTGCCATA ACTAACGAGA GTAGACGCCC      150
   CCGGTCACCG TGAATTATC AAGAACATGA TCACTGGTAC CTCCCAGGCT      200
   GACTGTGCTA TTCTCATCAT TGCTGCCGGT ACTGGTGAGT TCGAGGCTGG      250
   TATCTCCAAG GATGGCCAGA CCCGTGAGCA CGCTCTGCTC GCCTTCACCC      300
   TTGGTGTCAA GCAGCTCATC GTTGCCATCA ACAAGATGGA CACCACCAAC      350
60 TGGTCCGAGG ACCGTTTCAA GGAAATCATC AAGGAAGTCA CCAACTTCAT      400

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	CAAGAAGGTT	GGCTACGACC	CCAAGGGTGT	TCCATTCTGTT	CCAATCTCTG	450
	GTTTCAACGG	TGACAACATG	ATTGAGGCCT	CCACCAACTG	CCCATGGTAC	500
	AAGGGATGGA	ACAAGGAGAC	CAAGGCCGGT	GGTGCCAAGA	CTGGCAAGAC	550
	CCTCCTCGAG	GCCATCGATG	CCATCGACAT	GCCAACCCGT	CCTACCGACA	600
5	AGCCCCCTCCG	TCTCCCACCTC	CAGGATGTCT	ACAAGATCTC	TGGTATCGGA	650
	ACTGTACCAG	TCGGTTCGTGT	TGAGACCGGT	ATCATCAAGC	CCGGTATGGT	700
	CGTCACCTTC	GCCCCTGCCA	ACGTCAACCAC	TGAAGTCAAG	TCCGTCGAAA	750
	TGCACCACCA	GCAGCTTCAG	CAGGGTGTCC	CCGGTGACAA	CGTCGGCTTC	800
	AACGTCAAGA	ACGTTTCCGT	CAAGGAAGTC	CGCCGTGGTA	ACGTTGCCGG	850
10	TGACTCCAAG	AACGACCCAC	CATCCGGCTG	TGCCTCCTTC	AACGCCCAGG	900
	TCATCGTCCT	CAACCACCCC	GGCCAGATCG	GTGCTGGTTA	CGCCCCAGTC	950
	CTCGACTGCC	ACACTGCTCA	CATTGCTTGC	AAGTTCGCTG	AGCTCCTCGA	1000
	GAAGATTGAG	CGCCGTACCG	GTAAATCCGT	CGAAGCCAAC	CCCAAGTTCG	1050
	TCAAGTCTGG	TGATGCCGCT	ATCGCCAAGA	TGGTTCCATC	CAAGCCTATG	1100
15	TGCGTTGAGG	CTTTCACCTGA	CTACCCCCCA	CTTGGTCG		1138

2) INFORMATION FOR SEQ ID NO: 790

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

25

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

30

- (A) ORGANISM: *Bipolaris hawaiiensis*
 (B) STRAIN: ATCC 26067

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 790

35	CACCACCAAG	TGGTCTGAGG	AGCGTTACCA	GGAAATCATC	AAGGAGACCT	50
	CCAACCTTCAT	CAAGAAGGTC	GGCTACAACC	CCAAGCACGT	TCCCTTCGTC	100
	CCCATCTCTG	GTTTCAACGG	AGACAACATG	ATTGAGGCTT	CCACCAACTG	150
	CCCCTGGTAC	AAGGGTTGGG	AGAAGGAGAC	CAAGGCCAAG	GCCACTGGTA	200
	AGACCCTTCT	CGAGGCCATC	GACGCCATCG	ACCCCCCTGT	CCGTCCTACC	250
40	GACAAGCCCC	TCCGCCTTCC	CCTCCAGGAT	GTGTACAAGA	TTGGTGGTAT	300
	TGGCACGGTT	CCCGTCGGTC	GTGTCGAGAC	CGGTATCATC	AAGCCCGGTA	350
	TGGTCGTCAC	CTTCGCCCCC	GCTGGTGTCA	CCACTGAAGT	CAAGTCCGTC	400
	GAGATGCACC	ACGAGCAGCT	TGCCGAGGGT	GTCCCCGGTG	ACAACGTCGG	450
	CTTCAACGTC	AAGAACGTCT	CCGTCAAGGA	GATCCGTCGT	GGTAACGTTG	500
45	CCGGTGACTC	CAAGAACGAC	CCCCCAAGG	GTTGCGAGTC	CTTCAACGCC	550
	CAGGTCATCG	TCCTCAACCA	CCCCGGTCAG	GTCGGTGCCG	GTTACGCACC	600
	AGTCCTTGAC	TGCCACACTG	CCCACATTGC	TTGCAAGTTC	TCCGAGCTCC	650
	TCGAGAAGAT	TGACCGCCGT	ACCGGAAAGT	CTGTTGAGAA	CTCCCCCAAG	700
50	TTCATCAAGT	CCGGTGACGC	CGCCATCGTC	AAGATGGTTC	CCTCCAAG	748

2) INFORMATION FOR SEQ ID NO: 791

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 958 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

60

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Aspergillus fumigatus*

5 (B) STRAIN: ATCC 14110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 791

```

10 CGCTATTGTC GTTGTTGCTG CCTCCGACGG TCAGATGTAG GTGGAACATC      50
   TTGGGAAATA CGTCGTAAAA CACGGCGCTT ACGTTTTTCGC GAATAGGCCC      100
   CAGACTCGTG AGCATTGCTT GCTCGCCCGC CAGGTTGGTG TCCAGAAAGAT      150
   CGTTGTCTTC GTCAACAAAA TCGATGCTAT TGATGATCCG GAGATGCTGG      200
   AACTGGTCTGA ACTCGAGATG CGTGAGCTGC TGAACAGCTA CGGTTTCGAG      250
   GGTGAAGAGA CTCCGATCAT TTTCGTTTCC GCTCTCTGTG CTCTCGAAGG      300
15 ACGCCGTGAC GACATCGGTA AAGACAGAAT TGAGCAGCTT ATGAACGCTG      350
   TCGACACCTG GATCCCCACT CCTCAGCGTG ACCTCGACAA ACCTTTCTTG      400
   ATGTCTGTCTG AGGAAGTGTT CTCTATCGCC GGCCGTGGTA CCGTGGCTTC      450
   TGGTCGTGTC GAGCGTGGTA TCTTGAAGAA GGACTCTGAG GTTGAGATTG      500
   TTGGAGGCTC CTTCGAACCC AAGAAGACCA AAGTCACCGA CATTGAAACC      550
20 TTCAAGAAGA GCTGTGATGA ATCGCGTGCT GGTGACAACT CTGGTCTCCT      600
   CCTGCGTGGT ATCCGACGTG AAGACGTCAA GCGTGGTATG GTCATTGCTG      650
   TTCCCGGCAG CACCAAAGCT CACGACAAGT TCCTCGTCTC CATGTACGTC      700
   CTGACCGAGG CGGAGGGTGG TCGTCGTA CTGCTCGGTG CCAACTACCG      750
   TCCCCAAGTC TTCATCCGTA TGCAGGTAA GTTCCCGCAC ACCGTGTCCA      800
25 GATCTTCCGA GAGATTAGCG ATATATGCTA ATGATTCATC AGACGAGGCT      850
   GCTGACCTCA GCTTCCCTGA CGGCGACCAA TCTCGCAGAG TTATGCCTGG      900
   TGACAACGTC GAGATGATCC TGAAGACCCA CCACCCTGTT GCTGCTGAGG      950
   CTGGTCAA                                     958

```

30

2) INFORMATION FOR SEQ ID NO: 792

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 936 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

40 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Trichophyton mentagrophytes*

45 (B) STRAIN: ATCC 8125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 792

```

   CGTTGTCGCA GCTTCTGACG GTCAAATGTA ATTGAATGCC CGCCCAGACG      50
   GATGAAAGGA TTTGACGTTT CTAACATCAT TCTAGGCCTC AGACCAGAGA      100
50 ACATTGCTC CTTGCCCCGCC AGGTCGGTGT CCAGAAGCTG GTCGTTTTTCG      150
   TTAACAAGGT CGATGCCGTT GAGGACCCAG AGATGTTGGA GCTTGTCGAA      200
   CTTGAAATGC GTGAACTCCT CAGCCACTAC GGTTTCGAGG GTGAGGAGAC      250
   CCCCATCATT TTTGGCTCTG CTCTCTGTGC CCTCGAGTCC CGTCGACCTG      300
   AGCTTGGTGT CGAGAAGATT GACGAGCTAT TGAACGCCGT CGACACCTGG      350
55 ATCCCCACCC CCGAGCGCGC CACTGATAAG CCTTTCCTCA TGTCCATTGA      400
   GGAAGTGTTT TCTATCTCTG GTCGTGGTAC CGTCGTCTCC GGTCGTGTTG      450
   AGCGTGGTAT CCTCAAGAAG GATTCCGACG TCGAAATTGT TGGTGGCTCT      500
   ACCACCCCTA TCAAGACCAA GGTCACAGAT ATCGAAACCT TCAAGAAGTC      550
   CTGCGATGAA TCTCGAGCTG GTGACAACTC TGGTCTCCTT CTCCGAGGTA      600
60 TCAAGCGTGA GGACTTGAAG CGTGGAATGG TTGTTGCTGC CCCCAGATCC      650

```

	ACCAAGGCTC	ACACCGACTT	CATGGTCTCC	CTCTACGTCC	TGACTGAGGC	700
	TGAGGGTGGT	CGTTCCAACG	GCTTCACCCA	CAAGTACCGC	CCCCAAATGT	750
	TCATCCGTAC	TGCTGGTATG	TAACCCAAGT	TTCCGCTATT	TACTAAGTAG	800
	ATCATTTGCTA	ACTTGTATTT	CCTTCCGTAG	ACGAAGCCGC	ATCTTTCAGC	850
5	TGGCCTGGAG	AAGACCAAGA	CAAGAAGGCT	ATGCCTGGTG	ACAACGTCGA	900
	GATGATTTGC	AAGACCCTCC	ACCCCATTCG	TGCCGA		936

10 2) INFORMATION FOR SEQ ID NO: 793

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 793

TTATTGTTGC TGCTGGTACT

20

25 2) INFORMATION FOR SEQ ID NO: 794

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35 (vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Trypanosoma cruzi*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 794

40 GACGACAAGT CGGTGAACTT

20

45 2) INFORMATION FOR SEQ ID NO: 795

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

55 (vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Trypanosoma cruzi*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 795

60 ACTTGACACG GATGTGGCAG

20

2) INFORMATION FOR SEQ ID NO: 796

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 796

GGTCCAATGC CWCAAACWAG A

21

2) INFORMATION FOR SEQ ID NO: 797

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 797

CATTAAGAAT GGYTTATCTG TSKCTCT

27

2) INFORMATION FOR SEQ ID NO: 798

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 798

TGTTGTCCC AGCCGATCGT TT

22

2) INFORMATION FOR SEQ ID NO: 799

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 799

10 ACCTGTGAAT ACAAGCAATC T

21

2) INFORMATION FOR SEQ ID NO: 800

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: single

20

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

25

(A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 800

30 GATGAAATCT TCAACGAAGT TGAT

24

2) INFORMATION FOR SEQ ID NO: 801

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

40

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

45

(A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 801

50 ACAACACCGA GAAGATCCCA

20

2) INFORMATION FOR SEQ ID NO: 802

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

55

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

60

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 802

5 TTGCCATTTTC TGGTTTCGTT 20

10 2) INFORMATION FOR SEQ ID NO: 803

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

15 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

20 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 803

25 ACTTCAGTGG TAACACCAGC 20

30 2) INFORMATION FOR SEQ ID NO: 804

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

35 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

40 (A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 804

45 CCTGGGACGG CCTCTGGCAT 20

50 2) INFORMATION FOR SEQ ID NO: 805

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

55 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cryptosporidium parvum*

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 805

CTCTTGTCCA TCTTAGCAGT

20

5

2) INFORMATION FOR SEQ ID NO: 806

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cryptosporidium parvum*

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 806

AGCATCACCA GACTTGATAA G

21

25

2) INFORMATION FOR SEQ ID NO: 807

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

35

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 807

40

AAAGTGGCTT CAAAGGTTGC

20

45 2) INFORMATION FOR SEQ ID NO: 808

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 808

GCITTAIWRG CATTAGAARA YCCA

24

60

2) INFORMATION FOR SEQ ID NO: 809

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 809

TCTTCCTGTW GCAACTGTTC CTCT

24

2) INFORMATION FOR SEQ ID NO: 810

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 810

AGAGMWACAG ATAARSCATT CTTA

24

2) INFORMATION FOR SEQ ID NO: 811

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 811

TRAARTAGAA TTGTGGTCTR TATCC

25

2) INFORMATION FOR SEQ ID NO: 812

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 812

GTIACIGGIT CYTYRARRTT ICCICC

26

2) INFORMATION FOR SEQ ID NO: 813

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
10 (ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 813
15 AATCYGTYGA AATGCAYCAC GA 22

2) INFORMATION FOR SEQ ID NO: 814

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
25 (D) TOPOLOGY: Linear
(ii) MOLECULE TYPE: DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 814
30 GCIGGCACGT ACACIGCCTG 20

2) INFORMATION FOR SEQ ID NO: 815

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
40 (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
(ii) MOLECULE TYPE: DNA
45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 815
TGGTGCATYT CKACRGACTT 20

2) INFORMATION FOR SEQ ID NO: 816

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 bases
55 (B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
(ii) MOLECULE TYPE: DNA
60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 816

GCTACGACGA GATCAAGGGC

20

5

2) INFORMATION FOR SEQ ID NO: 817

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 817

TGGAAGAAGG CCGAGGAGTT

20

20

2) INFORMATION FOR SEQ ID NO: 818

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 818

35 AGCCGGGCTG GATCTTCTTC

20

35

2) INFORMATION FOR SEQ ID NO: 819

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 819

50 TCGAGCTTCT GGAGGAAGAG

20

50

55 2) INFORMATION FOR SEQ ID NO: 820

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single

60

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Trypanosoma brucei*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 820

10 GAAGGAGGTG TCTGCTTACA C

21

2) INFORMATION FOR SEQ ID NO: 821

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

20

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

25

(A) ORGANISM: *Trypanosoma brucei*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 821

30 GGCGCAAACG TCACCACATC A

21

2) INFORMATION FOR SEQ ID NO: 822

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

40

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

45

(A) ORGANISM: *Trypanosoma brucei*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 822

50 CGGCGGATGT CCTTAACAGA A

21

2) INFORMATION FOR SEQ ID NO: 823

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

60

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 823

GAGCGGTATG AYGAGATTGT

20

5

2) INFORMATION FOR SEQ ID NO: 824

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

10

15

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 824

GGCTTCTGCG GCACCATGCG

20

20

2) INFORMATION FOR SEQ ID NO: 825

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

25

30

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 825

ATGAGCARCG SAACCATCGT TCAGTG

26

35

2) INFORMATION FOR SEQ ID NO: 826

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

40

45

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 826

TCGATCGTGC CGACCATGTA GAACGC

26

50

2) INFORMATION FOR SEQ ID NO: 827

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 446 bases
- (B) TYPE: Nucleic acid

55

60

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Clostridium novyi*
(B) STRAIN: ATCC 19402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 827

```

5      CACCAACTTG CTAAATGGGG AGATGCCCAG ATTGTTGTAT ATATAGGCTG      50
      TGGAGAACGT GGAAATGAAA TGACAGATGT TCTTAATGAG TTTCCAGAAC      100
      TTAAAGATCC TAAGACTGGC AAATCAATAA TGGAAAGAAC AGTTTTAATA      150
15     GCAAATACTT CTAATATGCC AGTTGCAGCC CGTGAAGCTT GTATATATAC      200
      AGGAATCACA ATAGCAGAAT ATTTTAGAGA TATGGGATAT TCAGTAGCAC      250
      TTATGGCGGA TTCCACTTCA CGTTGGGCAG AGGCATTAAG AGAAATGTCT      300
      GGAAGACTTG AAGAAATGCC TGGTGATGAA GGTTACCCAG CTTATTTAGG      350
      ATCAAGACTT GCTGATTCTT ATGAAAGAGC TGGAAAAGTT GTGTGTTTAG      400
20     GAGACGATGA AAGAGAAGGT GCCATTACTG CAATAGGTGC TGTATC      446

```

2) INFORMATION FOR SEQ ID NO: 828

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 445 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Clostridium difficile*
(B) STRAIN: 9689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 828

```

40     CAGCATCAGC TTGCTAAATG GGCAGATGCA GATATAGTTG TATATATAGG      50
      CTGTGGCGAG CGTGGAAATG AAATGACAGA TGTCTTCTT GAATTTCTTG      100
      AATTAAAGA CCAAGAACA GGCAGATCAC TTATGCAAAG AACTGTGCTT      150
      ATAGCAAATA CATCAGATAT GCCGGTTGCT GCACGTGAAG CTTCTATATA      200
      CACTGGTATT ACAATAGCTG AATATTTTAG AGATATGGGA TATAGTGTTG      250
45     CACTTATGGC AGACTCTACA TCAAGATGGG CTGAGGCTCT TAGAGAGATG      300
      AGTGGTCGTT TAGAGGAGAT GCCTGGTGAA GAAGGTTATC CTGCATACTT      350
      AGGTTACAGT CTTGCTCAAT TCTATGAGAG AGCAGGAAAG GTAAATTGTC      400
      TAGGTATGGA TGAAAGAGAA GGAACACTTA CAGCAATTGG TGCAG      445

```

2) INFORMATION FOR SEQ ID NO: 829

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 445 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium septicum*
 (B) STRAIN: ATCC 12464

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 829

```

10 ATGCTATAGC TAAATGGGGA GACAGCGAAA TAGTTGTTTA CGTTGGATGT 50
    GGAGAACGTG GTAACGAAAT GACAGACGTT CTTAACGAAT TCCCAGAACT 100
    TATTGACCCA AAAACTGGGG AAAGTTTAAT GAAGAGAACA GTACTTATAG 150
    CTAATACTTC AAACATGCCA GTTGCTGCTA GAGAAGCTTG CATATACACA 200
    GGTATTACAA TAGCTGAATA CTTAGAGAT ATGGGATACT CAGTATCTAT 250
    AATGGCTGAT TCAACTTCAA GATGGGCAGA AGCATTAGA GAAATGTCAG 300
    GTAGACTTGA AGAAATGCCA GGTGATGAAG GATATCCAGC GTACTTAGGA 350
15 TCAAGACTTG CTGATTATTA CGAAAGAGCA GGTAAGGTTG TTTGTCTAGG 400
    TAAAGATGGT AGAGAAGGTG CTGTAACAGC AATTGGAGCT GTATC 445
  
```

20 2) INFORMATION FOR SEQ ID NO: 830

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 bases
 (B) TYPE: Nucleic acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium botulinum*
 (B) STRAIN: 20:3.1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 830

```

35 TCAAATTGCT AAATGGGGAG ATGCAGAAAT CGTTGTTTAC GTTGGATGCG 50
    GAGAACGTGG TAACGAAATG ACAGACGTTG TTAATGAGTT CCCAGAACTT 100
    ATTGACCCTA AGACTGGCGA AAGCTTAATG AAGAGAACAG TTCTTATAGC 150
    TAATACTTCA AACATGCCAG TTGCAGCGAG AGAAGCTTCA ATATATACAG 200
    40 GTATCACAAT AGCTGAATAT TTCAGAGATA TGGGATATGC AGTATCAATA 250
    ATGGCTGACT CAACTTCAAG ATGGGCTGAG GCATTAAGAG AAATGTCTGG 300
    TAGACTTGAA GAAATGCCTG GTGATGAAGG ATATCCAGCT TACCTTGGAT 350
    CAAGACTTGC TGATTACTAT GAAAGAGCTG GTAAGGTTGA ATGTTTAGGT 400
    AATGATGGAA GAATTGGTTC TATAACAGCA ATCGGTGCGG TATC 444
  
```

2) INFORMATION FOR SEQ ID NO: 831

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 456 bases
 50 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium perfringens*
 (B) STRAIN: ATCC 13124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 831

```

TAGTTCAGCA CCAAGTTGCT AAATGGGGAG ATACTGAGAT AGTTGTTTAC      50
GTTGGATGTG GAGAACGTGG TAACGAGATG ACAGACGTTC TTAACGAATT      100
5  CCCAGAACTT AAAGACCCTA AAAGTGGGGA AAGCTTAATG AAGAGAACAG      150
   TTCTTATTGC TAATACATCT AACATGCCAG TTGCTGCCAG AGAAGCATCA      200
   ATATATACTG GTATAACAAT AGCAGAGTAT TTCAGAGATA TGGGATACTC      250
   AGTATCAATC ATGGCTGACT CAACTTCACG TTGGGCAGAG GCTTTAAGAG      300
   AAATGTCAGG AAGACTTGAA GAAATGCCAG GAGACGAAGG TTACCCAGCA      350
10 TACTTAGGAT CAAGACTTGC TGATTACTAT GAAAGAGCTG GTAAAGTTGT      400
   AGCTTTAGGT AAAGATGGAA GAGAAGGAGC TGTACAGCT ATCGGAGCAG      450
   TATCCC                                     456

```

15 2) INFORMATION FOR SEQ ID NO: 832

(i) SEQUENCE CHARACTERISTICS:

```

20 (A) LENGTH: 444 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

```

   (A) ORGANISM: Clostridium tetani
   (B) STRAIN: ATCC 19406

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 832

```

30 CCAACTTGCA AAATGGGCTG ATGCTCAAAT AGTTGTGTAC ATAGGATGTG      50
   GAGAACGTGG AAATGAAATG ACAGACGTTT TAAATGAGTT CCCAGAATTA      100
   AAGGATCCTA AAACCGGGGA ATCTTTAATG AAAAGAACTG TGTTAATAGC      150
   AAATACATCT AATATGCCTG TTGCAGCTAG AGAAGCATCT ATATATACTG      200
35 GTATAACAAT AGGGGAATAT TTTAGAGATA TGGGATATTC AATAGCACTA      250
   ATGGCAGATT CGACTTCTAG ATGGGCAGAG GCTCTAAGAG AAATGTCTGG      300
   AAGACTAGAG GAGATGCCAG GTGAAGAAGG TTATCCAGCT TATTTAGGAT      350
   CTAGATTAGC AGAGTTCTAT GAAAGAGCAG GTAATGTTAT ATGTTTAGGT      400
   CAGGATGGAA GAGAAGGAGC ATTAACAGCT ATAGGAGCAG TTTC          444
40

```

2) INFORMATION FOR SEQ ID NO: 833

45 (i) SEQUENCE CHARACTERISTICS:

```

   (A) LENGTH: 1786 bases
   (B) TYPE: Nucleic acid
   (C) STRANDEDNESS: Double
   (D) TOPOLOGY: Linear

```

50 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

```

   (A) ORGANISM: Streptococcus pyogenes

```

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 833

```

TGAACCAAGG AAAAATAATA ACCGTTTCGG GACCTCTTGT TGTGGCTTCT      50
GGGATGCAAG AAGCTAATAT TCAAGATATT TGTCGTGTGG GACATCTTGG      100
60 CTTAGTCGGA GAAATTATTG AAATGCGTCG CGATCAAGCG TCTATTTCAGG      150

```

	TTTATGAGGA	AACATCAGGG	ATCGGTCCAG	GAGAACCAGT	AGTGACTACT	200
	GGTTGTCCCT	TGTCGGTCGA	GTTAGGCCCG	GGCCTGATTT	CAGAAATGTT	250
	TGACGGTATT	CAGCGACCGC	TTGATCGTTT	TCAAAAAGCA	ACGGACAGCG	300
	ACTTTTTAAT	CCGTGGTGTG	GCTATCCCAA	GTCTTGATCG	AAAGGCTAAG	350
5	TGGGCATTTA	TTCCCAAGCT	AAGTGTGGT	CAAGAAGTAG	TTGCAGGTGA	400
	TATTTTAGGA	ACTGTGCAAG	AAACAGCTGT	CATTGAGCAC	CGTATCATGG	450
	TTCTTTATAA	AGTTTCAGGG	ACCTTGGTGG	CTATTCATGC	AGGGGACTTC	500
	ACAGTAACAG	ATACAGTTTA	TGAAATTAAG	CAGGAAGACG	GTTCCATTTA	550
	CCAAGGTAGC	CTCATGCAGA	CTTGGCCAGT	TGGTCAAAGT	CGCCCTGTTG	600
10	CTCAAAAGCT	TATCCCAGTC	GAACCTTTGG	TTACAGGTCA	ACGGGTTATT	650
	GACACCTTTT	TCCCTGTTC	AAAAGGTGGT	GCCGCTGCCG	TTCCTGGACC	700
	ATTTGGGGCA	GGAAAAACAG	TTGTGCAGCA	TCAAATAGCT	AAATTTGCCA	750
	ACGTTGATAT	TGTTATTTAT	GTCGGTGTGT	GGGAACGCGG	CAACGAGATG	800
	ACCGACGTTT	TGAATGAGTT	TCCAGAGTTA	ATTGACCCAA	ATACAGGCCA	850
15	GTCCATTATG	GAGCGCACGG	TGTTAATTGC	AAACACCTCT	AATATGCCAG	900
	TAGCAGCGCG	TGAAGCGTCG	ATTTACACAG	GTATTACCAT	TGCCGAATAT	950
	TTCCGTGATA	TGGGCTATTC	TGTGGCTATC	ATGGCAGACT	CGACATCACG	1000
	TTGGGCAGAA	GCTCTGCGCG	AGATGTCAGG	ACGCCTACAA	GAAATGCCTG	1050
	GTGATGAAGG	CTACCCGGCT	TACTTAGGGA	GTCGTATTGC	CGAATATTAT	1100
20	GAACGGGCTG	GTCGTGTTCC	GACCTTGGGA	AGTCAAGAAC	GTGAGGGAAC	1150
	CATTACAGCC	ATCGGCGCGG	TTTCTCCTCC	TGGAGGGGAT	ATTTTCAGAGC	1200
	CTGTCACTCA	AAACACCCTT	CGGATTGTCA	AAGTTTTCTG	GGGGCTCGAC	1250
	GCGCCTCTTG	CGCAACGGCG	TCACTTCCCA	CGGATTAACT	GGCTGACGTC	1300
	TTATTCAATTG	TATCAAGATG	ATGTAGGAAG	CTATATTGAC	CGTAAACAGC	1350
25	AATCTAATTG	GTCCAACAAG	GTAACCTCGT	CCATGGCTAT	TTTGCAGCGT	1400
	GAAGCCAGTC	TAGAAGAAAT	TGTACGCTTG	GTGGGGCTTG	ATTCACTGTC	1450
	TGAACAAGAT	CGTTTGACCA	TGGCTGTTGC	CCGGCAAATT	CGGGAGGATT	1500
	ATCTCCAGCA	AAATGCCTTT	GATTCGGTGG	ATACCTTTAC	TTCCTTTCCG	1550
	AAACAAGAGG	CCATGCTAAC	CAATATTTTG	ACCTTTAATG	AGGAAGCCAG	1600
30	CAAAGCCCTT	TCTTTGGGAG	CTTATTTTAA	TGAGATTATG	GAAGGCACTG	1650
	CTCAGGTACG	CGATCGCATC	GCACGCAGCA	AATTTATCCC	AGAAGAAAAC	1700
	TTAGAGCAGA	TTAAAGGGCT	TACTCAGAAG	GTTACCAAAG	AGATTCACCA	1750
	CGTTTTAGCA	AAGGGAGGAA	TTTAGATGAG	CGTTCT		1786

35

2) INFORMATION FOR SEQ ID NO: 834

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 499 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Babesia bovis*
- (B) STRAIN: Suarez-3
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 834

	TATCTCACGT	AAGTTTTTGC	GCGGCGGTTA	TATATCACTC	CAGGCCCTGG	50
	CTAAGTACGC	TAATACTGAC	GTTACTGTCT	ATGTGGGATG	TGGAGAGCGT	100
55	GGAAACGAGA	TTGCGGAGGT	GCTTAAGGAG	TTCCCTGAGC	TGAAGACCAA	150
	GGTTGATGGC	AAGGAAGTGA	GCATTATGAA	ACGCACTTGC	TTGGTGGCCA	200
	ATACTTCAAA	CATGCCAGTG	GCCGCCAGGG	AGGCTAGTAT	CTACACTGGC	250
	ATTACCTTAT	GTGAATACTT	CAGGGATATG	GATACAACG	CCTGTGTGAT	300
	GGCGGATTCC	ACCAGTCGTT	GCGCTGAGGC	TTTGCCTGAG	ATATCAGGTC	350
60	GTTTAGCTGA	GATGCCTGCT	GATTCAGGTT	ATCCCGCCTA	CCTTGCTTCT	400

AGGCTTTTCGG CGTTCTATGA GCGTGCTGGT ACAGCTGAGT GTATTGGAAC 450
 ACCACTTCGT GAAGGTTTCAG TTACCATTGT TGGTGCTGTA TCTCCACCA 499

5

2) INFORMATION FOR SEQ ID NO: 835

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 464 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

15

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cryptosporidium parvum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 835

20 TTTCTCAAGC TTTGAGTAAA TATAGTAACT CTGATGTTAT TATTTACATT 50
 GGTGTGGAG AAAGAGGAAA TGAAATGGCA GAAGTTCTTA CAGAATCCC 100
 TGAGCTTTAT ACTATGGTTG ATGGAAAGAA GGAGTCAATT ATGCAAAGAA 150
 CTTGTTTAGT AGCTAATACA TCAAATATGC CTGTCGCTGC TAGAGAAGCT 200
 25 TCCATCTACA CTGGTATTAC ACTTTCTGAA TACTTTAGAG ATATGGGATG 250
 TAATGTTTCT ATGATGGCAG ATTCAACTTC TCGTTGGGCT GAAGCTCTTA 300
 GAGAAATTTT TGGTAGATTA GCTGAAATGC CTGCAGATTC GGGTTACCCA 350
 GCATATTTAG GCGCCAGACT TGCTTCATTC TATGAAAGAT CAGGAAGAGT 400
 TAAATGTATG GGTTCGCCAG ATAGAGAAGG TACAGTAACA ATTGTTGGTG 450
 30 CAGTTTCTCC ACCT 464

2) INFORMATION FOR SEQ ID NO: 836

35

3)

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 446 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- 45 (A) ORGANISM: *Leishmania donovani* subsp. *infantum*
 (B) STRAIN: MOU

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 836

50 GCCCTCTCCA AGTACTCCAA CTCCGATTGC GTCATCTATG TCGGCTGCGG 50
 CGAGCGCGGT AATGAGATGG CCGAGGTGCT CATGGAGTTC CCGACCCTGA 100
 CGACCGTGAT CGATGGCCGC GAGGAGTCGA TCATGAAGCG CACCTGCCTC 150
 GTGGCGAACA CCTCGAACAT GCCAGTCGCA GCGCGTGAGG CCTCTATTTA 200
 CACCGGCATC ACCCTGGCCG AGTACTACCG TGATATGGGC AAGCATATCG 250
 55 CCATGATGGC TGA CTGACG TCTCGCTGGG CCGAGGCGCT TCGTGAGATT 300
 TCGGGTCGTC TGGCGGAGAT GCCGGCGGAT GGTGGCTACC CCGCCTACCT 350
 CAGCGCTCGT CTCGCCTCCT TCTACGAGCG CGCCGGCCTC GTCACCTGCA 400
 TCGGCGGGCC GAAGCGCCAG GGCTCCGTCA CGATCGTCGG TGCCGT 446

60

2) INFORMATION FOR SEQ ID NO: 837

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 456 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania major*
 (B) STRAIN: ATCC 50122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 837

TTAGTCAGGC	CCTCTCCAAG	TACTCCAAC	CCGACTGCGT	CATCTATGTC	50
GGCTGCGGCG	AGCGCGGTAA	TGAGATGGCT	GAGGTGCTCA	TGGATTTC	100
AACTCTGACG	ACCGTGATCG	ATGGTCGCGA	GGAGTCCATC	ATGAAGCGCA	150
CCTGCCTCGT	GGCAAACACT	TCGAACATGC	CAGTCGCAGC	CCGCGAGGCC	200
TCTATTTACA	CCGGCATCAC	CCTGGCCGAG	TACTACCGTG	ATATGGGCAA	250
GCATATTGCC	ATGATGGCCG	ACTCGACATC	TCGCTGGGCC	GAGGCGCTTC	300
GTGAGATTTT	CGGTCGTCTG	GCGGAGATGC	CAGCCGATGG	TGGCTACCCT	350
GCCTACCTCA	GCGCTCGTCT	CGCCTCCTTC	TACGAGCGCG	CCGGCCTCGT	400
CACCTGCATC	GGCGGGCCGA	AGCGCCAGGG	CTCCGTCACG	ATCGTCGGTG	450
CTGTGT					456

2) INFORMATION FOR SEQ ID NO: 838

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania tarentolae*
 (B) STRAIN: MOU-2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 838

AGGCCCTCTC	CAAGTACTCC	AACTCCGACT	GCGTCATCTA	CGTCGGCTGC	50
GGCGAGCGCG	GTAATGAGAT	GGCCGAGGTG	CTCATGGAGT	TCCCGACCTT	100
GACGACTGTG	ATTGATGGCC	GTGAGGAGTC	GATCATGAAG	CGGACCTGCC	150
TCGTGGCCAA	CACCTCCAAC	ATGCCAGTCG	CAGCCCCTGA	AGCCTCTATT	200
TAACTGGTA	TCACCCTGGC	CGAATACTAC	CGTGATATGG	GCAAGCATAT	250
CGCCATGATG	GCTGACTCGA	CGTCTCGCTG	GGCGGAGGCG	CTTCGTGAGA	300
TTTCGGGTG	CCTGGCGGAG	ATGCCGGCTG	ATGGTGGGTA	CCCCGCCTAC	350
CTTAGTGCTC	GTCTTGCTC	CTTCTACGAG	CGTGCCGCGC	TCGTCACCTG	400
CATCGGTGGG	CCGAAGCGCC	AGGGCTCCGT	CACGATCGTC	GGTGCCGTGT	450

2) INFORMATION FOR SEQ ID NO: 839

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma brucei*
 (B) STRAIN: EATRO 795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 839

15	GCACTCTCGA	AGTACTCGAA	CAGTGACGCT	GTTATTTACG	TGGGTTGTGG	50
	TGAGCGTGGC	AATGAGATGG	CGGAGGTGCT	CATGGACTTT	CCCACCCCTCA	100
	CCACCATTAT	TGATGGACGT	GAGGAGTCTA	TCATGAAGCG	CACATGCCTG	150
	GTGGCAAATA	CTTCCAATAT	GCCTGTTGCT	GCTCGTGAGG	CATCTATTTA	200
	CACTGGTATC	ACCTTAGCTG	AGTATTATCG	GGATATGGGA	AAACACATCG	250
20	CCATGATGGC	CGATTCAACC	TCCCCTGGG	CTGAGGCTTT	GCGTGAGATT	300
	TCCGGTCGTC	TTGCTGAAAT	GCCTGCAGAT	GGAGGTTATC	CCGCGTACCT	350
	CAGCGCCCGT	TTGGCCTCCT	TCTACGAGCG	TGCTGGCCGT	GTGACATGCA	400
	TCGGTGGGCC	GAAGCGTGAA	GGGTCTGTAA	CAATTGT		437

2) INFORMATION FOR SEQ ID NO: 840

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1052 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma cruzi*
 (B) STRAIN: MM3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 840

	TGAAGGCTGA	GCGCGAGCGC	GGCATCACGA	TCGACATCGC	GCTCTGGAAG	50
	TTCGAGTCGC	CCAAGTCTGT	GTTACAGATC	ATCGACGCCC	CCGGCCACCG	100
45	CGACTTCATC	AAGAACATGA	TCACGGGCAC	GTCTCAGGCG	GACGCCGCCG	150
	TCCTTGTCAT	TGCGTCATCG	CAGGGTGAGT	TTGAGGCGGG	CATCTCGAAG	200
	GACGGCCAGA	CACGCGAGCA	CGCGCTGCTC	GCCTTCACGC	TCGGCGTGAA	250
	GCAGATGGTT	GTGTGCTGCA	ACAAGATGGA	CGACAAGTCG	GTGAACTTCG	300
	CCCAGGAGCG	CTACGATGAG	ATTGTGAAGG	AGGTGTCGGC	GTACCTGAAG	350
50	AAGGTTGGGT	ACAACGTGGA	GAAGGTGCGC	TTCATCCCCA	TCTCCGGCTG	400
	GCAGGGCGAC	AACATGATTG	ACAAGTCGGA	AAATATGCCG	TGGTACAAGG	450
	GCCCCACGCT	GCTGGAGGCA	CTCGACATGC	TGGAGCCCCC	GGTGCGCCCC	500
	AGCGACAAGC	CGCTGCGCCT	GCCGCTGCAG	GACGTGTACA	AGATCGGCGG	550
	TATCGGCACC	GTGCCGGTCG	GTCGCGTGGA	GACGGGCACG	ATGAAGCCCG	600
55	GCGACGTGGT	GACGTTTGCG	CCCGCCAACG	TGACGACGGA	GGTGAAGTCG	650
	ATTGAGATGC	ACCACGAGCA	GCTGGCCGAG	GCCACGCCCC	GCGACAACGT	700
	CGGCTTCAAC	GTGAAGAACG	TGTCCGTGAA	GGACATCCGC	CGTGGCAACG	750
	TGTGCGGCAA	CTCGAAGAAC	GACCCCCCAA	AGGAGGCGGC	CGACTTCACG	800
	GCGCAGGTGA	TCATCCTGAA	CCACCCCGGC	CAGATCGGCA	ACGGCTATGC	850
60	GCCGGTGCTC	GACTGCCACA	CCTGCCACAT	CGCGTGCAAG	TTCGCCGAGA	900

TCGAGTCCAA	GATCGACCGC	CGCTCCGGCA	AGGAGCTTGA	GAAGAACCCC	950
AAGTCGATCA	AGTCCGGTGA	CGCCGCCATG	GTGCGCATGG	TGCCGCAGAA	1000
GCCCATGTGC	GTGGAGGTGT	TCAACGACTA	CGCTCCTCTT	GGCCGCTTTG	1050
CC					1052

5

2) INFORMATION FOR SEQ ID NO: 841

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1061 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma cruzi*
- (B) STRAIN: CGL-1

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 841

TGAAGGCTGA	GCGCGAGCGC	GGCATCACGA	TCGACATCGC	GCTCTGGAAG	50
TTGAGTTCGC	CCAAGTCTGT	GTTACAGATC	ATCGACGCCC	CCGGCCACCG	100
CGACTTCATC	AAGAACATGA	TCACGGGCAC	GTCTCAGGCG	GATGCCGCCG	150
TCCTTGTCAT	TGCGTCATCG	CAGGGTGAGT	TTGAGGCGGG	CATCTCGAAG	200
GACGGCCAGA	CACGCGAGCA	CGCGCTGCTC	GCCTTCACGC	TCGGCGTGAA	250
GCAGATGGTT	GTGTGCTGCA	ACAAGATGGA	CGACAAGTCG	GTGAACTTTG	300
CCCAGGAGCG	CTACGATGAG	ATTGTGAAGG	AGGTGTCGGC	GTACCTGAAG	350
AAGGTTGGGT	ACAACGTGGA	GAAGGTGCGC	TTCATCCCCA	TCTCCGGCTG	400
GCAGGGCGAC	AACATGATTG	ACAAGTCGGA	AAATATGCCG	TGGTACAAGG	450
GCCCCACGCT	GCTGGAGGCA	CTCGACATGC	TGGAGCCCCC	GGTGCGCCCC	500
AGCGACAAGC	CGCTGCGCCT	GCCGCTGCAG	GATGTGTACA	AGATCGGCGG	550
TATCGGCACC	GTGCCGGTCG	GTCGCGTGGA	GACGGGCACG	ATGAAGCCCG	600
GCGACGTGGT	GACGTTTGCG	CCCGCCAACG	TGACGACGGA	GGTGAAGTCG	650
ATTGAGATGC	ACCACGAGCA	GCTGGCCGAG	GCCACGCCCC	GCGACAACGT	700
CGGCTTCAAC	GTGAAGAACG	TGTCCGTGAA	GGACATCCGC	CGTGGCAACG	750
TGTGCGGCAA	CTCGAAGAAC	GATCCCCCAA	AGGAGGCGGC	CGACTTCACG	800
GCCGAGGTGA	TCATCCTGAA	CCACCCCGGC	CAGATCGGCA	ACGGCTATGC	850
GCCGGTGCTT	GACTGCCACA	CCTGCCACAT	CGCGTGCAAG	TTGCGCGAGA	900
TCGAGTCCAA	GATCGACCGC	CGCTCCGGCA	AGGAGCTTGA	GAAGAACCCC	950
AAGTCGATCA	AGTCCGGTGA	CGCCGCCATG	GTGCGCATGG	TGCCGCAGAA	1000
GCCCATGTGC	GTGGAGGTGT	TCAACGACTA	CGCTCCTCTT	GGCCGCTTTG	1050
CCGTGCGTGA	C				1061

45

2) INFORMATION FOR SEQ ID NO: 842

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1062 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

55

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma cruzi*

60

(B) STRAIN: PCU-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 842

5	GCTGAAGGCT	GAGCGCGAGC	GCGGCATCAC	GATCGACATC	GCGCTCTGGA	50
	AGTTCGAGTC	GCCCAAGTCT	GTGTTACGA	TCATCGACGC	CCCCGGCCAC	100
	CGCGACTTCA	TCAAGAACAT	GATCACGGGC	ACGTCTCAGG	CGGACGCCGC	150
	CGTCCTTGTC	ATTGCGTCAT	CGCAGGGTGA	GTTTGAGGCG	GGCATCTCGA	200
	AGGACGGCCA	GACACGCGAG	CACGCGCTGC	TCGCCTTCAC	GCTCGGCGTG	250
10	AAGCAGATGG	TTGTGTGCTG	CAACAAGATG	GACGACAAGT	CGGTGAACTT	300
	CGCCCAGGAG	CGCTACGATG	AGATTGTGAA	GGAGGTGTCG	GCGTACCTGA	350
	AGAAGGTTGG	GTACAACGTG	GAGAAGGTGC	GCTTCATCCC	CATCTCCGGC	400
	TGGCAGGGCG	ACAACATGAT	TGACAAGTCG	GAAAATATGC	CGTGGTACAA	450
	GGGCCCCACG	CTGCTGGAGG	CACTCGACAT	GCTGGAGCCC	CCGGTGCGCC	500
15	CCAGCGACAA	GCCGCTGCGC	CTGCCGCTGC	AGGACGTGTA	CAAGATCGGC	550
	GGTATCGGCA	CCGTGCCCGT	CGGTCGCGTG	GAGACGGGCA	CGATGAAGCC	600
	CGGCGACGTG	GTGACGTTTG	CGCCCGCCAA	CGTGACGACG	GAGGTGAAGT	650
	CGATTGAGAT	GCACCACGAG	CAGCTGGCCG	AGGCCACGCC	CGGCGACAAC	700
	GTCGGGTTCA	ACGTGAAGAA	CGTGTCCGTG	AAGGACATCC	GCCGTGGCAA	750
20	CGTGTGCGGC	AACTCGAAGA	ACGACCCCCC	AAAGGAGGCG	GCCGACTTCA	800
	CGGCGCAGGT	GATCATCTCT	AACCACCCCG	GCCAGATCGG	CAACGGCTAT	850
	GCGCCGGTGC	TCGACTGCCA	CACCTGCCAC	ATCGCGTGCA	AGTTCGCCGA	900
	GATCGAGTCC	AAGATCGACC	GCCGCTCCGG	CAAGGAGCTT	GAGAAGAACC	950
	CCAAGTCGAT	CAAGTCCGGT	GACGCCGCCA	TGGTGCGCAT	GGTGCCGCAG	1000
25	AAGCCCATGT	GCGTGGAGGT	GTTCAACGAC	TACGCTCCTC	TTGGCCGCTT	1050
	TGCCGTGCGT	GA				1062

30 2) INFORMATION FOR SEQ ID NO: 843

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 1057 bases
	(B) TYPE: Nucleic acid
35	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

40 (vi) ORIGINAL SOURCE:

	(A) ORGANISM: <i>Babesia bovis</i>
	(B) STRAIN: Suarez-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 843

45	TACATTGACA	GCTGCATTGA	CCAAGGTCTG	TTCGATGGGT	GGTCATGGCG	50
	AGTACACTCC	TTATGAAGCA	ATTGACCGTG	CTCCTGAGGA	GCGTAAACGT	100
	GGTATTACTA	TAAATTCGAC	ACATGTTGAA	TATGAGACTA	AGAACCGTCA	150
	TTACGGTCAC	GTGGACTGTC	CAGGTCACCT	TGATTATGTG	AAGAACATGA	200
50	TATCTGGCGC	TGCTCAGATG	GATGGTGCCA	TATTGGTTGT	TTCTTGTTGT	250
	GACGGTCCCA	TGCCTCAGAC	TAAGGAGCAC	GTGTTGCTTG	CTAAGCAGAT	300
	TGGTGTACCT	CGTTTAGTTG	TGTTTTTGAA	CAAGCTTGAC	ATGTTAGAGG	350
	ACTCTGAGCT	ATTGGAGTTG	GTGGAGTTAG	AGGTTTCGTG	GTTATTGAGT	400
	GAGTTTGGTT	ACGACGGTGA	CAACACGCCT	ATCGTTTCGT	GCAGTGCTAT	450
55	AAAGGCATTG	AACAGTAGTT	CCGAGGCTGA	CATTAAGCCA	ATTCAGGATT	500
	TATTGGATGC	GTGTGATGCC	TTTTTACTGA	CTCCAGAACG	TAAGGATGAC	550
	ATGCCGCTCT	TGGTTGCTAT	TGACGATGTT	CTTGCCATTG	CTGGCAAGGG	600
	TACTGTTGTA	ACCGGTAGGA	TAGAGCAGGG	CAAGATTCGT	TGTGGTGACC	650
	CTATTGAGGT	TTGCCCGCGT	CCGAAGTCCG	GCAAGAAGAC	TGTGTGTGTT	700
60	GGTCTTRARA	TGTTCCGCAA	GAGTCTCAGT	RAGGGTATTG	CTGGTGACCA	750

	GATTGGTGT	TTGCTCAAGG	GTGTGAAGCG	CGACRAGGTA	GAGCGCGGGT	800
	TTGTATTGAT	TCAACCCGGA	AGTTACAAAT	GTCACGGTGA	ATTGATGCT	850
	GACTTGCTACG	TGTTGACTAC	GRAGGAAGGT	GGGCGCAAGC	ATCCGTTTGT	900
	GTCTAACTAC	CGTCCTCAGG	CGTTTATACG	TACTGGAGAC	GTTTGCTGCT	950
5	CAGTTCATTT	GGATRAGGGT	GTTGAGATGG	CAGCTCCTGG	TGACAACGTG	1000
	CGTTGCAAGA	TCAAGTTACT	TTATCCCATG	CCTGTCCATG	AAGGTTTACG	1050
	ATTTGCG					1057

10

2) INFORMATION FOR SEQ ID NO: 844

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 943 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania aethiopica*
- (B) STRAIN: ATCC 50119

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 844

	CGGTGGCATC	ATTGTGGTGG	CGGCCACCGA	CGGCGTCATG	CCGCAGACAC	50
	GCGAGCACCT	CCTGATCTGC	TCGCAGATTG	GGCTTCCGGC	GCTCGTAGGG	100
	TTCATCAACA	AAGTGGATAT	GACGGACGAG	GACACGTGCG	ACCTGGTGGA	150
30	CATGGAGGTG	CGCGAGCAGC	TGGAGAAATA	CAAGTTTCCG	GCGGAGGAGA	200
	CACCAATCGT	GCGCGGCTCG	GCCCTCAAGG	CCGTCGAGGG	CGACGCGAAG	250
	TACGAGGAGA	ACATCCTCGA	ACTGGTGCGG	AAGTGCGACG	AGTGGATCCC	300
	CGACCCGCCG	CGCAACACAG	ACAAGCCTTT	CCTTATGGCC	ATCGAGCACG	350
	TTTACGAGAT	CGGCAAGGAC	AAGAAGAGCG	TCATCGTGAC	CGGCCGCGTC	400
35	GATCAGGGCG	TGCTGAAGCT	CAACACAGAC	GCCGAGCTGG	CCGGCTTCAG	450
	CGCCAAGAAG	TCGACGGTGA	GGGTGACGGG	CATCGAGATG	TACCACAAGA	500
	CGCTGAGCGA	GTGCATGCCC	GGTGACTCCG	TCGGCGTCAG	CATTGTCTGGC	550
	ACCGGCGACA	CAACCAGTCT	GTCCAAGGAC	AACGTGGAAC	GCGGCATGGT	600
	AATGGCGGCG	ACGGGTAGCA	CGAACCTGTA	CAACAAGGTG	AAGGCGCAGG	650
40	TGTACGTGCT	GACGAAGGAT	GAGGCGGGCC	GCCACACCGG	CTTCAGCCCC	700
	CACTACCGCC	CGCAGCTCTT	CTTCCATTGC	GCTGACGTGA	CAGCGGACAT	750
	GAGCTTCCCG	GAGGCGGAGA	AGCACC GGGA	GGAGCTGAAC	AAGAAATTCG	800
	GCCGCGGCCC	CGAGGAGGAC	AAGAAGAAAG	AGGCGGAGAT	GAAGGAGTTC	850
	GAGAGCAAGC	TCGTCTGCAT	GCCGGGCGAT	AACCGCGAGC	TGATCCTGAC	900
45	GCTCGCGTAC	CCGATGCCCA	TTGAAAAGGG	CCTGAAGTTC	ACC	943

2) INFORMATION FOR SEQ ID NO: 845

50

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 939 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

60

- (A) ORGANISM: *Leishmania amazonensis*

(B) STRAIN: ATCC 50131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 845

5	CGGTGGCATC	ATTGTGGTGG	CGGCCACCGA	CGGCGTCATG	CCGCAGACAC	50
	GCGAGCATCT	CTTGATCTGC	TCGCAGATTG	GGCTTCCGGC	GCTCGTAGGG	100
	TTCATCAACA	AAGTGGACAT	GACGGACGAG	GACACGTGCG	ACCTGGTGGA	150
	CATGGAGGTG	CGTGAGCAGC	TGGAGAAATA	CAAGTTTCCG	GCGGAAGAGA	200
	CGCCCATCGT	GCGCGGCTCG	GCCCTCAAAG	CCGTCGAGGG	CGACGCGAAG	250
10	TACGAGGAGA	ACATCCTCGA	ACTGGTGCGG	AAGTGCAGAC	AATGGATCCC	300
	CGACCCGCCG	CGCAACACAG	ACAAGCCTTT	CCTTATGGCC	ATTGAGCACG	350
	TTTACGAGAT	CGGCAAGGAC	AAGAAGAGCG	TCATCGTGAC	CGGCCGCGTC	400
	GATCAGGGCG	TGCTGAAGCT	CAACACAGAC	GCCGAGCTGG	CCGGCTTCAG	450
	CGCCAAGAAG	TCGACGGTGA	GGGTGACGGG	CATCGAGATG	TACCACAAGA	500
15	CGCTGAGTGA	GTGCATGCCC	GGTGACTCCG	TCGGCGTCAG	CATTGTCCGGC	550
	ACCGGCGACA	CGATCAGTCT	CTCCAAGGAC	AACGTTGAAC	GCGGCATGGT	600
	AATGGCGGCA	ACGGGTAGCA	CGAACCTGTA	CAACAAGGTG	AAGGCGCAGG	650
	TGTACGTGCT	GACGAAGGAT	GAGGGCGGCC	GCCACACTGG	CTTCAGCCCC	700
	CACTACCGCC	CGCAGCTCTT	CTTCCATTGT	GCTGACGTGA	CGGCGGACAT	750
20	GAGCTTCCCG	GAGGCGGAGA	AGCACCGCGA	GGAGCTCAAC	AAGAAATTTC	800
	GCCGCGGCC	CGAGGAGGAC	AAGCAGAAGG	AGGCGGAGAT	GAAAGAGTTC	850
	GAGAGCAAGC	TCGTCTGCAT	GCCGGGCGAC	AACCGCGAGC	TGATCCTGAC	900
	GCTGGCGTAC	CCGATGCCCA	TTGACAAGGG	TCTGAAGTT		939

25

2) INFORMATION FOR SEQ ID NO: 846

(i) SEQUENCE CHARACTERISTICS:

30	(A) LENGTH: 945 bases
	(B) TYPE: Nucleic acid
	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear

35 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

	(A) ORGANISM: <i>Leishmania donovani</i> subsp. <i>donovani</i>
	(B) STRAIN: ATCC 50212

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 846

	CATTGTGGTG	GCGGCCACCG	ACGGCGTCAT	GCCGCAGACA	CGCGAGCACC	50
	TCCTGATCTG	CTCGCAGATC	GGGCTTCCGG	CGCTCGTAGG	GTTCATCAAC	100
45	AAGGTGGACA	TGACGGACGA	GGACACGTGC	GACCTGGTGG	ACATGGAGCT	150
	GCGCGAGCAG	CTGGAGAAAT	ACAAGTTTCC	GGCGGAGGAG	ACGCCAATCG	200
	TGCGCGGCTC	AGCCCTCAAA	GCCGTCGAGG	GCGATGCGAA	GTACGAGGAG	250
	AACATTCTCG	AACTGGTGCG	GAAGTGTGAC	GAGTGGATCC	CTGACCCGCC	300
	GCGCAACACA	GACAAGCCTT	TCCTTATGGC	CATCGAGCAC	GTTTACGAGA	350
50	TCGGCAAGGA	CAAGAAGAGC	GTTGTCTGTA	CCGGCCGCGT	CGATCAGGGC	400
	ATTCTGAAGC	TCAACACAGA	CGCCGAGCTG	GCCGGCTTCA	GCTCCAAGAA	450
	GTCGACGGTG	AGGGTGACGG	GCATCGAGAT	GTACCACAAG	ACGCTGAGCG	500
	AGTGCAATGC	TGGTGACTCC	GTCGGCGTCA	GCATTGTCCG	GACCGGCGAC	550
	ACGACCAATC	TATCCAAGGG	CAACGTGGAA	CGCGGCATGG	TGATGGCGGC	600
55	GACGGGTAGC	ACGAACCTGT	ACACAAGGT	GAAGGCGCAG	GTGTACGTGC	650
	TGACGAAGGA	TGAGGGCGGC	CGCCACACTG	GCTTTAGTCC	TCACTACCGC	700
	CCGCAGCTCT	TCTTCCATTG	TGCTGACGTG	ACGGCGGACA	TGAGCTTCCC	750
	GGAGGCGGAG	AAGCACCGCG	AAGAGCTCAA	CAAGAAATTC	GGCCGCGGCC	800
	CCGAGGAGGA	CAAGAAGAAA	GAGGCAGCGA	TGAAGGAGTT	CGAGAGCAAG	850
60	CTCGTCTGCA	TGCCGGGCGA	TAACCGCGAG	CTGATCCTGA	CGCTGGCGTA	900

CCCGATGCCC ATTGAAAAGG GTCTGAAGTT CACCATCCGT GAGGG

945

5 2) INFORMATION FOR SEQ ID NO: 847

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 939 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania donovani* subsp. *infantum*
 (B) STRAIN: MOU

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 847

20 GGCATCATTG TGGTGGCGGC CACCGACGGC GTCATGCCGC AGACACGCGA 50
 GCACCTCCTG ATCTGCTCGC AGATCGGGCT TCCGGCGCTC GTAGGGTTCA 100
 TCAACAAGGT GGACATGACG GACGAGGACA CGTGCGACCT GGTGGACATG 150
 GAGCTGCGCG AGCAGCTGGA GAAATACAAG TTTCCGGCGG AGGAGACGCC 200
 25 AATCGTGCGC GGCTCAGCCC TCAAAGCCGT CGAGGGCGAT GCGAAGTACG 250
 AGGAGAACAT TCTCGAACTG GTGCGGAAGT GTGACGAGTG GATCCCTGAC 300
 CCGCCGCGCA ACACAGACAA GCCTTTCTTT ATGGCCATCG AGCACGTTTA 350
 CGAGATCGGC AAGGACAAGA AGAGCGTTGT CGTGACCGGC CGCGTCGATC 400
 AGGGCGTTCT GAAGCTCAAC ACAGACGCCG AGCTGGCCGG CTTCAGCTCC 450
 30 AAGAAGTCGA CGGTGAGGGT GACGGGCATC GAGATGTACC ACAAGACGCT 500
 GAGCGAGTGC ATGCCTGGTG ACTCCGTCGG CGTCAGCATT GTCGGCACCG 550
 GCGACACGAC CAGTCTATCC AAGGGCAACG TGGAACGCGG CATGGTGATG 600
 GCGGCGACGG GTAGCACGAA CCTGTACAAC AAGGTGAAGG CGCAGGTGTA 650
 CGTGCTGACG AAGGATGAGG GCGGCCGCCA CACTGGCTTT AGTCCTCACT 700
 35 ACCGCCCCGA GCTCTTCTTC CATTGTGCTG ACGTGACGGC GGACATGAGC 750
 TTCCCGGAGG CGGAGAAGCA CCGCGAAGAG CTCAACAAGA AATTCGGCCG 800
 CGGCCCCGAG GAGGACAAGA AGAAAGAGGC AGCGATGAAG GAGTTCGAGA 850
 GCAAGCTCGT CTGCATGCCG GGCGATAACC GCGAGCTGAT CCTGACGCTG 900
 40 GCGTACCCGA TGCCCATTTGA AAAGGGTCTG AAGTTCACC 939

2) INFORMATION FOR SEQ ID NO: 848

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 933 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania enriettii*
 (B) STRAIN: ATCC 50120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 848

60 CACCGACGGC GTCATGCCGC AGACACGGGA GCACCTGCTC ATCTGCTCGC 50
 AGATCGGGCT GCCGGCGCTT GTAGGGTTCA TCAATAAAGT TGACATGACG 100

	GACGAGGATA	CGTGCGACCT	CGTGGACATG	GAGGTGCGGG	AACAGCTGGA	150
	GAAGTACAAG	TTTCCGGCCG	AGGAGACGCC	CATCGTACGT	GGCTCGGCCC	200
	TCAAGGCCCT	CGAGGGGGAT	GCGCAATACG	AGGGGAGTAT	TCTCGAGCTG	250
	GTGCGAAAGT	GCGACGAGTG	GATCCCCGAC	CCGCCGCGCA	ACACCGAAAA	300
5	GCCTTTCTCTC	ATGGCTATCG	AGCACGTTTA	CGAGCTCGGC	AAAGACAAGA	350
	AGAGCGTCAT	CGTTACCGGC	CGCGTCGATC	AAGGTGTGCT	GAAGCTCAAC	400
	ACAGACGCCG	AGCTGGCCCG	CTTCAGCGCC	AAGAAGGCGA	CAGTCAAAGT	450
	GACGGGCATC	GAGATGTATC	ACAAGACACT	CAATGAGTGC	ATGCCCCGGCG	500
	ACTCTGTCTCG	TGTCAGCATC	GTCGGTACCG	GTGACACGAC	CAGCTTATCC	550
10	AAGGATAATG	TTGAGCGCGG	TATGGTAATG	GCGGCAACGG	GTAGCACGAA	600
	CCTGTACAAC	AAGCTGAAGG	CGCAGGTTTA	CGTGCTGACA	AAGGAGGAGG	650
	GTGGCCGCCA	CACCGGGTTC	AGCCCCCACT	ACCGCCCGCA	GCTCTTCTTC	700
	CACTGCGCTG	ACGTGACCGC	AGACATGAGC	TTCCCGGAGG	CGGAGAAGTA	750
	CCGCGAGGAG	CTCAACAAGA	AGTTCGGCCG	TGGCCCTGAG	GAGGACAAGA	800
15	AGAAAGAGGC	GGAGATGAAG	GAGTTCGAAA	GCAAACCTGT	CTGCATGCCA	850
	GGCGATAACC	GCGAGCTGAT	CCTAACTCTG	GCGTACCCGA	TGCCCATCGA	900
	CAAGGGCCTG	AAGTTCACCA	TCCGTGAGGG	CGG		933

20

2) INFORMATION FOR SEQ ID NO: 849

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 943 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

30

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania gerbilli*
- (B) STRAIN: ATCC 50121

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 849

	CGGTGGCATC	ATTGTGGTGG	CGGCCACCGA	CGGCGTCATG	CCGCAGACAC	50
	GCGAGCACCT	CCTGATCTGC	TCGCAGATTG	GGCTTCCGGC	GCTCGTAGGG	100
	TTCATCAACA	AAGTGGACAT	GACGGACGAG	GACACGTGCG	ACCTGGTGGA	150
40	CATGGAGGTG	CGCGAGCAGC	TGGAGAAATA	CAAGTTTCCG	GCGGAGGAGA	200
	CACCAATCGT	GCGCGGCTCG	GCCCTCAAGG	CCGTCGAGGG	CGACGCGAAG	250
	TACGAGGAGA	ACATCCTCGA	ACTGGTGCGG	AAGTGCGACG	AGTGGATCCC	300
	CGACCCGCCG	CGCAACACAG	ACAAGCCTTT	CCTTATGGCC	ATCGAGCACG	350
	TTTACGAGAT	CGGCAAGGAC	AAGAAGAGCG	TCATCGTGAC	CGGCCGCGTC	400
45	GATCAGGGCG	TGCTGAAGCT	CAACACGGAC	GCCGAGCTGG	CCGGCTTCAG	450
	CGCCAAGAAG	TCGACGGTGA	GGGTGACGGG	CATTGAGATG	TACCACAAGA	500
	CGCTGAGCGA	GTGCATGCCC	GGTGACTCCG	TCGGCGTCAG	CATTGTCTGC	550
	ACCGGCGACA	CGACCAGTCT	GTCCAAGGAC	AACGTGGAAC	GCGGCATGGT	600
	AATGGCGGCG	ACGGGTAGCA	CGAACCTGTA	CAACAAGGTG	AAGGCGCAGG	650
50	TGTACGTGCT	GACGAAGGAT	GAGGGCGGCC	GCCACACTGG	CTTCAGCCCC	700
	CACTACCGCC	CGCAGCTCTT	CTTCCATTGC	GCTGACGTGA	CAGCGGACAT	750
	GAGCTTCCCG	GAGGCGGAGA	AGCACGCGCA	GGAGCTCAAC	AAGAAATTCG	800
	GCCGCGGCC	CGAGGAGGAC	AAGAAGAAAG	AGGCGGAGAT	GAAGGAGTTC	850
	GAGAGCAAGC	TCGTCTGCAT	GCCGGGCGAT	AACGCGAGC	TGATCCTGAC	900
55	GCTGGCGTAC	CCGATGCCCA	TTGAAAAGGG	TCTGAAGTTC	ACC	943

2) INFORMATION FOR SEQ ID NO: 850

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 918 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania major*
 (B) STRAIN: ATCC 50122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 850

```

15  GGCATCATTG TGGTGGCGGC CACCGACGGC GTCATGCCGC AGACACGCGA      50
    ACACCTCCTG ATCTGCTCGC AAATTGGCCT TCCGGCGCTC GTAGGGTTCA      100
    TCAACAAAGT GGACATGACG GACGAGGACA CGTGTGACCT GGTGGACATG      150
    GAGGTGCGCG AGCAGCTGGA GAAATACAAG TTTCCGGCGG AGGAGACACC      200
    AATCGTGCGC GGCTCGGCCC TCAAGGCCGT CGAGGGCGAC GCGAAGTACG      250
20  AGGAGAACAT CCTCGAACTG GTGCGGAAGT GCGACGAGTG GATCCCCGAC      300
    CCGCCGCGCA ACACAGACAA GCCTTTCCTT ATGGCCATCG AGCACGTTTA      350
    CGAGATCGGC AAGGACAAGA AGAGCGTCAT CGTGACCGGC CGCGTCGATC      400
    AGGGCGTGCT GAAGCTCAAC ACAGACGCCG AGCTGGCCGG CTTCAGCGCC      450
    AAGAAGTCGA CGGTGAGGGT GACGGGCATT GAAATGTACC ACAAGACGCT      500
25  GAGCGAGTGC ATGCCCGGTG ACTCCGTCGG CGTCAGCATT GTCGGCACCG      550
    GCGACACGAC CAGTCTGTCC AAGGACAACG TGGAGCGCGG CATGGTAATG      600
    GCGGCGACGG GTAGCACGAA CCTGTACAAC AAGGTGAAGG CGCAGGTGTA      650
    CGTGCTGACG AAGGATGAGG GCGGCCGCCA CACTGGCTTC AGCCCCCACT      700
    ACCGCCCCGA GCTCTTCTTC CATTGCGCTG ACGTGACAGC GGACATGAGC      750
30  TTCCCGGAGG CGGAGAAGCA CCGCGAGGAG CTCAACAAGA AATTCGGCCG      800
    CGGCCCCGAG GAGGACAAGA AGAAAGAGGC GGAGATGAAG GAGTTCGAGA      850
    GCAAGCTCGT CTGCATGCCG GGCGATAACC GCGAGCTGAT CCTGACGCTG      900
    GCGTACCCGA TGCCCAT      918
  
```

2) INFORMATION FOR SEQ ID NO: 851

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 939 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania mexicana*
 (B) STRAIN: ATCC 50156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 851

```

    CCGTGGCATC ATTGTGGTGG CGGCCACCGA CGGCGTCATG CCGCAGACAC      50
    GCGAGCATCT CCTGATCTGC TCGCAGATTG GGCTTCCGGC GCTCGTAGGG      100
55  TTCATCAACA AAGTGGACAT GACGGACGAG GACACGTGCG ACCTGGTGGA      150
    CATGGAGGTG CGTGAGCAGC TGGAGAAATA CAAGTTTCCG GCGGAAGAGA      200
    CGCCCATCGT GCGCGGCTCG GCCCTCAAGG CCGTCGAGGG CGACGCGAAG      250
    TACGAGGAGA ACATCCTCGA ACTGGTGC GGAGTGCAGC AATGGATCCC      300
    CGACCCGCCG CGCAACACAG ACAAGCCTTT CCTTATGGCC ATTGAGCACG      350
60  TTTACGAGAT CGGCAAGGAC AAGAAGAGCG TCATCGTGAC CGGCCGCGTC      400
  
```

```

GATCAGGGCG TGCTGAAGCT CAACACAGAC GCCGAGCTGG CCGGCTTCAG 450
CGTCAAGAAG TCGACGGTGA GGGTGACGGG CATCGAGATG TACCACAAGA 500
CGCTGAGTGA GTGCATGCCC GGTGACTCCG TCGGCGTCAG CATTGTCGGC 550
ACCGGCGACA CGATCAGTCT CTCCAAGGAC AACGTTGAAC GCGGCATGGT 600
5 AATGGCGGCA ACGGGTAGCA CGAACCTGTA CAACAAGGTG AAGGCGCAGG 650
TGTACGTGCT GACGAAGGAT GAGGGCGGCC GCCACACTGG CTTCAGCCCC 700
CACTACCGCC CGCAGCTCTT CTTCCATTGT GCTGACGTGA CGGCGGACAT 750
GAGCTTCCCG GAGGCGGAGA AGCACCGCGA GGAGCTCAAC AAGAAATTCTG 800
GCCGCGGCCC CGAGGAGGAC AAGCAGAAGG AGGCGGAGAT GAAAGAGTTC 850
10 GAGAGCAAGC TCGTCTGCAT GCCGGGCGAC AACCGCGAGC TGATCCTGAC 900
GCTGGCGTAC CCGATGCCCA TTGAGAAGGG TCTGAAGTT 939

```

15 2) INFORMATION FOR SEQ ID NO: 852

(i) SEQUENCE CHARACTERISTICS:

```

(A) LENGTH: 912 bases
(B) TYPE: Nucleic acid
20 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

25 (vi) ORIGINAL SOURCE:

```

(A) ORGANISM: Leishmania tarentolae
(B) STRAIN: MOU-2

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 852

```

30 TCATTGTGGT GGCCGCCACC GACGGCGTCA TGCCGCAAAC ACGGGAGCAC 50
CTTTTGATCT GCTCGCAGAT CGGGCTGCCG GCGCTCGTAG GGTTCATCAA 100
CAAAGTGGAC ATGACAGACG AAGACACGTG CGACCTGGTA GACCTGGAGG 150
TGCGTGAGCA GCTGGAGAAG TACAAGTTTC CGGCAGAGGA AACACCAATC 200
35 GTGCGTGGCT CGGCCCTCAA GGCCGTTGAG GGCGATGCAA AGTACGAGGA 250
GAACATCCTC GAACTGGTGC GGAAGTGC GAAGTGGATC CCAGACCCGC 300
CACGCAATAC GGACAAGCCT TTCCTTATGG CCATTGAACA CGTGTACGAG 350
ATCGGCAAGG ATAGGAAAAG CGTCATCGTA ACCGGCCGCG TCGATCAAGG 400
TGTGCTGAAG CTGAACACAG ACGCCGAGCT GGCCGGCTTC AGCGCCAAGA 450
40 AGTCGACGGT GAAAGTGACG GGCATTGAGA TGTACCACAA GACACTGACA 500
GAGTGTCATGC CCGGCGACTC TGTGCGCGTC AGCATTGTGG GCACTGGYGA 550
CACGACCAGC CTCTCTAAGG ACAATGTTGA GCGTGGCATG GTACTGGCCG 600
CTACGGGTAG CACGAACCTG TACAACAAAG TAAAGGCGCA GGTGTATGTA 650
CTCACGAAGG ATGAGGGCGG CCGCCACACC GGCTTCAGCC CCCACTACCG 700
45 TCCGCAGCTC TTCTTCCACT GCGCTGACGT AACGGCGGAC ATGAGCTTCC 750
CGGAGGCGGA GAAGCACCGC GAGGAACTCA ATAAGAAATT CGGCCGCGGC 800
CCCAGGAGG ACAAGAAAAA GGAGGCGGAG ATGAAGGAGT TCGAGAGCAA 850
GCTGGTCTGC ATGCCAGGCG ATAACGCGA GCTGATCCTG ACATTGGCGT 900
ACCCGATGCC TA 912
50

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2) INFORMATION FOR SEQ ID NO: 853

(i) SEQUENCE CHARACTERISTICS:

```

55 (A) LENGTH: 936 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
60 (D) TOPOLOGY: Linear

```

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Trypanosoma cruzi*

(B) STRAIN: MM3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 853

```

10  ATTCTTGTGG TGGCAGCTAA CGACGGATGC ATGCCGCAGA CGCGTGAGCA 50
    CCTGCTTATT TGTTCGCAGA TTGGCCTTCC TGCTCTTGTA TGCTTTATCA 100
    ATAAGTGTGA CATGATGCAA GGGCAGGAGG AAATGATTGA ACTTGTTGAA 150
    ATGGAGGTAC GTGAACTTT GGAGAAGTAC AAGTTCCCTG CGGAGGAGAC 200
    GCCATTTGTG CCGGGGTCTG CGGTGAAGGC ATTGGAGGGT GATGCTGAAA 250
    ATGAAGGAAA GATTTTGGAG CTTGTAAAAA AATGTGATGA ATGGATTCCC 300
15  GACCCACCGC GTGCCATTGA AAAACCGTTC CTTATGGCCA TTGAGCACGT 350
    TTTTGAGGTT GGAAAGGATA AGAAGGCCGT TGTGTGAGC GGGCGTGTGG 400
    ACCAGGGGCA GTTGAAGGTC GGCGCAGATG CAGAACTTTC CGGGTTTAGC 450
    GCAAAGAAGC TGACGGTGAA GGTGTGCTAG ATCGAAATGT ACCATAAAAT 500
    TCTGGAGGAT TGCATGCCTG GTGACTCTGT TGGCGCGAAG ATCGTTGGCA 550
20  GCGGTGAAAC AGTGAACCTG TCGAAGGAAA ATGTGGAACG CGGCATGGTA 600
    CTCTCCGCAC CAGGTGCAAC GACACTGTTC AACAAGGTCC GCGCGCAGGT 650
    GTACGTGTTG ACAAAGGAAG AAGGCGGTCG TCACACAGCC TTTAGTCCTC 700
    ACTATCGTCC GCAGCTTTTC TTCCACTGTG CTGATGTCAC GGCAGATATT 750
    AACTTCCCCG AAAGCGAGAA GCTTGCAGGG GAGCTGAACA AAAAGTATGG 800
25  CCGTGATGCG GCGGAACAGA AGAAGAAGGA GGCAGAACTG AAAGAGTTTG 850
    AAAAGACGCT TGTCTGCATG CCTGGTGATA ACCGCGAACT CCTGCTCACC 900
    CTTGCCTATC CAATGCCAAT GGAAAAGGGA CTCAAG 934

```

2) INFORMATION FOR SEQ ID NO: 854

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 934 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Trypanosoma cruzi*

(B) STRAIN: PCU-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 854

```

    CGGCATTCTT GTGGTGGCAG CTAACGACGG ATGCATGCCG CAGACGCGTG 50
    AGCACCTGCT TATTTGTTCT CAGATTGGCC TTCCTGCTCT TGTATGCTTT 100
    ATCAATAAGT GTGACATGAT GCAAGGGCAG GAGGAAATGA TTGAGCTTGT 150
50  TGAAATGGAG GTACGTGAAC TTTTGGAGAA GTACAAGTTC CCTGCGGAGG 200
    AGACGCCATT TGTGCGGGGG TCTGCGGTGA AGGCATTGGA GGGTGATGCT 250
    GAAAATGAAG GAAAGATTTT GGAGCTTGTA AAAAAATGTG ATGAATGGAT 300
    TCCCGACCCA CCGCGTGCCA TTGAAAAACC GTTCCTTATG GCCATTGAGC 350
    ACGTTTTTGA GGTTGGAAG GATAAGAAG CCGTTGTTGT GAGCGGGCGT 400
55  GTGGACCAGG GGCAGTTGAA GGTGCGCGCA GATGCAGAAC TTTCCGGGTT 450
    TAGTGCAAAG AAGCTGACGG TGAAGGTTGC TAGCATCGAA ATGTACCATA 500
    AAATTCTGGA GGATTGCATG CCTGGTGA CTATTGGCGC GAAGATCGTT 550
    GGCAGCGGTG AAACAGTGAA CCTGTCGAAG GAAAATGTGG AACCGGGCAT 600
    GGTACTCTCC GCACCAGGTG CAACGACACT GTTCAACAGG GTCCGCGCGC 650
60  AGGTGTACGT GTTGACAAAG GAAGAAGGCG GTCGTACAC AGCCTTTAGT 700

```

	CCTCACTATC	GTCCGCAGCT	TTTCTTCCAC	TGTGCTGATG	TCACGGCGGA	750
	TATTAACCTC	CCGGAAAGCG	AGAAGCTTGC	AGGGGAGCTG	AACAAAAAGT	800
	ATGGCCGTGA	CGCGGCGGAA	CAGAAGAAGA	AGGAGGCAGA	ACTGAAAGAG	850
	TTTGAAAAGA	CGCTTGTCTG	CATGCCTGGT	GATAACCGCG	AACTCCTGCT	900
5	CACCCTTGCC	TATCCAATGC	CAATGGAAAA	GGGA		934

2) INFORMATION FOR SEQ ID NO: 855

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 937 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Trypanosoma cruzi*
- (B) STRAIN: CGL-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 855

25	TGGCGGCATT	CTTGTGGTGG	CAGCTAACGA	CGGATGCATG	CCGCAGACGC	50
	GTGAGCACCT	GCTTATTTGT	TCGCAGATTG	GCCTTCCTGC	TCTTGTATGC	100
	TTTATCAATA	AGTGTGACAT	GATGCAAGGG	CAGGAGGAAA	TGATTGAACT	150
	TGTTGAAATG	GAGGTACGTG	AACTTTTGGA	GAAGTACAAG	TTCCCTGCGG	200
	AGGAGACGCC	ATTTGTGCGG	GGGTCTGCGG	TGAAGGCATT	GGAGGGTGAT	250
30	GCTGAAAATG	AAGGAAAGAT	TTTGGAGCTT	GTAAAAAAT	GTGATGAATG	300
	GATTCCTGAC	CCACCGCGTG	CCATTGAAAA	ACCGTTCCTT	ATGGCCATTG	350
	AGCACGTTTT	TGAGGTTGGA	AAGGATAAGA	AGGCCGTTGT	TGTGAGCGGG	400
	CGTGTGGACC	AGGGGCAGTT	GAAGGTCGGC	GCAGATGCAG	AACTTTCCGG	450
	GTTTAGCGCA	AAGAAGCTGA	CGGTGAAGGT	TGCTAGCATC	GAAATGTACC	500
35	ATAAAATTCT	GGAGGATTGC	ATGCCTGGTG	ACTCTGTTGG	CGCGAAGATC	550
	GTTGGCAGCG	GTGAAACAGT	GAACCTGTCTG	AAGGAAAATG	TGGAACGCGG	600
	CATGGTACTC	TCCGCACCAAG	GTGCAACGAC	ACTGTTCAAC	AAGGTCCGCG	650
	CGCAGGTGTA	CGTGTTGACA	AAGGAAGAAG	GCGGTCGTCA	CACAGCCTTT	700
	AGTCCTCACT	ATCGTCCGCA	GCTTTTCTTC	CACTGTGCTG	ATGTCACGGC	750
40	AGATATTAAC	TTCCCGGAAA	GCGAGAAGCT	TGCAGGGGAG	CTGAACAAAA	800
	AGTATGGCCG	TGATGCGGCG	GAACAGAAGA	AGAAGGAGGC	AGAAGTGAAG	850
	GAGTTTGAAA	AGACGCTTGT	CTGCATGCCT	GGTGATAACC	GCGAACTCCT	900
	GCTCACCCCTT	GCCTATCCAA	TGCCAATGGA	AAAGGGA		937

2) INFORMATION FOR SEQ ID NO: 856

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 888 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Babesia bigemina*
- (B) STRAIN: Suarez-2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 856

	CTTATTATGG	AGCTGATCAA	CAACGTCGCG	AAGAAGCACG	GTGGTTTCTC	50
	CGTGTTTCGCC	GGCGTCGGCG	AGCGCACCAG	GGAGGGCAAC	GAGCTGTACC	100
5	ACGAGATGAT	GGAGACCGGC	GTCATCAAGC	GCCGCCAGCT	GGATGACGGC	150
	ACGTTTCGACT	TCTCCGGCTC	CAAGGCCGCG	CTGGTGTACG	GCCAGATGAA	200
	CGAGCCGCCA	GGTGCCAGGG	CGCGTGTTGC	CCTCACTGGC	CTGACGGTGG	250
	CCGAGTACTT	CCGTGATGAG	GACGGCCAGG	ACGTGCTGCT	CTTCATCGAC	300
	AACATCTACC	GTTTCACCCA	GGCTGGTTCT	GAGGTGAGTG	CCCTTTTGGG	350
10	GCGCATCCCG	TCCGCCGTCG	GTTACCAAGC	GACCCTCGCC	ACCGACCTTG	400
	GCGCGCTGCA	GGAGCGTATC	ACGACGACCA	ACAAGGGCTC	CATCACCTCC	450
	GTGCAGGCCG	TCTACGTGCC	GGCCGACGAT	ATCACCGACC	CGGCGCCTGC	500
	GACCACCTTC	ACCCATCTGG	ACGCGACCAC	TGTGCTCTCC	CGTTCCATCG	550
	CCGAGCTGGG	TATCTACCCC	GCCGTCGACC	CGCTCGACTC	CACCTCGCGT	600
15	ATGCTGTCCG	CGAACATCGT	CGGCGAGGAG	CAGTACAACG	TGGCGCGTGG	650
	CGTGCAGAAA	ATACTGCAGG	ACTACAAATC	GCTGCAGGAT	ATCATCGCCA	700
	TCCTGGGTAT	GGACGAGCTG	TCTGAGCAGG	ACAAGTTCGT	CGTCGCGCGT	750
	GCGCGCAAGG	TTCAGCGTTT	CCTATCCCAG	CCCTTCCAGG	TGGCTGAGGT	800
	ATTACCCGGC	AAGCCCGGAC	GTTTCGTCGA	GCTGCAGGAC	ACCATCAGCG	850
20	GCGTCAAGGA	GATTTTGGAC	GGCGAGTGCG	ACGACATG		888

2) INFORMATION FOR SEQ ID NO: 857

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 884 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

30

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

35

- (A) ORGANISM: *Babesia bovis*
- (B) STRAIN: Suarez-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 857

40	TGATTATGGA	ATTGATCAAC	AATGTCGCCA	AGAAACACGG	TGGGTTCTCC	50
	GTGTTTCGCTG	GTGTTGGTGA	ACGTACGAGG	GAAGGTAACG	AACTGTACCA	100
	TGAAATGATG	GAAACGGGTG	TCATCAAGCG	CCGTCAACTG	GAAGACGGAA	150
	CATTTGACTT	CTCGGGCTCT	AAAGCTGCTT	TGGTGTACGG	ACAAATGAAC	200
	GAACCACCAG	GTGCTAGAGC	CCGTGTTGCA	CTCACGGGAT	TGACCGTTGC	250
45	CGAGTATTTT	CGTGATGAAG	AGGGGCAGGA	TGTGCTACTC	TTCATCGATA	300
	ACATCTACCG	TTTCACCCAG	GCCGGTTCCG	AAGTGAGTGC	GCTGTTAGGA	350
	AGAATTCCAT	CCGCCGTGGG	TTATCAACCT	ACATTGGCCA	CTGATCTCGG	400
	AGCACTCCAG	GAACGCATTA	CTACAACCAA	CAAGGGTTTCG	ATTACATCAG	450
	TCCAGGCAGT	ATACGTCCCA	GCCGATGATA	TCACTGATCC	CGCTCCAGCT	500
50	ACCACTTTCT	CGCACTTGGA	TGCCACTACA	GTGCTTTCTC	GTTCAATTGC	550
	GGAGTTGGGT	ATTTACCCCTG	CGGTCGACCC	GCTTGACTCA	ACGTCACGTA	600
	TGCTGTCCGC	CAACATTGTA	GGACAGGAAC	AGTACGATGC	CGCACGTGGT	650
	GTACAGAAAA	TTTTACAGGA	CTACAAATCA	CTGCAGGATA	TCATTGCCAT	700
	TCTGGGTATG	GACGAGCTGT	CTGAGCAGGA	CAAGTTCGTT	GTAGCACGCG	750
55	CCCGTAAGGT	ACAGCGTTTC	CTGTCTCAGC	CGTTCCAAGT	GGCTGAGGTG	800
	TTCACCGGCA	AGCCTGGGAG	GTTTCGTTGAA	CTACAGGATA	CCATCAGCGG	850
	TGTCAAGGAA	ATCTGGAAGG	TGAGTGTGAC	GATA		884

60

2) INFORMATION FOR SEQ ID NO: 858

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 871 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Babesia microtti*
 (B) STRAIN: Persing-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 858

TGGA	ACTGAT	TAATA	ATGTG	GCCAAA	AAGC	ATGG	CGGTTA	CTCT	GTTTTT	50
GCAG	GTGTAG	GTGAA	AGGAC	GAGGG	AGGGT	AATG	AATTGT	ACCA	TGAAAT	100
GATG	GAGACA	GGTGT	TATAA	AGAAA	AAGGC	ACTA	GGTGGT	GGGA	AGTTTG	150
ATTT	CAGTGG	ATCTA	AAGCA	GCGCT	TGGTCT	ATGG	ACAAAT	GAAC	GAGCCA	200
CCTG	GGGGCCC	GTGCT	AGAGT	GGCACT	AACT	GGAT	TAAACAG	TCGC	AAGAATA	250
TTTC	CGTGAC	GAACA	AGGAC	AAGAC	TGTT	GTTG	TTTTATT	GATA	AATATTT	300
ACCG	ATTTAC	TCAGG	CAGGG	TCTGA	GGTTT	CAGC	CTTGCT	AGGC	CGTATA	350
CCTT	CAGCTG	TGGGA	TACCA	GCCTA	CATTG	GCAAC	AGATC	TTGG	CTGTTT	400
ACA	AGAACGA	ATTAC	TACGA	CCAA	ATCTGG	TTCA	ATCACC	AGTG	TACAAG	450
CTGT	GTATGT	GCCAG	CAGAT	GATAT	TACTG	ATCC	AGCGCC	TGCC	CAAACT	500
TTTA	CTCACT	TGGAC	GCTAC	TACTG	TACTT	AGCA	GGCCAA	TTGT	CTGAACT	550
CGGT	ATTTAT	CCAGC	GGTAG	ACCCG	TTGGA	TTCA	ACAAGC	CGTA	TGCTAA	600
GCGC	GAACAT	TGTGG	GAAAT	GAACA	CTATA	GTGT	AGCCCG	TTCC	GTGCAG	650
AAGA	TACTGC	AAGAT	TACAA	ATCG	CTTCAG	GACAT	TATTG	CCAT	TTTGGG	700
TATG	GATGAA	CTGTC	GGAAC	AAGAC	AAAAA	TATAG	TAGCC	CGAG	CAAGGA	750
AGAT	GCAAAG	GTTCT	TATCA	CAGCC	ATTCC	AAGT	GGCGGA	AGTT	TTTTACT	800
GGTA	AACCGG	GAAGA	TTTGT	GGAAT	TGGAA	GATA	CAATTG	CCGG	GGGCACG	850
AGAT	AATAATT	GCGGG	TAATT	G						871

2) INFORMATION FOR SEQ ID NO: 859

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1286 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania guyanensis*
 (B) STRAIN: ATCC 50126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 859

TCTC	GGAGGG	CGTCCC	GCCC	GTGCT	GACGG	CGCT	GGATGT	GACG	GAGGAC	50
CTTG	GCCGCG	ATGAG	CCGCT	GACG	CTGGAG	ATCG	TGCAGC	ACCT	GGACGC	100
GAAC	ACCGGC	CGTGT	CATTG	CGAT	GCAGAC	GACG	GACCTG	CTGA	AGCTGA	150
AGTC	GAAAGT	TGTGT	CGACC	GGCG	GCAACA	TCTCT	TGTGCC	GGTG	GGCCGT	200
GAGAC	GCTGG	GCCGC	ATCTT	CAAC	GTGCTG	GGCG	ACGCGA	TCGA	CCAGCG	250
CGG	CCCCGTG	GGTG	AGAAGA	TGCG	CATGGC	GATCC	ACGCC	GAGG	CCCCGA	300
AGCT	GGCGGA	TCAGG	CCGCG	GAGG	ACACGA	TCCT	GACGAC	CGGC	CATCAAG	350

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GTGATCGACC TGATTCTGCC CTACTGCAAG GGTGGCAAGA TCGGCCTGTT 400
TGGCGGCGCC GGTGTGGGCA AGACCGTGAT CATCATGGAG CTGATTAACA 450
ACGTCGCGAA GGGCCACGGT GGTTCCTCGG TGTTCGCCGG CGTTGGCGAG 500
CGCACGCGCG AGGGCACGGA CCTGTACCTG GAGATGATGC AGTCGAAGGT 550
5 GATTGACCTG AAGGGCGAGT CGAAGTGCCT GCTTGTGTAC GGGCAGATGA 600
ACGAGCCCCC GGGTGCGCGC GCGCGCGTTG CGCAGTCTGC GCTGACGATG 650
GCGGAGTACT TCCGAGACGT GGAGGGCCAG AATGTGCTGC GTTTCATCGA 700
CAACATCTTC CGCTTCACGC AGGCGAACTC CGAGGTCTCT GCGCTGCTGG 750
GCCGCATTCC GGCCGCCGTG GGCTACCAGC CGACGCTTGC GGAGGATCTT 800
10 GGTATGCTGC AGGAGCGCAT CACGTCGACG ACGAAGGGGT CGATCACGTC 850
CGTGCAAGGC GTGTACGTGC CTGCGGATGA TATCACGGAT CCGGCGCCCCG 900
CGACGACGTT CTCGCACCTG GACGCGACGA CTGTGCTGGA CCGCGCGGTG 950
GCGGAGTCGG GGATCTACCC TGCCGTGAAC CCGCTGGAGT GCGCGTCGCG 1000
TATCATGGAC CCCGATGTGA TCGACGTGGA CCACTACAAC GTTGCGCAGG 1050
15 ATATCGTGCA GATGCTGACC AAGTACAAGG AGCTGCAGGA TATCATTGCG 1100
GTGCTTGGA TCGACGAGCT GAGCGAGGAG GACAAGGTCG TGGTGGACCG 1150
CGCGCGCAAG GTGACCCGGT TCCTGTGCGA GCCGTTCCAG GTTGCGGAGG 1200
TGTTACGGG CATGACGGC CACTACGTGC AGCTGGCCGA CACGGTGGAG 1250
TCGTTCTCTG GGCTGCTGAT GGGGTCGTAC GACCAG 1286
20

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2) INFORMATION FOR SEQ ID NO: 860

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25 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 1222 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
30 (ii) MOLECULE TYPE: Genomic DNA
    (vi) ORIGINAL SOURCE:
    (A) ORGANISM: Leishmania mexicana
35 (B) STRAIN: ATCC 50156
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 860

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CTCGGAGGGC GTCCCGCCCC TGCTGACGGC GCTGGATGTG ACGGAGGACC 50
40 TTGGCCGCGA TGAGCCGCTG ACGCTGGAGA TCGTGACGCA CCTGGACGCG 100
AACACCGGCC GCTGCATTGC GATGCAGACG ACGGACCTGC TGAAGCTGAA 150
GTCGAAGGTT GTGTGACCG GCGGCAACAT CTCTGTGCCG GTGGGCCGTG 200
AGACGCTGGG CCGCATCTTC AACGTGCTGG GCGACGCGAT CGACCAGCGC 250
GGCCCCGTGG GTGAGAAGAT GCGCATGGCG ATCCACGCCG AGGCCCCGAA 300
45 GCTGGCGGAT CAGGCCGCGG AGGACACGAT CCTGACGACC GGCATCAAGG 350
TGATCGACCT GATTCTGCCC TACTGCAAGG GTGGCAAGAT CGGCCTGTTT 400
GGCGGCGCCG GTGTGGGCAA GACCGTGATC ATCATGGAGC TGATTAACAA 450
CGTCGCGAAG GGCCACGGTG GTTTCCTCGG GTTTGCCGGC GTTGGCGAGC 500
GCACGCGCGA GGGCACGGAC CTGTACCTGG AGATGATGCA GTCGAAGGTG 550
50 ATTGACCTGA AGGGCGAGTC GAAGTGCGTG CTTGTGTACG GGCAGATGAA 600
CGAGCCCCCG GGTGCGCGCG CCGCGCTTGC GCAGTCTGCG CTGACGATGG 650
CGGAGTACTT CCGAGACGTG GAGGGCCAGA ATGTGCTGCT GTTCATCGAC 700
AACATCTTCC GCTTCACGCA GGCGAACTCC GAGGTCTCTG CGCTGCTGGG 750
CCGCATTCCG GCCGCCGTGG GCTACCAGCC GACGCTTGCG GAGGATCTTG 800
55 GTATGCTGCA GGAGCGCATC ACGTCGACGA CGAAGGGGTC GATCACGTCC 850
GTGCAGGCCG TGTACGTGCC TGCGGATGAT ATCACGGATC CGGCGCCCGC 900
GACGACGTTT TCGCACCTGG ACGCGACGAC TGTGCTGGAC CGCGCGGTGG 950
CGGAGTCGGG GATCTACCCT GCCGTGAACC CGCTGGAGTG CGCGTCGCGT 1000
ATCATGGACC CCGATGTGAT CGACGTGGAC CACTACAACG TTGCGCAGGA 1050
60 TATCGTGACG ATGCTGACCA AGTACAAGGA GCTGCAGGAT ATCATTGCGG 1100

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TGCTTGGTAT CGACGAGCTG AGCGAGGAGG ACAAGGTCGT GGTGGACCGC 1150
 GCGCGCAAGG TGACCCGGTT CCTGTGCGAG CCGTTCCAGG TTGCGGAGGT 1200
 GTTCACGGGC ATGACGGGCC AC 1222

5

2) INFORMATION FOR SEQ ID NO: 861

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1246 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

15 (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Leishmania tropica*
 (B) STRAIN: ATCC 50129

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 861

CCGTGCTGAC GCGCTGGAT GTGACGGAGG ACCTTGGCCG CGATGAGCCG 50
 CTGACGCTGG AGATCGTGCA GCACTTGGAC GCGAACACCG GCCGCTGCAT 100
 25 TGCATGTCAG ACGACGGACC TGCTGAAGCT GAAGTCGAAG GTTGTGTCTGA 150
 CCGGCGGCAA CATCTCTGTG CCGGTGGGCC GTGAGACGCT GGGCCGCATC 200
 TTCAACGTTT TGGGCGACGC GATCGACCAG CGCGGCCCCG TGGGCGAGAA 250
 GATGCGCATG GCGATCCACG CCGAGGCCCC GAAGCTGGCG GATCAGGCCG 300
 CGGAGGACAC GATCCTGACG ACCGGCATCA AGGTGATCGA CCTGATTCTG 350
 30 CCCTACTGCA AGGGTGGCAA GATCGGCCTG TTCGGCGGTG CCGGTGTGGG 400
 CAAGACTGTG ATCATCATGG AGCTGATCAA CAACGTCGCG AAGGGCCACG 450
 GTGGTTTCTC CGTGTTTGCC GCGTTTGGCG AGCGCACGCG CGAGGGCACG 500
 GACCTGTACC TGGAGATGAT GCAGTCGAAG GTGATTGACC TGAAGGGCGA 550
 GTCGAAGTGC GTGCTTGTGT ACGGGCAGAT GAACGAGCCC CCGGGTGCGC 600
 35 GCGCGCGCGT TGCAGTCTT TGCCTGACGA TGGCGGAGTA CTTCCGCGAC 650
 GTGGAGGGCC AGAACGTGCT GCTGTTTCATC GACAACATCT TCCGCTTCAC 700
 GCAGGCGAAC TCCGAGGTGT CTGCGCTGCT GGGCCGCATT CCGGCCGCCG 750
 TGGGCTACCA GCCGACGCTT GCGGAGGATC TTGGTATGCT GCAGGAGCGC 800
 ATCACGTCGA CAACGAAGGG GTCGATCACG TCCGTGCAGG CCGTGTACGT 850
 40 GCCAGCGGAT GATATCACGG ATCCCGCGCG CGCGACGACG TTCTCGCACC 900
 TGGACGCGAC GACTGTGCTG GACCGCGCGG TGGCGGAGTC GGGCATCTAC 950
 CCTGCCGTGA ACCCGCTGGA GTGCGCGTCG CGTATCATGG ACCCCGATGT 1000
 GATCGATGTG GACCACTACA ACGTTGCGCA GGATATCGTG CAGATGCTGA 1050
 CCAAGTACAA GGAGCTGCAG GATATCATTG CCGTGCTTGG CATCGACGAG 1100
 45 CTGAGCGAGG AAGACAAGGT GTTGTGGAC CGCGCGCGCA AGGTGACCCG 1150
 GTTCCTGTCT CAGCCGTTCC AGGTTGCGGA GGTGTTTACG GGCATGACGG 1200
 GCCACTACGT GCAGCTGGTC GACACGGTGG AGTCGTTCTC TGGCCT 1246

50

2) INFORMATION FOR SEQ ID NO: 862

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 1265 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

60

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania tropica*

(B) STRAIN: ATCC 30815

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 862

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GGCGTGCCGC CCGTGCTGAC GGCGCTGGAT GTGACGGAGG ACCTTGGCCG      50
CGATGAGCCG CTGACGCTGG AGATCGTGCA GCACTTGGAC GCGAACACGG      100
GCCGCTGCAT TGCATGACAG ACGACGGACC TGCTGAAGCT GAAGTCGAAG      150
10 GTCGTGTCGA CCGGCGGCAA CATCTCTGTG CCGGTGGGCC GTGAGACGCT      200
GGGCCGCATC TTCAAYGTTC TGGGCGACGC GATCGACCAG CGCGGCCCCG      250
TGGGCGAGAA GATGCGCATG GCGATCCACG CCGAGGCCCC GAAGCTGGCG      300
GATCAGGCCG CGGAGGACAC GATCCTGACG ACCGGCATCA AGGTGATCGA      350
CCTGATTCTG CCCTACTGCA AGGGTGGCAA GATCGGCCTG TTCGGCGGTG      400
15 CCGGTGTGGG CAAGACTGTG ATCATCATGG AGCTGATCAA CAACGTCGCG      450
AAGGGCCACG GCGGTTTCTC CGTGTGTTGCC GGCGTTGGCG AGCGCACGCG      500
CGAGGGCACG GACCTGTACC TGGAGATGAT GCAGTCGAAG GTGATTGACC      550
TGAAGGGCGA GTCGAAGTGY GTGCTTGTGT ATGGGCAGAT GAACGAGCCC      600
CCGGGTGCGC GCGCGCGCGT TGCGCAGTCT GCGCTGACGA TGGCGGAGTA      650
20 CTTCCGCGAC GTGGAGGGCC AGAACGTGCT GCTGTTCATC GACAACATCT      700
TCCGCTTCAC GCAGGCGAAC TCCGAGGTGT CTGCGCTGCT GGGCCGCATT      750
CCGGCCGCCG TGGGCTACCA GCCGACGCTT GCGGAGGATC TTGGTATGCT      800
GCAGGAGCGC ATCAGTCGA CAACGAAGGG GTCGATCACG TCCGTGCAGG      850
CCGTGTACGT GCCAGCGGAT GATATCACGG ATCCCGCGCC CGCGACGACG      900
25 TTCTCGCACC TGGACGCGAC GACTGTGCTG GACCGCGCGG TGGCGGAGTC      950
GGGCATCTAC CCTGCCGTGA ACCCGCTGGA GTGCGCGTCG CGTATCATGG      1000
ACCTGATGTG GATCGATGTG GACCACTACA ACGTTGCGCA GGATATCGTG      1050
CAGATGCTGA CCAAGTACAA GGAGCTGCAG GATATCATTG CCGTGCTTGG      1100
CATCGACGAG CTGAGCGAGG AAGACAAGGT TGTGTGGGAC CGCGCGCGCA      1150
30 AGGTGACCCG GTTCCTGTCT CAGCCGTTCC AGGTTGCGGA GGTGTTACG      1200
GGCATGACGG GCCACTACGT GCAGCTGGTC GACACGGTGG AGTCGTTCTC      1250
TGGCCTGCTG ATGGG

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2) INFORMATION FOR SEQ ID NO: 863

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 1191 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

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45

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Bordetella pertussis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 863

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50 ATGGCAAAAG GCAAGTTTGA ACGTACCAAG CCGCACGTGA ACGTGGGTAC      50
GATTGGTCAC GTTGACCACG GCAAAACGAC GTTGACGGCG GCGATCACGA      100
CGGTGCTGTC GAACAAGTTC GCGGCGGAGG CTCGCGGCTA CGACCAGATT      150
55 GACGCGGCGC CGGAAGAGAA GGCGCGTGGG ATCACGATCA ACACCTCGCA      200
CGTTGAGTAC GAGACGGAGA CGCGTCACTA CGCGCACGTT GATTGCCCGG      250
GTCACGCTGA CTACGTGAAG AACATGATCA CGGGTGCTGC GCAGATGGAC      300
GGCGCGATCC TGGTGGTGTG GGCCGCGAGC GGCCCGATGC CGCAGACGCG      350
CGAGCACATT TTGCTGTCTG GCCAGGTTGG CGTGCCGTAC ATCATCGTGT      400
TCCTGAACAA GGCGGACATG GTTGATGACG CCGAGCTGCT CGAGCTGGTG      450
60 GAGATGGAAG TCCGCGAACT GCTGAGCAAG TACGATTTCG CGGGCGATGA      500

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CACGCCGATC GTGAATGGTG CGGCCAAGCT GCGCTGGAA AGCGACAACG 550
GCGACCTGGG CGAGCAGGCG ATTCTGTGCG TGGCGCAAGC GCTGGACACG 600
TACATTCCGA CGCCGAGCG CGCGGTGCG GGTGCGTTCC TGATGCCGGT 650
GGAAGACGTG TTCTCGATCT CGGGCCGTGG CACGGTGGTG ACTGGCCGTA 700
5 TCGAGCGCGG CGTGGTGAAG GTTGGCGAGG AAATCGAAAT CGTGGGCATC 750
AAGCCGACGG TGAAGACGAC CTGCACGGGC GTGGAGATGT TCCGCAAGCT 800
GCTGGACCAG GGCCAGGCGG GCGACAACGT GGGTATCTTG CTGCGCGGCA 850
CCAAGCGTGA AGACGTGCG CGTGGCCAGG TGCTGGCCAA GCCGGGTTTCG 900
ATCAACCCGC ACACGGAATT CACGGCCGAG GTGTACATTC TGTCCAAGGA 950
10 AGAGGGTGCG CGTCACACGC CGTTCTTCAA CGGCTATCGT CCGCAGTTCT 1000
ACTTCCGCAC GACGGACGTG ACCGGCACGA TCGACCTGCC GCGGACAAG 1050
GAAATGGTGC TGCCGGGCGA CAACGTGTCG ATGACCGTCA AGCTGCTGGC 1100
CCCGATCGCC ATGGAAGAAG GTCTGCGTTT CGCCATCCGT GAAGGCGGTC 1150
GTACCGTCCG TGCCGGCGTC GTCGCCAAGA TCATCAAGTA A 1191
15

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2) INFORMATION FOR SEQ ID NO: 864

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20 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 1350 bases
    (B) TYPE: Nucleic acid
    (C) STRANDEDNESS: Double
    (D) TOPOLOGY: Linear
25 (ii) MOLECULE TYPE: Genomic DNA
    (vi) ORIGINAL SOURCE:
    (A) ORGANISM: Trypanosoma brucei
30 (B) STRAIN: LVH/75/USAMRU-K/18
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 864

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ATGGGAAAGG AAAAGGTGCA CATGAATCTT GTGGTGGTGG GCCACGTCGA 50
35 TGCCGGTAAA TCCACTGCAA CGGGTCACTT GATCTACAAG TGCGGTGGTA 100
TTGACAAACG TACGATCGAG AAGTTCGAGA AAGAAGCTGC CGACATTGGT 150
AAGGCCTCAT TCAAGTACGC ATGGGTGCTG GACAAAGCTGA AGGCTGAGCG 200
CGAACGTGGT ATCACGATCG ACATTGCACT GTGGAAATTC GAGTCACCCA 250
AGTCTGTCTT CACTATTATT GATGCTCCTG GGCACCGTGA CTTTCATCAAG 300
40 AACATGATCA CCGGCACATC GCAAGCCGAC GCAGCCATCC TCATCATTGC 350
CTCTGCGCAG GGTGAGTTTC AGGCTGGTAT CTCCAAGGAT GGACAGACCC 400
GCGAGCACGC GTTGCTGGCC TTCACCTTGG GTGTGAAGCA GATGGTTGTG 450
TGCTGCAACA AAATGGACGA CAAGACTGTG AACTACGGAC AGGAGCGGTA 500
TGACGAGATT GTGAAGGAGG TGTCTGCTTA CATCAAGAAG GTTGGGTACA 550
45 ACGTGGAGAA GGTGCGCTTC GTCCCCATCT CCGGATGGCA GGGCGACAAC 600
ATGATTGAGA AATCCGAGAA GATGCCATGG TACAAGGGTC CAACGCTCCT 650
GGAGGCACTA GACATGCTGG AGCCACCAGT GCGTCCGAGC GACAAGCCCC 700
TGCGTCTGCC ACTGCAGACG TGTACAAAGA TCGGTGGTAT TGGCACCGTG 750
CCCGTTGGTC GTGTGGAGAC CGGCGTGATG AAGCCTGGTG ATGTGGTGAC 800
50 GTTTGCCCCC GCCAACGTGA CGACCGAGGT GAAATCGATC GAGATGCACC 850
ACGAGCAGCT CGCTGAGGCG ACCCCCGGTG ACAACGTCGG CTTTAACGTG 900
AAGAACGTTT CTGTAAAGGA CATCCGCCGT GGCAACGTCT GCGGTAACAC 950
CAAGAACGAC CCCCCAAAGG AGGCCGCCGA CTTACGGCA CAGGTGATCA 1000
TCCTGAACCA CCCCAGACAG ATTGGAAACG GTTATGCGCC CGTGTGGAC 1050
55 TGCCACACAT CGCACATTGC CTGCAAGTTC GCGGAGATCG AGTCGAAGAT 1100
CGACCGTCGC TCTGGCAAGG AGCTGGAGAA GGCTCCCAAG TCGATCAAGT 1150
CTGGCGACGC CGCGATCGTG CGCATGGTGC CGCAGAAGCC TATGTGCGTG 1200
GAGGTCTTCA ACGACTACGC GCCACTCGGC CGCTTTGCCG TGCGTGACAT 1250
GCGCCAGACC GTCGCTGTCT GTATCATCAA GGCCGTGACC AAGAAGGACG 1300
60 GTTCTGGTGG TAAGGTGACG AAGGCTGCGG TGAAGGCTTC GAAGAAATAA 1350

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